

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run On: June 14, 2003, 11:14:11 : Search time 4487 Seconds
(without alignments)
11168.939 Million cell updates/sec

Title: US-09-826-581-3
Perfect score: 1722
Sequence: 1 cctggccctcagatcaaga.....gatgagagctcggtcgga 1722

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_em.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_nam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1722	100.0	1722	6	AX281580	AX281580 Sequence
C 2	1719.4	99.8	152129	2	AC027416	AC027416 Homo sapi
C 3	1697	98.5	206854	9	AC009974	AC009974 Homo sapi
C 4	612.6	35.6	5888	4	AF214521	AF214521 Sus scrofa
C 5	209.4	12.2	227724	2	AF336381	AF336381 Mus muscf
C 6	196.2	11.4	146577	2	AC128070	AC128070 Rattus no
C 7	196.2	11.4	190183	2	AC129703	AC129703 Rattus no
C 8	168.2	9.8	1647	6	AX281582	AX281582 Sequence
C 9	168.2	9.8	2109	6	AX099776	AX099776 Sequence
C 10	168.2	9.8	2115	6	AX09802	AX09802 Sequence
C 11	168.2	9.8	2115	6	AX09802	AX09802 Sequence
C 12	168.2	9.8	2290	9	AF214519	AF214519 Homo sapi
C 13	151.2	8.8	192968	2	AC127107	AC127107 Rattus no
C 14	148	8.6	1867	6	AX099774	AX099774 Sequence
C 15	148	8.6	1873	4	AF214520	AF214520 Sus scrofa
C 16	148	8.6	1873	6	AX09800	AX09800 Sequence
C 17	148	8.6	1873	6	AX398331	AX398331 Sequence
C 18	148	8.6	1873	6	AX398333	AX398333 Sequence
C 19	148	8.6	1873	6	AX398335	AX398335 Sequence
C 20	148	8.6	1873	6	AX398337	AX398337 Sequence
C 21	148	8.6	1873	6	AX398339	AX398339 Sequence
C 22	148	8.6	2022	6	AX09804	AX09804 Sequence
C 23	91.4	5.3	106	11	G67375	G67375 A898 Human
C 24	91.2	5.3	192968	2	AC127107	AC127107 Rattus no
C 25	82.2	4.8	142903	2	AL627254	AL627254 Danio rer
C 26	79.4	4.6	14411	4	AF329081	AF329081 Bos tauru
C 27	77	4.5	73638	2	AC015613	AC015613 Homo sapi
C 28	74.2	4.3	81210	2	AC019242	AC019242 Homo sapi
C 29	74.2	4.3	174400	9	AC011603	AC011603 Homo sapi
C 30	74.2	4.3	183565	2	AC073610	AC073610 Homo sapi
C 31	74.2	4.3	189141	2	AC025256	AC025256 Homo sapi
C 32	70.4	4.1	1578	9	HS042412	U42412 Human 5'-AM
C 33	70.4	4.1	1677	9	BC000358	BC000358 Homo sapi
C 34	70.4	4.1	1683	9	AK097606	AK097606 Homo sapi
C 35	70.4	4.1	1774	6	AX364914	AX364914 Sequence
C 36	69.4	4.0	101215	9	AC006966	AC006966 Homo sapi
C 37	68	3.9	3497	3	AF094763	AF094763 Drosophil
C 38	68	3.9	80869	2	AC019671	AC019671 Drosophil
C 39	68	3.9	173634	3	AC009344	AC009344 Drosophil
C 40	68	3.9	195868	3	AC008308	AC008308 Drosophil
C 41	68	3.9	230266	3	AE003733	AE003733 Drosophil
C 42	67.6	3.9	7218	6	I66494	I66494 Sequence 14
C 43	65.8	3.8	1905	6	AX482695	AX482695 Sequence
C 44	65.8	3.8	2082	3	AF094764	AF094764 Drosophil
C 45	65.8	3.8	3210	3	AY084138	AY084138 Drosophil

ALIGNMENTS

RESULT 1
AX281580
LOCUS AX281580
DEFINITION Sequence 3 from Patent WO0177305.
ACCESSION AX281580
VERSION AX281580.1 GI:16608831
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Andersson, L., Luthman, H. and Marklund, S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 3 18-OCT-2001;

FEATURES		Atexis AB (SE)	Location/Qualifiers			
source		1. .1722				
BASE COUNT		321 a	504 c	534 g	363 t	
ORIGIN						
Query Match 100.0%; Score 1722; DB 6; Length 1722;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 1722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	CCTGGCCCTCAGATCAAGAGCCCTTCTTGTGCTCGTGCCCAACGGTGTGGGGCAGC	60			
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QY	61	CCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG	120			
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QY	121	GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTTGTCTGGGGCTGATCTCTGATAT	180			
Db	121	GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTTGTCTGGGGCTGATCTCTGATAT	180			
QY	181	ACCACAAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC	240			
Db	181	ACCACAAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC	240			
QY	241	GGAGTCTGCATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCGCT	300			
Db	241	GGAGTCTGCATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCGCT	300			
QY	301	ATGACCAAGCTGACACCTTTACCTCCGCTACTGATGATGCCCTGTGCCATAGGTGCTAGGG	360			
Db	301	ATGACCAAGCTGACACCTTTACCTCCGCTACTGATGATGCCCTGTGCCATAGGTGCTAGGG	360			
QY	361	AGCAAAATGGGGAGGACAGAGAAAGAGCCCACTTCTCAGGCCCTGGGGGCTGCCCC	420			
Db	361	AGCAAAATGGGGAGGACAGAGAAAGAGCCCACTTCTCAGGCCCTGGGGGCTGCCCC	420			
QY	421	ACTGTCTGTTCACAGTCCCACTGTGTCTCAGACAAAGACACTGGCAGGGTGGGA	480			
Db	421	ACTGTCTGTTCACAGTCCCACTGTGTCTCAGACAAAGACACTGGCAGGGTGGGA	480			
QY	481	GGGATCTGACCTCAACCTGCTTCACACCAAGGCCCGGGGTGACCTCTCTCCCGCC	540			
Db	481	GGGATCTGACCTCAACCTGCTTCACACCAAGGCCCGGGGTGACCTCTCTCCCGCC	540			
QY	541	CCTCCCTGCAGGATGCTGACCATCACTGACATCTCACTGCTGCTGCTGCTGCTGCTG	600			
Db	541	CCTCCCTGCAGGATGCTGACCATCACTGACATCTCACTGCTGCTGCTGCTGCTGCTG	600			
QY	601	GGTCCCCCTGGTGAGGAGTGGGCTGGGAATCTTATGGCACCCAGAGGGGGGGGGCGG	660			
Db	601	GGTCCCCCTGGTGAGGAGTGGGCTGGGAATCTTATGGCACCCAGAGGGGGGGGGCGG	660			
QY	661	AGGGAGTCTCTCGAGGCTGGTGGCCCTAGAGCCACAGCTTCTTCTGACTTCTGGAGTC	720			
Db	661	AGGGAGTCTCTCGAGGCTGGTGGCCCTAGAGCCACAGCTTCTTCTGACTTCTGGAGTC	720			
QY	721	CTGTGATGTCCTTAGTCCACATCTATGAGATTTGAACAACATTAAGATTGAGACCTGGAG	780			
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Db	781	GGGTGAGTGGGGAGAGGAACCCGGAAGAGGGCTGTGTGTATGTGTGGCCAGGGCTTAAG	840			
QY	841	GTGAGGATGGGAGTGGGGATGTCCTGGATGAAACAGGGGAGGGAACAATAGAGCCTCG	900			
Db	841	GTGAGGATGGGAGTGGGGATGTCCTGGATGAAACAGGGGAGGGAACAATAGAGCCTCG	900			
QY	901	GGTGCCTCAGGAAGGAAGCTGCTGGGACTGCAAGGTGAGGCAGAGGTGACCGGCTCCCC	960			

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QY	961	TGGCCTGACTCTGGCTCTTTCTCTCAGAGATPACCTGCAAGGTGCTTCAAGCCCTCTGGT	1020			
Db	961	TGGCCTGACTCTGGCTCTTTCTCTCAGAGATPACCTGCAAGGTGCTTCAAGCCCTCTGGT	1020			
QY	1021	CTCCATCTCTCTAATGATAGGTGGGTGCTCTGCTCATTTCACTGAGCCTCTCTCTCTCC	1080			
Db	1021	CTCCATCTCTCTAATGATAGGTGGGTGCTCTGCTCATTTCACTGAGCCTCTCTCTCTCC	1080			
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Db	1081	ACAGTCCCCCTTCCCCAGTCCCACTCAGCTCTGAACTCACTCTTCACTTAGCGGCACA	1140			
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Db	1321	ACTCCACATCTCTCACACACAAAGCCCTGCTCAAGTTCTCTGCACATCTTTGTAAAGCTTGG	1380			
QY	1381	CCAGGTGGGAGGAAGGGGAGACCTTGGGAGGTGATCAGAGGCCCTGAGGAGTCTTCAG	1440			
Db	1381	CCAGGTGGGAGGAAGGGGAGACCTTGGGAGGTGATCAGAGGCCCTGAGGAGTCTTCAG	1440			
QY	1441	CCCTAGCAGTCTGCTGGGGAAGAGCTGGGAGCCCTCTTTGAAGCTGCTGGATCCCTGATCTCC	1500			
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QY	1501	ACCTGTGCCCATCTCTAACAGGTTCCCTTGTGTCGCCGCCCTCTCTTCTTACCGAC	1560			
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QY	1561	TATCCAGATTTGGCATCGGCACATTCGAGACTTGGCTGTGCTGGAGAGCAGACACC	1620			
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QY	1621	CATCCTGACTGCACTGGACATCTTTTGTGGACCGGCTGTGTCTGCTGCTTGTGCTCA	1680			
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QY	1681	CGAATGTGTATCCACCCAGGATGAGAGGCTCGGGCTGGA	1722			
Db	1681	CGAATGTGTATCCACCCAGGATGAGAGGCTCGGGCTGGA	1722			

RESULT 2

AC027416/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

152129 bp

Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32

unordered pieces.

AC027416

AC027416.2

GI:8317289

HTG: HTGS_PHASE1; HTGS_DRAFT.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 152129)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-504G11

Unpublished

2 (bases 1 to 152129)

RESULT 2
AC027416/c 152129 bp DNA linear HTG 07-JUN-2000
LOCUS Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
DEFINITION
unordered pieces.
ACCESSION
AC027416
VERSION
AC027416.2 GI:8317289
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 152129)
AUTHORS
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE
Homo sapiens, clone RP11-504G11
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 152129)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavsky,L., Bouhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collimore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrum,J., Weneus,L., Mihova,T., Miranda,C., Mienda,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J.H., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L7458

Center clone name: 504_G_11

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 135376 bases at least Q40

Consensus quality: 143264 bases at least Q30

Consensus quality: 146503 bases at least Q20

Insert size: 161000; agarose-1p

Insert size: 145029; sum-of-contigs

Quality coverage: 3.1 in Q20 bases; agarose-1p

Quality coverage: 3.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1
1006 1105: contig of 1005 bp in length
1106 2402: contig of 1297 bp in length
2403 2502: gap of 100 bp
2503 3623: contig of 1321 bp in length
3624 3923: gap of 100 bp
3924 5020: contig of 1097 bp in length
5021 5120: gap of 100 bp
5121 6161: contig of 1041 bp in length
6162 6261: gap of 100 bp
6262 7547: contig of 1286 bp in length
7548 7647: gap of 100 bp
7648 9983: contig of 2336 bp in length
9984 10083: gap of 100 bp
10084 12556: contig of 2473 bp in length
12557 12656: gap of 100 bp
12657 15043: contig of 2387 bp in length

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*	17224 19466: contig of 2243 bp in length	1. .1005	/note="assembly_fragment"
*	19467 19566: gap of 100 bp	1106. .2402	/note="assembly_fragment"
*	19567 21928: contig of 2362 bp in length	2503. .3823	/note="assembly_fragment"
*	21929 22028: gap of 100 bp	3924. .5020	/note="assembly_fragment"
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*	27160 30170: contig of 3011 bp in length	12657. .15043	/note="assembly_fragment"
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*	46366 46465: gap of 100 bp		
*	46466 51285: contig of 4820 bp in length		
*	51286 51385: gap of 100 bp		
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*	55872 55971: gap of 100 bp		
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*	60596 60695: gap of 100 bp		
*	60696 66595: contig of 5900 bp in length		
*	66596 66996: gap of 100 bp		
*	66996 73219: contig of 6523 bp in length		
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*	73319 77115: contig of 3797 bp in length		
*	77116 77215: gap of 100 bp		
*	77216 85022: contig of 7807 bp in length		
*	85023 85122: gap of 100 bp		
*	85123 93314: contig of 8192 bp in length		
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*	101194 101293: gap of 100 bp		
*	101294 113090: contig of 11797 bp in length		
*	113091 113190: gap of 100 bp		
*	113191 123496: contig of 10306 bp in length		
*	123497 123596: gap of 100 bp		
*	123597 137837: contig of 14241 bp in length		
*	137838 137937: gap of 100 bp		
*	137938 152129: contig of 14192 bp in length.		

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misc_feature 1106. .2402

misc_feature 2503. .3823

misc_feature 3924. .5020

misc_feature 5121. .6161

misc_feature 6262. .7547

misc_feature 7648. .9983

misc_feature 10084. .12556

misc_feature 12657. .15043

misc_feature 15144. .17123

misc_feature 17224. .19466

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Query Match 99.8%; Score 1719.4; DB 2; Length 152129;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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Qy	61	CCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG	120
Db	36558	CCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG	36499
Qy	121	GGAGATGGAGGAGTGAGGGGAGATCTTTGTACGGTTGTTGTGGGGCTGATCTGATAT	180
Db	36498	GGAGATGGAGGAGTGAGGGGAGATCTTTGTACGGTTGTTGTGGGGCTGATCTGATAT	36439
Qy	181	ACCACAGCTTGGCTTCAGCCCAAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGC	240
Db	36438	ACCACAGCTTGGCTTCAGCCCAAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGC	36379
Qy	241	GGAGTGTGATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCCATCTGTGGAGCCGT	300
Db	36378	GGAGTGTGATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCCATCTGTGGAGCCGT	36319
Qy	301	ATGACAGCTGACACCTTTCACTCCGCTACTGCAATGCCCTGTGCCATAGTGTAGGG	360
Db	36318	ATGACAGCTGACACCTTTCACTCCGCTACTGCAATGCCCTGTGCCATAGTGTAGGG	36259
Qy	361	AGCAATGGGGAGGAGGAG	420
Db	36258	AGCAATGGGGAGGAGGAG	36199
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DEFINITION Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
ACCESSION AC009974
VERSION AC009974.9 GI:16799058
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 206854)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 95063792
PubMed 9847074
REFERENCE 2 (bases 1 to 206854)
AUTHORS Harris,A. and Cotton,M.
TITLE The sequence of Homo sapiens BAC clone RP11-459119
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 206854)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 8, 2001 this sequence version replaced gi:13431203.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
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Center project name: H_NH0459119
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

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DEFINITION	Sus scrofa AMPK gamma subunit (PRKAG3) gene, complete cds.		
ACCESSION	AF214521		
VERSION	AF214521.1		
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SOURCE	Sus scrofa		
ORGANISM	Sus scrofa		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
AUTHORS	Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P. and Andersson, L.		
TITLE	A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle		
JOURNAL	Science 288 (5469), 1248-1251 (2000)		
MEDLINE	20280150		
PUBMED	10818001		
REFERENCE	2 (bases 1 to 5888)		
AUTHORS	Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P. and Andersson, L.		
TITLE	Direct Submission		

JOURNAL	Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC Box 597, Uppsala 751 24, Sweden		
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Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC Box 597, Uppsala 751 24, Sweden

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AF336381
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ORGANISM Mus musculus.
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 227724)
JOURNAL Mouse chromosome 1 genomic sequence
REFERENCE 2 (bases 1 to 227724)
AUTHORS Rump,A.
TITLE Direct Submission
JOURNAL Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular
COMMENT Biotechnology, Reutemstr. 11, Jena 07745, Germany
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 19828 21056: contig of 1229 bp in length
* 21057 21156: gap of unknown length
* 21157 22212: contig of 1056 bp in length
* 22213 22312: gap of unknown length
* 22313 23955: contig of 1643 bp in length
* 23956 24055: gap of unknown length
* 24056 25259: contig of 1204 bp in length
* 25260 25359: gap of unknown length
* 25360 26830: contig of 1471 bp in length
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* 28578 29861: contig of 1284 bp in length
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* 29862 31921: contig of 1960 bp in length
* 31922 32021: gap of unknown length
* 32022 33511: contig of 1330 bp in length
* 33512 33451: gap of unknown length
* 33452 34840: contig of 1389 bp in length
* 34841 34940: gap of unknown length
* 34941 36055: contig of 1115 bp in length
* 36056 36155: gap of unknown length
* 36156 37400: contig of 1245 bp in length
* 37401 37500: gap of unknown length
* 37501 39325: contig of 1825 bp in length
* 39326 39425: gap of unknown length
* 39426 41018: contig of 1593 bp in length
* 41019 41118: gap of unknown length
* 41119 42881: contig of 1763 bp in length
* 42882 42981: gap of unknown length
* 42982 44680: contig of 1699 bp in length
* 44681 44780: gap of unknown length
* 44781 46581: contig of 1801 bp in length
* 46582 46681: gap of unknown length
* 46682 48263: contig of 1582 bp in length
* 48264 48363: gap of unknown length
* 48364 50052: contig of 1689 bp in length
* 50053 50152: gap of unknown length
* 50153 52170: contig of 2018 bp in length
* 52171 52270: gap of unknown length
* 52271 54551: contig of 2281 bp in length
* 54552 54651: gap of unknown length
* 54652 56097: contig of 1446 bp in length
* 56098 56197: gap of unknown length
* 56198 58382: contig of 2185 bp in length
* 58383 58482: gap of unknown length
* 58483 61080: contig of 2598 bp in length
* 61081 61180: gap of unknown length
* 61181 63663: contig of 2483 bp in length
* 63664 63763: gap of unknown length
* 63764 65596: contig of 1833 bp in length
* 65597 65696: gap of unknown length
* 65697 68133: contig of 2437 bp in length
* 68134 68233: gap of unknown length
* 68234 70208: contig of 1975 bp in length
* 70209 70308: gap of unknown length
* 70309 72377: contig of 2069 bp in length
* 72378 72477: gap of unknown length
* 72478 74018: contig of 1541 bp in length
* 74019 74118: gap of unknown length
* 74119 75814: contig of 1696 bp in length
* 75815 75914: gap of unknown length
* 75915 79266: contig of 3352 bp in length
* 79267 79366: gap of unknown length
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* 82867 84394: contig of 1528 bp in length
* 84395 84494: gap of unknown length
* 84495 86237: contig of 1743 bp in length
* 86238 86338: gap of unknown length
* 86339 89425: contig of 3088 bp in length
* 89426 89525: gap of unknown length
* 89526 92315: contig of 2790 bp in length

* 92316 92415: gap of unknown length
* 92416 94843: contig of 2428 bp in length
* 94844 94943: gap of unknown length
* 94944 98381: contig of 3438 bp in length
* 98382 98481: gap of unknown length
* 98482 102086: contig of 3605 bp in length
* 102087 102186: gap of unknown length
* 102187 104593: contig of 2407 bp in length
* 104594 104693: gap of unknown length
* 104694 107538: contig of 2845 bp in length
* 107539 107638: gap of unknown length
* 107639 111897: contig of 4259 bp in length
* 111898 111997: gap of unknown length

Query Match 11.4%; Score 196.2; DB 2; Length 145577;
Best Local Similarity 68.1%; Pred. No. 8.3e-38;
Matches 408; Conservative 0; Mismatches 123; Indels 68; Gaps 7;

Qy 1124 TCATCTAGGCGCACACAGGAGCCTTGTCCTCCCTCCCTCTTTTATTAGGGCC 1183
Db 113906 TCTTCTTGGGAACAGAGGATGAGGAACTTGGTTCCCTG-----TTAGGGACC 113855

Qy 1184 TGGATGAGGTGTCTCTCCCTAGGCTGCCCGAGGCTCACATGC--TCCATCTCTGAC 1242
Db 113854 TCAGATGAGGGCTCT---ACCATGTTCTCTCTGTTCTCACTGCTTCTGTTCCCTAAAG 113798

Qy 1243 CCTGTTTGAAGCTGTCTACACCTCATCAAGACCGATCCATCGCTGCCCTTCTTGA 1302
Db 113797 TCTATTTGAAGCTGTCTATGCCCCCTCATCAAGACCGAATCCCGCTGCCGGTCCCTGGA 113738

Qy 1303 CCCGTTTCAGGCAAGTACTCCACATCCTCACACAAACGCTGCTCAAGTTCTCTGCA 1362
Db 113737 CCTGTCTCTGGACATGTCTCTACATACTCACACAAAGAGGCTACTCAAGTTCTCTGCA 113678

Qy 1363 CATCTTTGAAGCTGGGCCCCAGGTGGAGGAAGGGGAGACCTGGGAGGTGATCAGAG 1422
Db 113677 TATATTTGAGCCTGGG---ATGGTGGAGCAAGGGAGAGCCTCGGGAGATGCTC--- 113625

Qy 1423 GGCCTGAGGAGTCTTCAGCCCTAGCAGTCTGTGGGAGAGAGCTGGGAGCCCTTGAAGCT 1482
Db 113624 -----TAGATCCAGTGTCT 113611

Qy 1483 GCTGATCCCTGTACTCCACCTGGTCCCATCTCAACAGGGTTCCCTGCTCCCGGCC 1542
Db 113610 TCATCTGATGAGTCACTACCGTGTCCCATCCC--AACAGGTGCCCTGTGCCCGGCC 113553

Qy 1543 CTCCTTCCTTACCGCACTATCCAGATTTGGGATCGGCACATTCGGAGACTTGGCTGT 1602
Db 113552 CTCCTTCCTTTCGGCAGTATCCAAAGTGGGATCGGCACATTCGGAGATTAGCTGT 113493

Qy 1603 GGTGCTGGAGACAGCCATCCTGACTGCACTGTCATCTTTGTGACCGCGGTGCTC 1662
Db 113492 AGTTCTGGAACAGCTCTATCCTGACTGCGCTGGATCTTTGTGGACCGAGAGTCT 113433

Qy 1663 TGCACCTGCTGTGCTAACGAATGTGGTACCCACCCAGGATGAGAGCTCGGGCTGG 1721
Db 113432 TGCACCTGCTGTGCTCAATCACTGGTA-CTACATCCAGGTGAAAGCTCCACCTAG 113375

RESULT 7
AC129703/c 190183 bp DNA linear HTG 24-AUG-2002
LOCUS Rattus norvegicus clone CH230-917, *** SEQUENCING IN PROGRESS ***,
DEFINITION 54 unordered pieces.
ACCESSION AC129703
VERSION AC129703.2 GI:22094278
KEYWORDS HTG; HTGS.PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 190183)

AUTHORS

Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, D., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Canta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwakaeme, O., Okwuonu, G., Olarunsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shwartsbeyn, A., Sisson, L., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willison, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (01-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Aug 3, 2002 this sequence version replaced gi:22038439.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GDEC

Center clone name: CH230-917

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 141109 bases at least Q40
Consensus quality: 148891 bases at least Q30
Consensus quality: 155675 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 1029: contig of 1029 bp in length
* 1030 1128: gap of unknown length
* 1130 2709: contig of 1580 bp in length
* 2710 2809: gap of unknown length
* 2810 4026: contig of 1217 bp in length
* 4027 4126: gap of unknown length
* 4127 5707: contig of 1581 bp in length
* 5708 5807: gap of unknown length
* 5808 7503: contig of 1696 bp in length
* 7504 7603: gap of unknown length
* 7604 9024: contig of 1420 bp in length
* 9024 9124: gap of unknown length
* 9124 10171: contig of 1048 bp in length
* 10172 10271: gap of unknown length
* 10272 11528: contig of 1257 bp in length
* 11529 11628: gap of unknown length
* 11629 12774: contig of 1146 bp in length
* 12775 12874: gap of unknown length
* 12875 14388: contig of 1514 bp in length
* 14389 14488: gap of unknown length
* 14489 15629: contig of 1141 bp in length
* 15630 15729: gap of unknown length
* 15730 17938: contig of 2209 bp in length
* 17939 18038: gap of unknown length
* 18039 19764: contig of 1726 bp in length
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* 19865 21240: contig of 1376 bp in length
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* 21341 23608: contig of 2268 bp in length
* 23609 23708: gap of unknown length
* 23709 25603: contig of 1895 bp in length
* 25604 25703: gap of unknown length
* 25704 26960: contig of 1257 bp in length
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* 29589 31541: contig of 1953 bp in length
* 31542 31641: gap of unknown length
* 31642 33991: contig of 2349 bp in length
* 33992 34090: gap of unknown length
* 34091 35734: contig of 1644 bp in length
* 35735 35834: gap of unknown length
* 35835 37109: contig of 1275 bp in length
* 37110 37209: gap of unknown length
* 37210 39860: contig of 2651 bp in length
* 39861 39960: gap of unknown length
* 39961 41991: contig of 2031 bp in length
* 41992 42091: gap of unknown length
* 42092 45782: contig of 3691 bp in length
* 45783 45882: gap of unknown length
* 45883 48519: contig of 2636 bp in length
* 48519 48618: gap of unknown length
* 48619 51700: contig of 3082 bp in length
* 51701 51800: gap of unknown length
* 51801 54495: contig of 2695 bp in length
* 54496 54595: gap of unknown length
* 54596 57736: contig of 3141 bp in length

RESULT 9					
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LOCUS	2109 bp	DNA	linear	PAT 02-APR-2001	
DEFINITION	Sequence 3 from Patent WO0120003.				
ACCESSION	AX099776				
VERSION	AX099776.1 GI:13538810				
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2109) Anderson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gallard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.				
AUTHORS	Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof				
TITLE	Patent: WO 0120003-A 3 22-MAR-2001;				
JOURNAL	INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ; Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)				
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BASE COUNT	458 a	621 c	560 g	470 t	
ORIGIN					
Query Match	9.8%; Score 168.2; DB 6; Length 2109;				
Best Local Similarity	95.6%; Pred. No. 1e-30;				
Matches 173; Conservative	0; Mismatches 8; Indels 0; Gaps 0;				
QY	1510	CCATCCTAACAGAGGTTCCTCGTGCGCCGCCGCCTTCCTCTACCGCACTATCCAAGA	1569		
Db	909	CCTGCACATCTTTGGTTCCTCGTGCGCCGCCGCCTTCCTCTACCGCACTATCCAAGA	968		
QY	1570	TTTGGCATCGGCACATTCGAGACTTGCTGCTGGTGGAGACACCCATCCTGAC	1629		
Db	969	TTTTGGCATCGGCACATTCGAGACTTGCTGCTGGTGGAGACACCCATCCTGAC	1028		
QY	1630	TGCACTGGACATCTTTGGACCGGCGTGTGCTGCACCTGCCTGTGTAACAAGATGTGG	1689		
Db	1029	TGCACTGGACATCTTTGGACCGGCGTGTGCTGCACCTGCCTGTGTAACAAGATGTGG	1088		
QY	1690	T 1690			
Db	1089	T 1089			
RESULT 10					
AX099802					
LOCUS	2115 bp	DNA	linear	PAT 02-APR-2001	
DEFINITION	Sequence 29 from Patent WO0120003.				
ACCESSION	AX099802				
VERSION	AX099802.1 GI:13538836				
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2115) Anderson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gallard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.				
AUTHORS	Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof				
TITLE	Patent: WO 0120003-A 3 22-MAR-2001;				
JOURNAL	INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ; Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)				
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BASE COUNT	460 a	622 c	562 g	471 t	
ORIGIN					
Query Match	9.8%; Score 168.2; DB 6; Length 2115;				
Best Local Similarity	95.6%; Pred. No. 1e-30;				
Matches 173; Conservative	0; Mismatches 8; Indels 0; Gaps 0;				
QY	1510	CCATCCTAACAGAGGTTCCTCGTGCGCCGCCGCCTTCCTCTACCGCACTATCCAAGA	1569		
Db	915	CTGCACATCTTTGGTTCCTCGTGCGCCGCCGCCTTCCTCTACCGCACTATCCAAGA	974		
QY	1570	TTTGGCATCGGCACATTCGAGACTTGCTGCTGGTGGAGACACCCATCCTGAC	1629		
Db	975	TTTGGCATCGGCACATTCGAGACTTGCTGCTGGTGGAGACACCCATCCTGAC	1034		
QY	1630	TGCACTGGACATCTTTGGACCGGCGTGTGCTGCACCTGCCTGTGTAACAAGATGTGG	1689		
Db	1035	TGCACTGGACATCTTTGGACCGGCGTGTGCTGCACCTGCCTGTGTAACAAGATGTGG	1094		
QY	1690	T 1690			
Db	1095	T 1095			
RESULT 11					
AF214519					
LOCUS	2115 bp	mRNA	linear	PRI 03-JUN-2000	
DEFINITION	Homo sapiens AMP-activated protein kinase gamma subunit (PKAG3); mRNA, complete cds.				
ACCESSION	AF214519				
VERSION	AF214519.1 GI:8215681				
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2115) Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gallard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. and Andersson,L.				
AUTHORS	A mutation in PKAG3 associated with excess glycogen content in pig skeletal muscle				
TITLE	Science 288 (5469), 1248-1251 (2000)				
JOURNAL	MEDLINE 20280150				
MEDLINE	PUBMED 10818001				
PUBMED	10818001				
REFERENCE	2 (bases 1 to 2115) Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gallard,C., Paul,S., Iannuccelli,N., Gellin,J., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P., and Andersson,L.				
AUTHORS					

[illegible]

Carron, T. F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleaveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R., Davila, M. L., Davis, C., Davy-Carroll, L., Dederich, D. A., Delaney, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J., Earhart, C., Edgar, D., Edwards, C. C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J. J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harries, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, J., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louissegh, H., Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Roife, M., Ruiz, S., Savary, G., Scherex, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaite, J., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GNHC
 Center clone name: CH230-206A13
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 130676 bases at least Q40
 Consensus quality: 139439 bases at least Q30
 Consensus quality: 146503 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 74 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1105: contig of 1105 bp in length
 * 1106 1205: gap of unknown length
 * 1206 2375: contig of 1170 bp in length
 * 2376 2475: gap of unknown length

2476 3807: contig of 1332 bp in length
 3808 3907: gap of unknown length
 3908 5168: contig of 1261 bp in length
 5169 5268: gap of unknown length
 5269 6310: contig of 1042 bp in length
 6311 6410: gap of unknown length
 6411 7459: contig of 1049 bp in length
 7460 7559: gap of unknown length
 7560 8578: contig of 1019 bp in length
 8579 8678: gap of unknown length
 8679 10354: contig of 1676 bp in length
 10355 10454: gap of unknown length
 11539: contig of 1085 bp in length
 11540 11639: gap of unknown length
 11640 13122: contig of 1483 bp in length
 13123 13222: gap of unknown length
 13223 14871: contig of 1649 bp in length
 14872 14971: gap of unknown length
 14972 16450: contig of 1479 bp in length
 16451 16550: gap of unknown length
 16551 17578: contig of 1028 bp in length
 17579 17678: gap of unknown length
 17679 18992: contig of 2214 bp in length
 18993 19992: gap of unknown length
 19993 21699: contig of 1707 bp in length
 21700 21799: gap of unknown length
 21800 22937: contig of 1138 bp in length
 22938 23037: gap of unknown length
 23038 24744: contig of 1707 bp in length
 24745 24844: gap of unknown length
 24845 26303: contig of 1459 bp in length
 26304 26403: gap of unknown length
 26404 28138: contig of 1735 bp in length
 28139 28238: gap of unknown length
 28239 29251: contig of 1013 bp in length
 29252 30836: contig of 1485 bp in length
 30837 30936: gap of unknown length
 30937 32824: contig of 1888 bp in length
 32825 32924: gap of unknown length
 32925 34524: contig of 1600 bp in length
 34525 36141: contig of 1517 bp in length
 36142 36241: gap of unknown length
 36242 38249: contig of 2008 bp in length
 38250 38349: gap of unknown length
 38350 39397: contig of 1048 bp in length
 39398 40778: contig of 1281 bp in length
 40779 40878: gap of unknown length
 40879 41965: contig of 1087 bp in length
 41966 42065: gap of unknown length
 42066 43902: contig of 1837 bp in length
 43903 44002: gap of unknown length
 44003 45359: contig of 1357 bp in length
 45360 45459: gap of unknown length
 45460 48027: contig of 2568 bp in length
 48028 48127: gap of unknown length
 48128 49860: contig of 1733 bp in length
 49861 51868: contig of 1908 bp in length
 51869 51968: gap of unknown length
 51969 53698: contig of 1730 bp in length
 53699 53798: gap of unknown length
 53799 55479: contig of 1681 bp in length
 55480 55579: gap of unknown length
 55580 57721: contig of 2142 bp in length
 57722 57821: gap of unknown length
 57822 59554: contig of 1733 bp in length
 59555 59654: gap of unknown length
 62119: contig of 2465 bp in length
 62120 62219: gap of unknown length
 62220 64137: contig of 1918 bp in length

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

Search completed: June 14, 2003, 16:15:58
Job time : 4498 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 14, 2003, 11:14:11 ; Search time 423 Seconds
(Without alignments)
9167.709 Million cell updates/sec

Title: US-09-826-581-3
Perfect score: 1722
Sequence: 1 cctggccctcagatcaaga.....gatgagagctcggtgga 1722

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1722	100.0	1722	22 AAH43683 PRKAG3 intron 4 -
2	351	20.4	378	22 ABA44706 Human breast cell
3	351	20.4	378	22 ABA55162 Human foetal liver
4	351	20.4	378	22 ABA24907 Probe #3373 for ge
5	351	20.4	378	22 AAK03423 Human brain expres
6	351	20.4	378	22 AAK02874 Human bone marrow
7	351	20.4	378	22 AAK13465 Probe #3398 for ge
8	351	20.4	378	22 AAI34821 Probe #3507 used t
9	351	20.4	378	22 AAI03344 Probe #3335 used t

C	10	351	20.4	378	24	ABS03407	Human genome-deriv
	11	196	11.4	547	22	ABA08485	Human AMP-activate
	12	168.2	9.8	1647	22	AAH43683	PRKAG3 CDNA.. Homo
	13	168.2	9.8	2109	22	AAD03296	Human AMPK gamma s
	14	168.2	9.8	2115	22	AAD03320	Human AMPK gamma s
	15	148	8.6	1867	22	AAD03295	Pig AMPK gamma sub
	16	148	8.6	1873	22	AAD03319	Pig AMPK gamma sub
	17	148	8.6	1873	22	AAD03319	Pig wild-type PRKA
	18	148	8.6	1873	24	RAD36457	Pig PRKAG3 polymor
	19	148	8.6	1873	24	RAD36458	Pig PRKAG3 polymor
	20	148	8.6	1873	24	RAD36459	Pig PRKAG3 polymor
	21	148	8.6	1873	24	RAD36460	Pig PRKAG3 polymor
	22	148	8.6	2022	22	AAD03321	Sus scrofa PRKAG3
C	23	74.2	4.3	16525	22	AAK73303	Human immune/haema
	24	70.4	4.1	602	22	AAH35203	Human colon cancer
	25	70.4	4.1	1578	24	ABK84324	Human cDNA differe
	26	70.4	4.1	1691	21	AAC98774	Human pancreatic c
	27	70.4	4.1	1774	24	ABL39755	Human NS cDNA sequ
	28	68.8	4.0	1576	18	AAT85927	Mammalian AMPK-gam
	29	68	3.9	39651	23	ABL18856	Drosophila melanog
	30	65.8	3.8	3261	23	ABL18857	Drosophila melanog
C	31	65	3.8	92	22	ABA49850	Human breast cell
	32	65	3.8	92	22	ABA67769	Human foetal liver
	33	65	3.8	92	22	ABA34826	Probe #13292 for g
	34	65	3.8	92	22	AAK16181	Human brain expres
	35	65	3.8	92	22	AAK11922	Human bone marrow
	36	65	3.8	92	22	AAI22692	Probe #12625 for g
	37	65	3.8	92	22	AAI47988	Probe #16674 used
	38	65	3.8	92	22	AAI08354	Probe #8345 used t
C	39	65	3.8	92	24	ABS15953	Human genome-deriv
	40	63.8	3.7	1435	20	AAK06882	Disease associated
	41	63.8	3.7	1467	23	AAH84265	DNA encoding novel
	42	63.8	3.7	2223	22	AAH14839	Human cDNA sequenc
	43	62.6	3.6	350	21	AAC01661	Human secreted pro
	44	57.2	3.3	735	22	AAH07561	Human cDNA clone (
	45	49.8	2.9	2303	23	AAH84267	DNA encoding novel

ALIGNMENTS

RESULT 1
AAH43683
ID AAH43683 standard; DNA; 1722 BP.

XX AC AAH43683;

XX XX 21-JAN-2002 (first entry)

XX XX PRKAG3 intron 4 - intron 10.

XX XX Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;

XX XX metabolic disease; diabetes; obesity; substitution; ds.

XX OS Homo sapiens.

XX XX Key Location/Qualifiers

FT FT intron 1..13

FT FT /*tag= a /number= "Intron 4"

FT FT /note= "3' portion of intron 4"

FT FT 14..95

FT FT /*tag= b /number= "Exon 5"

FT FT 96..552

FT FT /*tag= c /number= "Intron 5"

FT FT 553..611

FT FT /*tag= d /number= "Exon 6"

FT FT 612..736

FT FT /*tag= e /number= "Intron 6"


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FT      /tag= f
FT      /number= "Exon 7"
FT      783..986
FT      intron
FT      /tag= g
FT      /number= "Intron 7"
FT      987..1041
FT      exon
FT      /tag= h
FT      /number= "Exon 8"
FT      1042..1242
FT      intron
FT      /tag= i
FT      /number= "Intron 8"
FT      1243..1369
FT      exon
FT      /tag= j
FT      /number= "Exon 9"
FT      1370..1522
FT      intron
FT      /tag= k
FT      /number= "Intron 9"
FT      1523..1688
FT      exon
FT      /tag= l
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FT      1689..1722
FT      intron
FT      /tag= i
FT      /number= "Intron 10"
FT      /note= "5' portion of intron 10"
XX
XX      WO200177305-A2.
XX
XX      18-OCT-2001.
XX
XX      06-APR-2001; 2001WO-SE00765.
XX
XX      07-APR-2000; 2000US-195665P.
XX      (AREX-) AREXIS AB.
XX
XX      Andersson L, Luthman H, Marklund S;
XX
XX      WPI; 2001-657170/75.
XX
XX      New variants of human AMP-activated protein kinase gamma3 subunit
XX      associated with a metabolic disease e.g. diabetes or obesity and method
XX      for determining a risk estimate of diseases in subject by detecting the
XX      variant -
XX
XX      Example 1; Fig 3; 25pp; English.
XX
XX      The sequences given in AAH43681-84 represents genomic fragments
XX      encoding the human AMP-activated protein kinase gamma 3 subunit
XX      (PRAG3). Detecting the presence of the PRAG3 DNA, or a variant,
XX      is useful in determining a risk estimate of a metabolic disease,
XX      such as diabetes or obesity, in a subject. The variation may occur
XX      in exons 3, 4 or 10. In exon 3 variation may be a substitution of
XX      a G for a C at nucleotide 320, resulting in the amino acid
XX      substitution P1A; in exon 4 variation may be a substitution of a
XX      T for a C at nucleotide 550; and in exon 10 variation may be a
XX      substitution of a T for a C at nucleotide 1037, resulting in the
XX      amino acid substitution R340W. There may also be nucleotide variation
XX      in intron 6.
XX
XX      Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0 other;
XX
XX      Query Match      100.0%; Score 1722; DB 22; Length 1722;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 1722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX      1 CCTGGCCCTCAGATCAAGAGCCCTTCTTGTCTGTGTCGTCGACAGGTGTGGGGCAGC 60
XX      |
XX      1 CCTGGCCCTCAGATCAAGAGCCCTTCTTGTCTGTGTCGTCGTCGACAGGTGTGGGGCAGC 60
XX      |
XX      61 CCCTCTATGGACGACCAAGACAGCTTGTGGGTGAGGAGAGGCTGGGGAGGTGAAG 120
XX      |
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XX      |
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QY      121 GGAGATGGAGAGGTGAGGGGGAGATCTTGACGGTTGTTCTGGGGCTGATCTCTGATAT 180
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QY      121 GGAGATGGAGAGGTGAGGGGGAGATCTTGACGGTTGTTCTGGGGCTGATCTCTGATAT 180
QY      |
QY      181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGGAAGTCCATCC 240
QY      |
QY      181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGGAAGTCCATCC 240
QY      |
QY      241 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCCATCTGTGGAGCGGT 300
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QY      301 ATGACCAGCTGACACCTTTACCTCCCTACTGCATGCGCCCTGTGCCATAGGTGTGAGG 360
QY      |
QY      361 AGCAATATGGGGAGGAGGAGAGAAAGACCCACTTCTCAGGCCTGGGGCTCCGCC 420
QY      |
QY      361 AGCAATATGGGGAGGAGGAGAGAAAGACCCACTTCTCAGGCCTGGGGCTCCGCC 420
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QY      421 ACTGTCTGTCTCCACAGTCCCTACTGTCTCAGACAAAGACACTGGCAGGCTGGGA 480
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QY      |
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QY      |
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QY      |
QY      841 GTGGAGGATGGGAGTGGGATGCTCTGAGTGAACAGGGGAGGACAAATAGGAGCCTCG 900
QY      |
QY      901 GGTCCCTGACGAAAGGAAAGTCCCTGAGTGCAGGTGAGGAGGAGTGCAGGCTCCCG 960
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QY      |
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Db 1381 CCCAGTGGGAGGAAGGGGAGACCTGGGCAGTGATCAGAGGGCTGAGAGTCTTCAG 1440
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ID ABA44706 standard; DNA; 378 BP.
XX AC ABA44706;
XX AC ABA44706;
DT 01-FEB-2002 (first entry)
XX Human breast cell single exon nucleic acid probe #3401.
XX Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX Homo sapiens.
XX OS
XX PN W0200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00662.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX New spatially-addressable set of single exon nucleic acid probes,
PT

PT useful for measuring gene expression in sample derived from human
breast, comprises number of single exon nucleic acid probes -
XX Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English.
XX The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human breast and BT 474 cells. The method involves contacting
the probes with a collection of detectably labelled nucleic acids
derived from mRNA of human breast, and then measuring the label
bound to each probe of the microarray. The probes are useful for
verifying the expression of regions of genomic DNA predicted to
encode proteins. They are useful for gene discovery, and for
determining predisposition and/or prognosing breast disease. Gene
expression analysis is useful for assessing the toxicity of chemical
agents on cells. The microarray of this invention presents a far greater
diversity of probes for measuring gene expression, with far less bias
than expressed sequence tag microarrays. The method is suitable for
rapid production of functional information from genomic sequence. The
present sequence is a single exon nucleic acid probe of the invention.
Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
Query Match 20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CCTGGCCCCCTCAGATCAAGAAGCCCTTTCTTCTGCTGTCGCCAACGGTGTGCGGGCAGC 60
Db 362 CCTGGCCCCCTCAGATCAAGAAGCCCTTTCTTCTGCTGTCGCCAACGGTGTGCGGGCAGC 303
QY 61 CCTCTATGGGACAGCAGCAAGCAGAGCTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG 120
Db 302 CCTCTATGGGACAGCAGCAAGCAGAGCTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG 243
QY 121 GGAGATGGAGGAGGTGAGGGGAGATCTTGACGGTTGTTCTGGGCTCATCTGTATAT 180
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QY 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGCGGGCCAGGGTGGAGGAAGTCCATCC 240
Db 182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGCGGGCCAGGGTGGAGGAAGTCCATCC 123
QY 241 GGAGTCTCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
Db 122 GGAGTCTCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
QY 301 ATGACCAAGCTGACACCTTTTACCTCCGCTACTGTCATGCGCCCTGTGCCATAGTGTAGGG 360
Db 62 ATGACCAAGCTGACACCTTTTACCTCCGCTACTGTCATGCGCCCTGTGTG-CATAGGTGTAGGG 4
QY 361 AGC 363
Db 3 AGC 1
RESULT 3
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ID ABA55162 standard; DNA; 378 BP.
XX AC ABA55162;
XX AC ABA55162;
DT 01-FEB-2002 (first entry)
XX Human foetal liver single exon nucleic acid probe #3467.
DE Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
XX OS

QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTGTGGAGCGCT 300
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Db 122 GAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTGTGGAGCGCT 63
QY 301 ATGACCAAGTGCACACTTTCACCTCCGCTACTGATGAGCCCTGTGCCATAGGTGCTAGGG 360
|||||
Db 62 ATGACCAAGTGCACACTTTCACCTCCGCTACTGATGAGCCCTGTG-CATAGGTGCTAGGG 4
QY 361 AGC 363
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Db 3 AGC 1
RESULT 5
AAK03423/c
ID AAK03423 standard; DNA; 378 BP.
AC AAK03423;
XX
DT 05-NOV-2001 (first entry)
DE Human brain expressed single exon probe SEQ ID NO: 3414.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 3414; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
Query Match 20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CCTGGCCCTTCAGATCAAGAGCGCTTCTTGTCTGTGGCCACAGGTGTGCGGCAGC 60
|||||
Db 362 CCTGGCCCTTCAGATCAAGAGCGCTTCTTGTCTGTGGCCACAGGTGTGCGGCAGC 303
QY 61 CCCTCTATGGGACACCAAGACACCTTTTGGGTGAGGAGCGCTGGGGAGGTGAAG 120

Db 302 CCCTCTATGGGACACCAAGACAGAGCTTTGGGTGAGGAGCGCTGGGGAGGTGAAG 243
QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTGTCTGGGGCTGATCTCTGATAT 180
|||||
Db 242 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTGTCTGGGGCTGATCTCTGATAT 183
QY 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 240
|||||
Db 182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 123
QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTGTGGAGCGCT 300
|||||
Db 122 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTGTGGAGCGCT 63
QY 301 ATGACCAAGTGCACACTTTCACCTCCGCTACTGATGAGCCCTGTGCCATAGGTGCTAGGG 360
|||||
Db 62 ATGACCAAGTGCACACTTTCACCTCCGCTACTGATGAGCCCTGTG-CATAGGTGCTAGGG 4
QY 361 AGC 363
|||
Db 3 AGC 1
RESULT 6
AAK28874/c
ID AAK28874 standard; DNA; 378 BP.
XX
AC AAK28874;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 3431.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 3431; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

```
Query Match      20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 COTGGCCCTCAGATCAAGAAGGCTTCTTTGCTCTGTGGCCCAACGGTGTGCGGGCAGC 60
   |||||||
Db 362 COTGGCCCTCAGATCAAGAAGGCTTCTTTGCTCTGTGGCCCAACGGTGTGCGGGCAGC 303

QY 61 CCTCTATGGGACACGAAGAAGCAGAGCTTTTGTGGTGAGGAGAGCTGGGAGGTGAAG 120
   |||||||
Db 302 CCTCTATGGGACACGAAGAAGCAGAGCTTTTGTGGTGAGGAGAGCTGGGAGGTGAAG 243

QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTTGTTCTGGGCTGATCTCTGATAT 180
   |||||||
Db 242 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTTGTTCTGGGCTGATCTCTGATAT 183

QY 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCGAGGGTGGAGAAAGTCCATCC 240
   |||||||
Db 182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCGAGGGTGGAGAAAGTCCATCC 123

QY 241 GGAGTCTCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGGAGCCGCT 300
   |||||||
Db 122 GGAGTCTCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGGAGCCGCT 63

QY 301 ATGACAGCTGACACCTTTACCTCCGCTACTGTCATGGCCCTGTGTCATAGGTGCTAGGG 360
   |||||||
Db 62 ATGACAGCTGACACCTTTACCTCCGCTACTGTCATGGCCCTGTG-CATAGGTGCTAGGG 4

QY 361 AGC 363
   |||
Db 3 AGC 1

RESULT 7
AAI13465/c
ID AAI13465 standard; DNA; 378 BP.
XX
AC AAI13465;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #3398 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632386.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOI.E-) MOLECULAR DYNAMICS INC.
XX
PT Penn SC, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 3398; 487pp; English.
XX
```

```
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human Hela cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match      20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 COTGGCCCTCAGATCAAGAAGGCTTCTTTGCTCTGTGGCCCAACGGTGTGCGGGCAGC 60
   |||||||
Db 362 COTGGCCCTCAGATCAAGAAGGCTTCTTTGCTCTGTGGCCCAACGGTGTGCGGGCAGC 303

QY 61 CCTCTATGGGACACGAAGAAGCAGAGCTTTTGTGGTGAGGAGAGCTGGGAGGTGAAG 120
   |||||||
Db 302 CCTCTATGGGACACGAAGAAGCAGAGCTTTTGTGGTGAGGAGAGCTGGGAGGTGAAG 243

QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTTGTTCTGGGCTGATCTCTGATAT 180
   |||||||
Db 242 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTTGTTCTGGGCTGATCTCTGATAT 183

QY 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCGAGGGTGGAGAAAGTCCATCC 240
   |||||||
Db 182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCGAGGGTGGAGAAAGTCCATCC 123

QY 241 GGAGTCTCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGGAGCCGCT 300
   |||||||
Db 122 GGAGTCTCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGGAGCCGCT 63

QY 301 ATGACAGCTGACACCTTTACCTCCGCTACTGTCATGGCCCTGTGTCATAGGTGCTAGGG 360
   |||||||
Db 62 ATGACAGCTGACACCTTTACCTCCGCTACTGTCATGGCCCTGTG-CATAGGTGCTAGGG 4

QY 361 AGC 363
   |||
Db 3 AGC 1

RESULT 8
AAI134821/c
ID AAI134821 standard; DNA; 378 BP.
XX
AC AAI134821;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #3507 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
```

PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PT WPI; 2001-488897/53.
DR Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
PT Claim 25; SEQ ID No 3507; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCTGGCCCTCAGATCAAGAGCCCTTCTTCTGCTGTGGCCCAACGGTGTGGGGCAGC 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
362 CCTGGCCCTCAGATCAAGAGCCCTTCTTCTGCTGTGGCCCAACGGTGTGGGGCAGC 303

QY 61 CCTCTATGGGACAGCAGAGAGCTTTTGTGGGTGAGGAGAGGCTGGGAGGTGAAG 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
302 CCTCTATGGGACAGCAGAGAGCTTTTGTGGGTGAGGAGAGGCTGGGAGGTGAAG 243

QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTTCTGGGGCTGATCTCTGATAT 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
242 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTTCTGGGGCTGATCTCTGATAT 183

QY 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 123

QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
62 ATGACCAGCTGACACCTTTTCACCTCCGCTACTGTCATGCGCCCTGTG-CATAGGTGCTAGGG 4

QY 361 AGC 363
DB |||
3 AGC 1

RESULT 9
AA103344/C
ID AA103344 standard; DNA; 378 BP.
XX
AC AA103344;
XX
DT 09-OCT-2001 (first entry)
XX
DE Probe #3335 used to measure gene expression in human breast sample.
XX
KW Probe; human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX

PF 29-JAN-2001; 2001WO-US00661.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
DR Novel single exon nucleic acid probe used to measuring gene expression
XX in a human breast -
PT Claim 25; SEQ ID No 3335; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes.
CC The present sequence is one such probe. The probes are useful for
CC measuring human gene expression in a human breast sample, where the probe
CC hybridises at high stringency to a nucleic acid expressed in the human
CC breast. The probes are useful for predicting, diagnosing, grading,
CC staging, monitoring and prognosing diseases of the human breast,
CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCTGGCCCTCAGATCAAGAGCCCTTCTTGTGCTGTGGCCCAACGGTGTGGGGCAGC 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
362 CCTGGCCCTCAGATCAAGAGCCCTTCTTGTGCTGTGGCCCAACGGTGTGGGGCAGC 303

QY 61 CCTCTATGGGACAGCAGAGAGCTTTTGTGGGTGAGGAGAGGCTGGGAGGTGAAG 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
302 CCTCTATGGGACAGCAGAGAGCTTTTGTGGGTGAGGAGAGGCTGGGAGGTGAAG 243

QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTTCTGGGGCTGATCTCTGATAT 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
242 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTTCTGGGGCTGATCTCTGATAT 183

QY 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 123

QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
122 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63

QY 301 ATGACCAGCTGACACCTTTTCACCTCCGCTACTGTCATGCGCCCTGTGCCATAGGTGCTAGGG 360
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
62 ATGACCAGCTGACACCTTTTCACCTCCGCTACTGTCATGCGCCCTGTG-CATAGGTGCTAGGG 4

QY 361 AGC 363
DB |||
3 AGC 1

RESULT 10
ABS03407/C
ID ABS03407 standard; DNA; 378 BP.

XX ABS03407;
XX 19-AUG-2002 (first entry)
XX Human genome-derived single exon probe from lung SEQ ID No 3398.
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
XX Homo sapiens.
OS
XX
XX WO2001:86003-A2.
PN
XX
XX 15-NOV-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US00665.
XX
XX 04-FEB-2000; 2000US-180312P.
PR
XX 26-MAY-2000; 2000US-207456P.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-234687P.
PR
XX 27-SEP-2000; 2000US-236359P.
PR
XX 04-OCT-2000; 2000GB-0024263.
PR
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
XX Claim 1; SEQ ID No 3398; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary

CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemorrhoidosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a single exon
CC probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.4%; Score 351; DB 24; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCTGGCCCCCAGATCAAGAGCCCTCTTTGCTCTGTGTGGCCACGGTGTGGCGGCGAGC 60
Db |||||
QY 362 CCTGGCCCCCAGATCAAGAGCCCTCTTTGCTCTGTGTGGCCACGGTGTGGCGGCGAGC 303
Db |||||
QY 61 CCTCTATGGGACAGCAAGACAGAGCTTTGTGGGTGAGGAGAGCTGGGGAGGTGAAG 120
Db |||||
QY 302 CCTCTATGGGACAGCAAGACAGAGCTTTGTGGGTGAGGAGAGCTGGGGAGGTGAAG 243
QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTTGACGGTTGTTCTGGGGCTGATCTCTGATAT 180
Db |||||
QY 242 GGAGATGGAGAGGTGAGGGGAGATCTTTGACGGTTGTTCTGGGGCTGATCTCTGATAT 183
QY 181 ACCCAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGGAAGTCCATCC 240
Db |||||
QY 182 ACCCAAGCTTGGCTTCAGGCCAAGCCAGGGCCAGGGTGGAGGAAGTCCATCC 123
QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
Db |||||
QY 122 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
QY 301 ATGACCAGCTGACACCTTCACCTCGGTACTGATGGCCCTGTGCCATAGTGTCTAGGG 360
Db |||||
QY 62 ATGACCAGCTGACACCTTCACCTCGGTACTGATGGCCCTGTG-CATAGTGTCTAGGG 4
QY 361 AGC 363
Db |||||
QY 3 AGC 1
Db

RESULT 11
ABA08485
ID ABA08485 standard; cDNA; 547 BP.
XX
XX ABA08485;
AC
XX
XX 11-JAN-2002 (first entry)
DT
XX
XX Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261.
DE
XX
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytoskeletal; osteopathic; vasotropic; cardiac; virucide; antibacterial;
KW antifungal; vulnary; antiulcer; ss.
XX
XX Homo sapiens.
OS


```
CC of PRKAG3 and is useful in gene therapy.
XX
SQ Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;

Query Match      8.6%; Score 148; DB 22; Length 1867;
Best Local Similarity 88.9%; Pred. No. 7.5e-29;
Matches 160; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1510 CCATCCTAACCGGGTCCCTGTGCGCCCGGCCCTCCTTCCTTACCGCACTATCCAAGA 1569
Db      || | | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1570 TTGGGCATCGGCAGATCCGAGACTTGGCTGTGGTCTGGAGACAGACACCCATCCTTGAC 1629
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 969 TTGGGCATCGGCAGATCCGAGACTTGGCGTGGTGGTGGAAAGCGCGCCATCCTTGAC 1028
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1630 TGCACTGGACATCTTTGTGGACCGCGGTGTCTGTGACATGCTGTGGTCAACGAATGTGG 1689
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1029 CGCACTGGACATCTTCGTGGACCGCGGTGTCTGTGCGCTGCCCTGTGGTCAACGAACACTGG 1088
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: June 14, 2003, 16:23:08
Job time : 426 secs
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:14:11 ; Search time 2562 Seconds
(without alignments)
10885.491 Million cell updates/sec

Title: US-09-826-581-3
Perfect score: 1722
Sequence: 1 cctggccctcagatcaaga.....gatgagaggtcggctgga 1722

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: em_estba.*
 - 2: em_esthum.*
 - 3: em_estin.*
 - 4: em_estmu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_htc.*
 - 9: gb_est1.*
 - 10: gb_est2.*
 - 11: gb_htc.*
 - 12: gb_est3.*
 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: gb_gss.*
 - 18: em_gss_hum.*
 - 19: em_gss_inv.*
 - 20: em_gss_pln.*
 - 21: em_gss_vrt.*
 - 22: em_gss_fun.*
 - 23: em_gss_mam.*
 - 24: em_gss_mus.*
 - 25: em_gss_other.*
 - 26: em_gss_pro.*
 - 27: em_gss_fod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	8.6	572	13	BI344527 373008 MA
2	132.4	7.7	413	9	AA178898 zp38d10.r
3	116.8	6.8	1042	17	AL248229 Tetraodon
4	88.8	5.2	591	13	BJ495978 BJ495978
5	84.6	4.9	728	13	BJ504184 BJ504184
6	82.6	4.8	933	13	BC919314 60281782

7	82.2	4.8	633	13	BJ072114
8	81.8	4.8	536	13	BM488662
9	80.2	4.7	595	13	BM487789
10	80.2	4.7	636	12	BG713637
11	80.2	4.7	647	13	BM440762
12	80.2	4.7	649	9	AJ395115
13	80.2	4.7	687	9	AJ451523
14	78.6	4.6	758	9	AJ396118
15	76.4	4.4	576	10	AV603335
16	73	4.2	564	10	AV608257
17	71	4.1	775	13	BI833269
18	70.4	4.1	448	9	AA558845
19	70.4	4.1	450	12	BF351397
20	70.4	4.1	455	9	AA578219
21	70.4	4.1	469	9	AL047390
22	70.4	4.1	473	10	BE168881
23	70.4	4.1	508	10	BE168874
24	70.4	4.1	558	14	BM710850
25	70.4	4.1	583	10	AW379936
26	70.4	4.1	584	14	BM765123
27	70.4	4.1	586	12	BG609812
28	70.4	4.1	591	10	AW410926
29	70.4	4.1	598	10	BE148626
30	70.4	4.1	616	10	AW956906
31	70.4	4.1	634	12	BG740148
32	70.4	4.1	668	12	BG705895
33	70.4	4.1	676	14	BM782063
34	70.4	4.1	698	14	BM764743
35	70.4	4.1	708	10	AW411228
36	70.4	4.1	710	13	BI223705
37	70.4	4.1	714	14	BM783383
38	70.4	4.1	726	13	BI768590
39	70.4	4.1	742	13	BI914634
40	70.4	4.1	746	12	BF528081
41	70.4	4.1	756	13	BI859947
42	70.4	4.1	782	13	BI819312
43	70.4	4.1	782	13	BI821538
44	70.4	4.1	795	12	BB871189
45	70.4	4.1	803	14	BQ216967

ALIGNMENTS

RESULT 1
BI344527
LOCUS BI344527 572 bp mRNA linear EST 30-JUL-2001
DEFINITION 373008 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BI344527
VERSION BI344527.1 GI:15037807
KEYWORDS EST.
SOURCE Pig.
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 572)
AUTHORS Faurenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laedreid,W.W.
and Keele,J.W.

TITLE EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAACAGCTATGACCAT


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Query Match          6.8%; Score 116.8; DB 17; Length 1042;
Best Local Similarity 56.3%; Pred. No. 3.9e-17;
Matches 269; Conservative 0; Mismatches 192; Indels 17; Gaps 2;

QY 1238 TCCAGCCTGTTGAAGCTGCTTACACCTCATCAAGAACCGGATCCATGCGTGCCTGTT 1297
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 196 TCCAGCCTGTTGATGCTGTACAGCTCATCAAAACAAAATTCACCGCTGCCGTGC 255

QY 1298 CTTGACCGGTGTCAGGCAAGCTACTCCACATCTCTACACACACAAAGCCTGCTCAAGTTC 1357
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 ATTGATCCAGTACAGGAACACGCTTTACATCTCTACACACAAAGAGGATCCTCAAGTTC 315

QY 1358 CTGACATCTTTGTAAG-----CCTGGGCCAGGTGGGAGGAAGGGGAGACCTGG 1408
      || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 CTTACAGCTGTTGTGAGTGGACACATCCCATCAGTGTGTGACAAAGGCGCGTGNAT 375

QY 1409 GCAGGTGATCAGAGCGCTGAGAGTCTTCAGCCCTAGCAGTCTGGGGAGAGAGCTGGGA 1468
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 CCCACCTGTGGGGCGAGATCTGCCCATCTGTTCCCTAGTGGCCAAAGCCGAGA 435

QY 1469 GCCCTCTTGAGCTGCTG-----GATCCCTGATCTCCACCTGTGCTCCCATCTAACC 1520
      || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 CCTCCTGTTTGGCGCGGTGAACACACCCCTGTCTTACTTTGGCGCTTTGCTGCTTTCC 495

QY 1521 AGGGTTCCTGCTGCCCGCGCTCTCTCTACCGCACTATCCAAAGATTTGGGCATCG 1580
      || || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 AGATGTGTGAGAGCCAAAGCCGCTTCATTCAGCAGAGAGCCCTGAGGGAGCTGGCCATG 555

QY 1581 GCACATTCGAGACTTGGCTGTGGTGGAGACAGACCCATCTGACTGCACTGGGACA 1640
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 556 GTACATACCGGACATGCTTCATTCACCCCGACAGCCCATCATCAAGGGCTCAACA 615

QY 1641 TCTTTGGACCGCGTGTGTCTGCACCTGCTGTGTCAGGATGTGTACCCACCC 1698
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 616 TCTTTGTGGAGCGGCTGTCCGCGCTGGGAGCGACTCCGCTAGGACCC 673

RESULT 4
LOCUS      BJ495978      591 bp      mRNA      linear      EST 08-AUG-2002
DEFINITION BJ495978      MF01FSA cDNA Oryzias latipes cDNA clone MF01FSA040J15 5',
            mRNA sequence.
ACCESSION  BJ495978
VERSION     BJ495978.1 GI:22147904
KEYWORDS    EST.
SOURCE      Japanese medaka.
ORGANISM    Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1 (bases 1 to 591)
AUTHORS     Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
TITLE       Medaka EST Project in Takeda's lab
JOURNAL     Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
              1..591
                /organism="Oryzias latipes"
                /strain="d-r8"
                /db_xref="taxon:8090"
                /clone="MF01FSA040J15"
                /sex="mixture of female and male"
                /tissue_type="whole embryo"
                /dev_stage="fry stage 40"

FEATURES             source
BASE COUNT          182 a 161 c 174 g 210 t 1 others
ORIGIN
Query Match          4.9%; Score 84.6; DB 13; Length 728;
Best Local Similarity 77.9%; Pred. No. 1.6e-09;
Matches 102; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1241 AGCCTGTTGAAGCTGTCTACACCTCATCAAGAACCGGATCCATGCGCTGCTGCTTT 1300
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 AGCCTTTTGTGATGCACTGTACCCCTCATCAAAAAAATTCACCGTCTGCTGCTCAT 297

QY 1301 GACCGGTGTCAGGCAAGCTACTCCACATCTCTACACACACCGCTGCTCAAGTTCCTG 1360
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 GACCGTGTACAGGAATGCATTTTACCTCTCACACACAGAGGATCTCTCAAGTTCCTG 237

QY 1361 CACATCTTTGT 1371
      || ||| ||| |||
Db 236 CAACGTCTTAT 226
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```
BASE COUNT          150 a 177 c 130 g 133 t 1 others
ORIGIN
Query Match          5.2%; Score 88.8; DB 13; Length 591;
Best Local Similarity 73.1%; Pred. No. 1.5e-10;
Matches 114; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1228 CTCCCATCTCTGCAGCCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATCCATCG 1287
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 416 CACACCTGAGTCCAGCCTGTTTGCAGCCATCTACTCGCTGCTGAGNACAAGATCCACGG 475

QY 1288 COTGCTGTTTGTGACCCGGTGTGAGGAAAGTACTCCACATCTCTACACACAAACGCT 1347
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 476 TCTGCCCTCATCGACCCGAGCTCAGGAAAGCTCTCCACATCTCTCACTCACAAAGCAT 535

QY 1348 GCTCAAGTCTCTGACATCTTTTGAAGCCTGGGCC 1383
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 536 CQTCAAAATCTCCACATCTTTTGGGTCCATGATCC 571

RESULT 5
BJ504184/c
LOCUS      BJ504184      728 bp      mRNA      linear      EST 08-AUG-2002
DEFINITION BJ504184      MF01FSA cDNA Oryzias latipes cDNA clone MF01FSA006A14 3',
            mRNA sequence.
ACCESSION  BJ504184
VERSION     BJ504184.1 GI:22156146
KEYWORDS    EST.
SOURCE      Japanese medaka.
ORGANISM    Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1 (bases 1 to 728)
AUTHORS     Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
TITLE       Medaka EST Project in Takeda's lab
JOURNAL     Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
              1..728
                /organism="Oryzias latipes"
                /strain="d-r8"
                /db_xref="taxon:8090"
                /clone="MF01FSA006A14"
                /sex="mixture of female and male"
                /tissue_type="whole embryo"
                /dev_stage="fry stage 40"

BASE COUNT          182 a 161 c 174 g 210 t 1 others
ORIGIN
Query Match          4.9%; Score 84.6; DB 13; Length 728;
Best Local Similarity 77.9%; Pred. No. 1.6e-09;
Matches 102; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1241 AGCCTGTTGAAGCTGTCTACACCTCATCAAGAACCGGATCCATGCGCTGCTGCTTT 1300
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 AGCCTTTTGTGATGCACTGTACCCCTCATCAAAAAAATTCACCGTCTGCTGCTCAT 297

QY 1301 GACCGGTGTCAGGCAAGCTACTCCACATCTCTACACACACCGCTGCTCAAGTTCCTG 1360
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 GACCGTGTACAGGAATGCATTTTACCTCTCACACACAGAGGATCTCTCAAGTTCCTG 237

QY 1361 CACATCTTTGT 1371
      || ||| ||| |||
Db 236 CAACGTCTTAT 226
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RESULT 6
BG919314
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

BG919314 933 bp mRNA linear EST 05-JUN-2001
 602817782F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4946661 5',
 mRNA sequence.
 BG919314 GI:14299790
 BG919314.1 house mouse.
 EST.
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 933)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapps@email.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LHAM10895 row: d column: 22
 High quality sequence stop: 498.
 Location/Qualifiers
 1..933
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4946661"
 /clone_lib="NCI_CGAP_Mam6"
 /sex="female_virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /name="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH
 244 a 292 c 238 g 159 t

BASE COUNT 244 a 292 c 238 g 159 t
 ORIGIN

Query Match 4.8%; Score 82.6; DH 13; Length 933;
 Best Local Similarity 52.1%; Pctd. NO. 5.5e-09;
 Matches 232; Conservative 0; Mismatches 209; Indels 4; Gaps 2;

```

QY      1242 GCCTGTGTTGAAGCTGTACACCCTCATCAGAAGCGGATCCATCGCGTGGCTGTGTTTG 1301
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB       7 GTCCGGTGTGCTCTCTCTTCATTAAATTCGAAATAAGATCCACAGGTCCTCAAGTATCG 66

QY      1302 ACCGGTGTACAGCAACGTACTCCATCATCTCACACAACAGCGCTGCTCAAGTTCCTGCG 1361
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB       67 ACCCAGAGTCAGGCAACACCTTGTACATCTTACTCACAAGCGGATCCTCAAAGTTCCTCA 126

QY      1362 ACATCTTTGTAG---CCTGGGCCAGCTGGGAGGAAGGGGAGACCTGGGCAGGTGATC 1418
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      137 AGTTGTTGTTAAGTAACCTCAGGCCATCATCCGATTAGCTGCTGAATTCGACACACAC 186

QY      1419 AGAGGGCTGAGGAGTCTTCAGCCCTAGCAGCTGTGGGGAAGAGCTGGGGGCCCTCTTGA 1478
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      187 AGACGGTTGGGACAGAGAGCGGTGTGGTGTGTGATGATTTAGCGTAGACATCCCATG 246

QY      1479 AGCTGTGGATCCCTGATCTCCACCTGGTCCCATCTTCAACAGGGTTCCTGCTGCCCC 1538
          || || || || || || || || || || || || || || || || || || || || ||
DB      247 CTCT-ATCCGGAAGCACCTCGACGCAATGCCCTTCTCTCAGATCACCGAGTTCGCCA 305

QY      1539 GGCGCTCTTCTCTACTACCGCACTATCCAGATTTGGGATCGGCACATTCGACACTTGG 1598
          |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
  
```

Db	306	AGCGGAAATTCATGCTTAAGTCTCTCAAGAGACTCGAGTGGCACTATGCGCAATATG	365
Qy	1599	CTGTGGTGTGGAGACAGACACCATCTGACTGCATCTGGACATCTTTGTGGACCGCGT	1658
Db	366	CCATGGTCCGTACTACACGCGCTGTCTAGCTGGCTCTGGCATCTTGTACAGACCGAG	425
Qy	1659	TGCTGCAGTGCCTGTCTCAAGA	1683
Db	426	TCTCCGCTTACCTGTAGTGATGA	450
RESULT 7			
LOCUS	BJ072114	633 bp mRNA linear	EST 11-DEC-2001
DEFINITION	BJ072114 N1BB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL096j16 5', mRNA sequence.		
ACCESSION	BJ072114		
VERSION	BJ072114.1	GI:17502303	
KEYWORDS	EST.		
SOURCE	African clawed frog.		
ORGANISM	Xenopus laevis		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.		
AUTHORS	Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara,Y.		
TITLE	Expressed genes in X. laevis embryo		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Tadasu Shin-i Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.		
FEATURES	Location/Qualifiers		
source	1. .633 /organism="Xenopus laevis" /db_xref="taxon:8355" /clone="XL096j16" /clone_lib="N1BB Mochii normalized Xenopus tailbud library" /tissue_type="whole embryo" /dev_stage="stage 25" /note="Vector: pBSRN3; Site.1: NotI; Site.2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieukoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."		
BASE COUNT	144 a 162 c 148 g 179 t		
ORIGIN			
Query Match	4.8%;	Score 82.2;	DB 13; Length 633;
Best Local Similarity	73.4%;	Prod. No. 5.8e-09;	
Matches 105;	Conservative	0; Mismatches 38;	Indels 0; Gaps 0;
Qy	1228	CTCCCATCTCTGCAGCGCTGTTGAAGCTGTCATACCCCTCATCAAGACCGGATCCATCG	1287
Db	10	CTCCCCAGCAGACGCGCTTTCCCAAGCTGTGTATTCATCTCATCAAGTAAGATCCACCG	69
Qy	1288	CCTGCCCTGTTCTTGACCCGGTGTGAGCAACGCTACTCCACATCTCTACACACAAACGCT	1347
Db	70	GCTACCAAGTAAGTATCCGCTATCTGCAACATCTTGCAATCTCTCACGCATAACGCT	129
Qy	1348	GCTCAAGTTCCTGCACATCTTTG	1370
Db	130	ACTCAAGTTCCTTCACCTCTTG	152
RESULT 8			
LOCUS	BM488662	536 bp mRNA linear	EST 07-FEB-2002

DEFINITION pgm2n.pk008.g21 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk008.g21 5' similar to gb|AAC52580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus], mRNA sequence.

ACCESSION BM488662 GI:18609593

VERSION BM488662.1

KEYWORDS EST.

SOURCE chicken.

ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 536)

AUTHORS Cogburn, L.A. and Monsonego-Ornan, E.

TITLE ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome Project

JOURNAL Unpublished (2002)

COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
source
1..536
/organism="Gallus gallus"
/strain="Commercial broiler and Ottawa Res. Centre
Strains 90 & 21"
/db_xref="taxon:9031"
/clone="pgm2n.pk008.g21"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
/tissue_type="Breast muscle, leg muscle and epiphyseal
growth plate"
/dev_stage="Breast, leg; Embryo(d19); post-hatch(1d,1,3,5,7,9
11 weeks); growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH108"
/note="Vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue (embryonic
muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
plate 33.3% of the final RNA pool). Single pass sequencing
from 5'-end"

BASE COUNT 117 a 171 c 132 g 116 t

ORIGIN
Query Match 4.8%; Score 81.8; DB 13; Length 536;
Best Local Similarity 70.1%; Pred. No. 6.7e-09;
Matches 110; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1228 CTCCATCTCTGCAGCGCTTTTGAAGCTGTCTACACCTCTCATCAGACCGGATCCATCG 1287

Db 85 CTCCCCAAGCGGACCGCTTTTGTATGCGCTCTCTCCCTGTGATCGCAATAGATCCACCG 144

QY 1288 CTTGCTGTCTTGACCGGGTCTCAGGCAACGTACTCCACATCTCTACATCTCTCCACCAACGCCT 1347

Db 145 CTTCCCGTCATCGACCGCGTCTCGGCAACATCTCTACATCTCTCCACCAACGCAT 204

QY 1348 GCTCAAGTTCCTGCACATCTTTTGAAGCCTGGGCCA 1384

Db 205 CTTCAAGTTCCTCAAACTCTTTATTGCGAGGTCCTCA 241

RESULT 9

BM487789

LOCUS

DEFINITION pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk005.j24 5' similar to gb|AAC52580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus], mRNA sequence.

ACCESSION BM487789

VERSION BM487789.1

KEYWORDS EST.

SOURCE chicken.

ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 595)

AUTHORS Cogburn, L.A. and Monsonego-Ornan, E.

TITLE ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome Project

JOURNAL Unpublished (2002)

COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
source
1..595
/organism="Gallus gallus"
/strain="Commercial broiler and Ottawa Res. Centre
Strains 90 & 21"
/db_xref="taxon:9031"
/clone="pgm2n.pk005.j24"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
/tissue_type="Breast muscle, leg muscle and epiphyseal
growth plate"
/dev_stage="Breast, leg; Embryo(d19); post-hatch(1d,1,3,5,7,9
11 weeks); growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH108"
/note="Vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue (embryonic
muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
plate 33.3% of the final RNA pool). Single pass sequencing
from 5'-end"

BASE COUNT 126 a 199 c 137 g 133 t

ORIGIN
Query Match 4.7%; Score 80.2; DB 13; Length 595;
Best Local Similarity 69.4%; Pred. No. 1.7e-08;
Matches 109; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1228 CTCCATCTCTGCAGCGCTTTTGAAGCTGTCTACACCTCTCATCAGACCGGATCCATCG 1287

Db 289 CTCCCCAATGCCAGCGCTTTTGTATGCGCTCTCTCCCTGTGATCGCAATAGATCCACCG 348

QY 1288 CTTGCTGTCTTGACCGGGTCTCAGGCAACGTACTCCACATCTCTACATCTCTCCACCAACGCCT 1347

Db 349 CTTCCCGTCATCGACCGCGTCTCGGCAACATCTCTACATCTCTCCACCAACGCAT 408

QY 1348 GCTCAAGTTCCTGCACATCTTTTGAAGCCTGGGCCA 1384

Db 409 CTTCAAGTTCCTCAAACTCTTTATTGCGAGGTCCTCA 445

RESULT 10

BM713637

LOCUS

DEFINITION pg1ln.pk008.cl3 Normalized Liver Library Gallus gallus cDNA clone pg1ln.pk008.cl3 5' similar to gi|4506061 ref|NP_02724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens] gi|12737489 ref|XP_006778.2| protein kinase, AMP-activated, gamma 1 non-mRNA sequence.

ACCESSION BM713637

VERSION BM713637.1

KEYWORDS EST.

SOURCE chicken.

ACCESSION BM487789

VERSION BM487789.1

KEYWORDS EST.

SOURCE chicken.

ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 595)

AUTHORS Cogburn, L.A. and Monsonego-Ornan, E.

TITLE ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome Project

JOURNAL Unpublished (2002)

COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
source
1..595
/organism="Gallus gallus"
/strain="Commercial broiler and Ottawa Res. Centre
Strains 90 & 21"
/db_xref="taxon:9031"
/clone="pgm2n.pk005.j24"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
/tissue_type="Breast muscle, leg muscle and epiphyseal
growth plate"
/dev_stage="Breast, leg; Embryo(d19); post-hatch(1d,1,3,5,7,9
11 weeks); growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH108"
/note="Vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue (embryonic
muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
plate 33.3% of the final RNA pool). Single pass sequencing
from 5'-end"

BASE COUNT 126 a 199 c 137 g 133 t

ORIGIN
Query Match 4.7%; Score 80.2; DB 13; Length 595;
Best Local Similarity 69.4%; Pred. No. 1.7e-08;
Matches 109; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1228 CTCCATCTCTGCAGCGCTTTTGAAGCTGTCTACACCTCTCATCAGACCGGATCCATCG 1287

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Db 349 CTTCCCGTCATCGACCGCGTCTCGGCAACATCTCTACATCTCTCCACCAACGCAT 408

QY 1348 GCTCAAGTTCCTGCACATCTTTTGAAGCCTGGGCCA 1384

Db 409 CTTCAAGTTCCTCAAACTCTTTATTGCGAGGTCCTCA 445

RESULT 10

BM713637

LOCUS

DEFINITION pg1ln.pk008.cl3 Normalized Liver Library Gallus gallus cDNA clone pg1ln.pk008.cl3 5' similar to gi|4506061 ref|NP_02724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens] gi|12737489 ref|XP_006778.2| protein kinase, AMP-activated, gamma 1 non-mRNA sequence.

ACCESSION BM713637

VERSION BM713637.1

KEYWORDS EST.

SOURCE chicken.

ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 636)
AUTHORS Burnside, J., Morgan, R.W. and Cogburn, L.A.
TITLE Chicken ESTs from a normalized liver library
JOURNAL Unpublished (2001)
COMMENT Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1345
Fax: 302-831-3411
Email: joan@udel.edu, www.chickest.udel.edu.
FEATURES
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/organism="Gallus gallus"
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/clone_lib="Normalized Liver Library"
/sex="Male and Female"
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/note="Vector: pCMVSPORT 6"
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Best Local Similarity 69.4%; Pred. No. 1.7e-08;
Matches 109; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1228 CTCACATCTCTGCAGCGCTGTTCAGCGCTCTACACCTCATCAAGACCGGATCCATCG 1287
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Db 489 CTTCCCGCTGATCGACCGCCACTCGGGCAACACTCTCTACATCTCTACCCACAAAGCAT 548
QY 1348 GCTCAAGTCTCTGCACATCTTTTGTAAAGCTTGGGCCA 1384
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Db 549 CCTCAAGTCTCTCAACTCTTTATTCAGAGGTGCCA 585
RESULT 11
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LOCUS pgrln.pk002.19 Normalized chicken Reproductive Tract cDNA Library
DEFINITION (pgrln) Gallus gallus cDNA clone pgrln.pk002.19 5' similar to
gi14506061 ref|NP_002724.1| protein kinase, AMP-activated, gamma 1
non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated,
noncatalytic, gamma-1 [Homo sapiens] gi12737489 ref|XP_006778.2|
protein kinase, AMP-activated, gamma 1, mRNA sequence.
BM440762
VERSION BM440762.1 GI:18471537
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 647)
AUTHORS Cogburn, L.A. and Nys, Y.
TITLE ESTs from Normalized Chicken Reproductive Tract cDNA library-
University of Delaware and INRA, Tours-Poultry Unit Project
JOURNAL Unpublished (2002)
COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
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/organism="Gallus gallus"
/strain="Commercial broiler and layer"
/db_xref="taxon:9031"
/clone_lib="Normalized Chicken Reproductive Tract cDNA
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/sex="Male and Female"
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/dev_stage="Various stages; embryonic, post-hatch, immature
and sexually-mature"
/lab_host="E. coli EMDH10B"
/note="Vector: pCMVSPORT6; Library made from three total
RNA pools from each tissue (testis 25%, ovary 25%, and
oviduct 50% of final RNA pool); Single pass sequencing
from 5'-end"
BASE COUNT 137 a 222 c 160 g 128 t
ORIGIN
Query Match 4.7%; Score 80.2; DB 13; Length 647;
Best Local Similarity 69.4%; Pred. No. 1.7e-08;
Matches 109; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1228 CTCACATCTCTGCAGCGCTGTTCAGCGCTCTACACCTCATCAAGACCGGATCCATCG 1287
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QY 1288 CTGCGCTGTCTTGCAGCGGTGTACGGCAACGTACTCCACATCTCTCACACACAAAGCGCT 1347
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Db 453 CTCGCCGTCTGACCGCCACTCGGGCAACACTCTCTACATCTCTACCCACAAAGCAT 512
QY 1348 GCTCAAGTCTCTGCACATCTTTTGTAAAGCTTGGGCCA 1384
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Db 513 CCTCAAGTCTCTCAACTCTTTATTCAGAGGTGCCA 549
RESULT 12
AJ395115 549 bp mRNA linear EST 25-JAN-2001
LOCUS AJ395115 dkfz426 Gallus gallus cDNA clone 21c2r1, mRNA sequence.
DEFINITION AJ395115
ACCESSION AJ395115
VERSION AJ395115.1 GI:7125706
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 649)
AUTHORS Abdrakhmanov, I., Lodygin, D., Geroth, P., Arakawa, H., Law, A., Plachy
J., Korn, B. and Buerstedde, J.M.
TITLE A large database of chicken bursal ESTs as a resource for the
analysis of vertebrate gene function
JOURNAL Genome Res. 10 (12), 2062-2069 (2000)
MEDLINE 20568495
COMMENT Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20521 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
FEATURES
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/strain="CB"
/db_xref="taxon:9031"
/clone="21c2r1"
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/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
BASE COUNT 130 a 227 c 155 g 137 t
ORIGIN

Search completed: June 14, 2003, 15:00:53
Job time : 2570 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:14:12 ; Search time 90 Seconds
(without alignments)
5867.749 Million cell updates/sec

Title: US-09-826-581-3
Perfect score: 1722
Sequence: 1 cctggccctcagatcaaga.....gatgagagctcggtgga 1722

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA:*
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2: /cgn2_6/ptodata/1/ina/5B-COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	68.8	4.0	1576	3	US-09-101-146-63
2	67.6	3.9	7218	1	US-08-232-463-14
3	63.8	3.7	1435	2	US-08-878-989-14
4	63.8	3.7	1435	4	US-09-272-796-14
5	61	3.5	7218	1	US-08-232-463-14
6	39.4	2.3	289	4	US-09-007-005-17
7	39.4	2.3	289	4	US-09-244-796-17
8	39	2.3	53526	3	US-08-658-136-2
9	39	2.3	53577	3	US-08-658-136-1
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11	38.6	2.2	320	4	US-09-165-264-14
12	37.4	2.2	319	4	US-09-165-264-8
13	36.2	2.1	320	4	US-09-165-264-13
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24	34.2	2.0	6306	1	US-08-466-390-3
25	34.2	2.0	6306	1	US-08-470-950-3
26	34.2	2.0	6306	1	US-08-467-781-3
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C 32	34	2.0	6232	4	US-08-456-200B-11	Sequence 11, Appli
C 33	34	2.0	7175	1	US-08-455-543A-8	Sequence 8, Appli
C 34	34	2.0	7175	2	US-08-193-078B-8	Sequence 8, Appli
C 35	34	2.0	7175	2	US-08-223-305C-8	Sequence 8, Appli
C 36	34	2.0	7175	2	US-08-149-097D-8	Sequence 8, Appli
C 37	34	2.0	7175	3	US-08-949-386-8	Sequence 8, Appli
C 38	34	2.0	7175	3	US-08-450-562-8	Sequence 8, Appli
C 39	34	2.0	7175	4	US-08-984-709A-8	Sequence 8, Appli
C 40	34	2.0	7175	4	US-08-450-272-8	Sequence 7, Appli
C 41	34	2.0	7177	4	US-08-268-163-7	Sequence 7, Appli
C 42	34	2.0	7266	3	US-08-713-118-1	Sequence 1, Appli
C 43	34	2.0	7266	3	US-09-452-007-1	Sequence 1, Appli
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C 45	34	2.0	7362	2	US-08-193-078B-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-101-146-63
; Sequence 63, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincents Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1576
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
US-09-101-146-63

Query Match 4.0%; Score 68.8; DB 3; Length 1576;
Best Local Similarity 67.4%; Pred. No. 4.9e+09;
Matches 97; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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Db 561 TGACCAAGTACAGCAAGTACTTGTACATCTCCACCAAGCGCATCTGAAGTTCTT 620

Qy 1360 GCACATCTTCTAAGCCTGGGCC 1383

Db 621 CAAATGTTTACACTGAGTTCC 644

RESULT 2

US-08-232-463-14

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: pTZgpt-F15

US-08-232-463-14

Query Match 3.98; Score 67.6; DB 1; Length 7218;

Best Local Similarity 6.28; Pred. No. 1.9e-08;

Matches 25; Conservative 223; Mismatches 152; Indels 0; Gaps 0;

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Qy 1026 TCTCTCCTTAAGTAGTAGTGGGTGTCTCTGCTCAITTCACCTGAGGCTCTCTCCACACT 1085

Db 1138 YY 1197

Qy 1086 CCCTTCCCACTCCCACTCAGCTCTGAACCTCACTCTTCACTCTAGCGGCACACAGAC 1145

Db 1198 YY 1257

Qy 1146 AAGGAGCCTTGGTCCCTCCCTCTTTTAGGGGCTGGGATGGAGTGTCTCTCC 1205

Db 1258 YY 1317

Qy 1206 TAGGCTGCCGAGGCTCACTGCTCCATCTCTGAGCTGTGAGCTGTCTACACC 1265

Db 1318 YY 1377

Qy 1266 TCATCAAGACGGATCCATCGCTCGCTCGCTGCTTGTGACC 1305

Db 1378 YY 1417

RESULT 3

US-08-878-989-14

; Sequence 14, Application US/08878989

; Patent No. 5885803

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl G.

; APPLICANT: Lal, Preeti

; APPLICANT: Goli, Surya K.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

; TITLE OF INVENTION: KINASES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/878,989

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J J

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0321 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1435 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: PENITUT01

; CLONE: 1452972

US-08-878-989-14


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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-658-136-2

Query Match 2.3%; Score 39; DB 3; Length 53526;
Best Local Similarity 52.1%; Pred. No. 2;
Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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Db 34640 GGAGGAGAGGGGGAGGAGAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34581

QY 837 TAAGGTGAGGATGGGAGTGGGATGTCCTGGAGTGAACAGGGGAGGACAAATAGGAGC 896
Db 34580 GACAGAGGGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34521

QY 897 CTCGGGTGCTGACGAAGGAAGCTGCTGGGACTGCAAGGTGAGG 943
Db 34520 GAGGGGAGGAGGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34474

RESULT 9
US-08-658-136-1/c
; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDER, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: OLAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
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; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-658-136-1

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Best Local Similarity 52.1%; Pred. No. 2;
Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 777 GGAGGGTGAGTGGGAGAGAACCCGGAAGGGGCTGTGGTGATGTTGGCCAGGGCT 836
Db 34635 GGAGGAGAGGGGGAGGAGGAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34576

QY 837 TAAGGTGAGGATGGGAGTGGGATGTCCTGGAGTGAACAGGGGAGGACAAATAGGAGC 896
Db 34575 GACAGAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34516

QY 897 CTCGGGTGCTGACGAAGGAAGCTGCTGGGACTGCAAGGTGAGG 943
Db 34515 GAGGGGAGGAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 34469

RESULT 10
US-09-165-264-7
; Sequence 7, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinayamoorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Locl Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
; US-09-165-264-7

Query Match 2.2%; Score 38.6; DB 4; Length 320;
Best Local Similarity 50.3%; Pred. No.0.33;
Matches 95; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 777 GGAGGGTGAGTGGGAGAGAACCCGGAAGGGGCTGTGGTGATGTTGGCCAGGGCT 836
Db 126 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 185

QY 837 TAAGGTGAGGATGGGAGTGGGATGTCCTGGAGTGAACAGGGGAGGACAAATAGGAGC 896
Db 186 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 245

QY 897 CTCGGGTGCTGACGAAGGAAGCTGCTGGGACTGCAAGGTGAGGACAGGTACCGGT 956
Db 246 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 305

QY 957 CCCTGGCC 965
Db 306 AGCCATGCC 314
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[illegible]

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 16:16:05 ; Search time 288 Seconds
(without alignments)
8658.197 Million cell updates/sec

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Perfect score: 1722
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues
Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published_Applications_NA:*
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 - 2: /cgn2.6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2.6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2.6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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 - 12: /cgn2.6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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 - 14: /cgn2.6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	351	20.4	378	10	US-09-864-761-3373
3	168.2	9.8	1647	10	US-09-826-581-5
4	70.4	4.1	1691	10	US-09-925-297-2
5	68	3.9	11527	9	US-10-108-605-70
6	65	3.8	92	10	US-09-864-761-20146
7	44.2	2.6	1064	10	US-09-804-682-29
8	43	2.5	910	9	US-10-123-155-112
9	42.4	2.5	671	9	US-10-184-644-346
10	42.4	2.5	671	9	US-10-184-634-346
11	40.8	2.4	1512	9	US-09-984-271-18
12	40.6	2.4	671	9	US-10-184-644-346
13	40.6	2.4	671	9	US-10-184-634-346
14	40.2	2.3	1184	9	US-10-123-155-394
15	40	2.3	12733	9	US-10-032-393-47
16	40	2.3	12739	9	US-10-032-393-8
17	39.8	2.3	4158	10	US-09-827-998-15
18	39.8	2.3	5313	10	US-09-827-998-9
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21	39.8	2.3	6719	10	US-09-827-998-1	Sequence 1, Appli
c 22	39.2	2.3	594	9	US-10-123-155-10	Sequence 10, Appli
23	39.2	2.3	40090	10	US-09-820-004-3	Sequence 3, Appli
c 24	39	2.3	53522	9	US-09-904-968A-1	Sequence 1, Appli
25	38.8	2.3	882	9	US-10-184-644-574	Sequence 574, App
26	38.8	2.3	882	9	US-10-184-634-574	Sequence 574, App
27	38.4	2.2	931	9	US-10-198-846-8585	Sequence 8585, Ap
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29	38.2	2.2	2531	10	US-09-764-870-49	Sequence 49, Appli
30	37.6	2.2	777	9	US-10-184-644-348	Sequence 348, App
31	37.6	2.2	777	9	US-10-184-634-348	Sequence 348, App
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c 33	37.2	2.2	463	10	US-09-864-761-5509	Sequence 5509, Ap
c 34	37.2	2.2	531	10	US-09-864-761-22281	Sequence 22281, A
35	37.2	2.2	21423	10	US-09-764-877-2835	Sequence 2835, Ap
c 36	37.2	2.2	659158	9	US-09-771-208-20	Sequence 20, Appli
37	37	2.1	155074	9	US-10-026-188-6	Sequence 6, Appli
c 38	36.8	2.1	440	9	US-10-184-644-202	Sequence 202, App
c 39	36.8	2.1	440	9	US-10-184-634-202	Sequence 202, App
c 40	36.8	2.1	1065	10	US-09-804-682-33	Sequence 33, Appli
41	36.6	2.1	98829	9	US-10-017-724-3	Sequence 3, Appli
c 42	36.4	2.1	765	9	US-10-123-155-38	Sequence 28, Appli
c 43	36.4	2.1	802	9	US-10-184-644-312	Sequence 312, App
c 44	36.4	2.1	802	9	US-10-184-634-312	Sequence 312, App
c 45	36.4	2.1	987	10	US-09-804-682-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1
US-09-826-581-3
; Sequence 3, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SU
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3

Query Match	100.0%;	Score 1722;	DB 10;	Length 1722;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1722;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCTGGCCCTCAGATCAAGAGCCCTTCTTGCTGCTGGTGGCCCAACGGTGTGGGGCAGC	60	
Db	1	CCTGGCCCTCAGATCAAGAGCCCTTCTTGCTGCTGGTGGCCCAACGGTGTGGGGCAGC	60	
Qy	61	CCCTCTATGGGACAGCAGAGAGCTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG	120	
Db	61	CCCTCTATGGGACAGCAGAGAGCTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG	120	
Qy	121	GGAGATGAGGAGGTGAGGGGAGATCTTTGACGGTTGTTCTGGGGCTGATCTCTGATAT	180	
Db	121	GGAGATGAGGAGGTGAGGGGAGATCTTTGACGGTTGTTCTGGGGCTGATCTCTGATAT	180	
Qy	181	ACCACAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCGAGGTGGAGGAAGTCCATCC	240	
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QY 301 ATGACAGCTGACACTTTACCTTCGCTACTCCATGCGCCCTGTGCCATAGGTGCTAGGG 360
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QY 541 CTTCCCTCGAGGATGCTGACCACTGACCTGACCTGACCTGACCTGACCTGACCTGAC 600
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QY 661 AGGGAGTCTCTCTGGAGCTGTGCTCCCTAGAACGCCAGCTTTCTGACTTCTGGAGTC 720
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QY 961 TGGCTGACTTGGCTCTCTGAGAGATCTACCTGCAAGGCTGCTTCAAGCTCTGCT 1020
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QY 1501 ACCTGGTCCCATCTTAACACAGGCTTCCCTGCTGCCCCCGGCTCTCTTCTTACGCGAC 1560
Db 1501 ACCTGGTCCCATCTTAACACAGGCTTCCCTGCTGCCCCCGGCTCTCTTCTTACGCGAC 1560
QY 1561 TATCCAAAGATTTGGGATCGGCACATTTCCGAGACTTGGCTGTGTGGAGACAGCACCC 1620
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Db 1621 CATCTGACTGCTGAGGACTTGTGTGGACCGGCTGTGTGCTGACTGCTGTGTGCTGCTGCT 1680
QY 1681 CGAATGTGTGATCCACCCAGGATGAGAGCTCGGGCTGGA 1722
Db 1681 CGAATGTGTGATCCACCCAGGATGAGAGCTCGGGCTGGA 1722

RESULT 2

US-09-864-761-3373/c
; Sequence 3373, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weisheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687

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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3373
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN BLAD, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4
; OS=09-864-761-3373
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Query Match 20.4%; Score 351; DB 10; Length 378;
Best Local Similarity 99.7%; Pred. No. 4.6e-93;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db	302	CCCTCTATGGGACACGAAGAAGACAGACTTTGTGGTGCAGGAGAGGCTGGGAGGTGAAG	243
QY	121	GGAGTGGAGGAGGTGAGGGGGAGATCTTTACGGTTGTTCTGGGGCTGATCTCTGATAT	180
Db	242	GGAGTGGAGGAGGTGAGGGGGAGATCTTTACGGTTGTTCTGGGGCTGATCTCTGATAT	183
QY	181	ACCACAGCTTGGCTTCAGGCCCAAGCCCAAGGGCCAGGGTGGAGGAAGTCCATCC	240
Db	182	ACCACAGCTTGGCTTCAGGCCCAAGCCCAAGGGCCAGGGTGGAGGAAGTCCATCC	123
QY	241	GGAGTGTGATGGCCAGCTGGGACACCTCTGGGCTCAATTTCCCACCTCTGTGGAGCCGT	300
Db	122	GGAGTGTGATGGCCAGCTGGGAGACCTTGGGCTCAATTTCCCACCTCTGTGGAGCCGT	63
QY	301	ATGACCAGCTGCACCTTCACTTCCCTACTGCATGSCCCTGTGCCATAGGTGCTAGGG	360
Db	62	ATGACCAGCTGCACCTTTCACCTCCCTTACCTGCCATGSCCCTGTG-CATAGGTGCTAGGG	4
QY	361	AGC 363	
Db	3	AGC 1	

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RESULT 3
US-09-826-581-5
: Sequence 5, Application US/09826581
: Patent No. US20020142310A1
: GENERAL INFORMATION
: APPLICANT: Andersson, Leif
: APPLICANT: Lutman, L. Holger
: APPLICANT: Marklund, Stefan
: TITLE OF INVENTION: VARIANTS OF THE HUMAN
: FILE REFERENCE: 11145-007001
: CURRENT APPLICATION NUMBER: US/09/826,581
: CURRENT FILING DATE: 2001-04-05
: PRIOR APPLICATION NUMBER: US 60/195,665
: PRIOR FILING DATE: 2000-04-07
: NUMBER OF SEQ IDS: 14

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20... (1486)
US-09-826-581-5

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Query Match 9.8%; Score 168.2; DB 10; Length 1647;
Best Local Similarity 95.6%; Pred. No. 2.7e-39;
Matches 173; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy	1510	CCATCTTACCAAGGTTCTGCTGCTGCCCGGGCCCTCTTCTCTACCGCACTATCCAAGA	1569	TTTTGGGATCGGCACATCTCCGAGACTTTGGCTGTGGTGTGGAGACACGCCATCTGCAC	1629	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1689	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1748
Db	1009	CCTGCACATCTTTGGTGTCCCTGTGCTGCCCGGGCCCTCTTCTCTACCGCACTATCCAAGA	1068	TTTTGGGATCGGCACATCTCCGAGACTTTGGCTGTGGTGTGGAGACACGCCATCTGCAC	1128	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1188	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1247
Qy	1570	TTTTGGGATCGGCACATCTCCGAGACTTTGGCTGTGGTGTGGAGACACGCCATCTGCAC	1629	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1689	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1748	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1807
Db	1069	TTTTGGGATCGGCACATCTCCGAGACTTTGGCTGTGGTGTGGAGACACGCCATCTGCAC	1128	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1188	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1247	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1306
Qy	1630	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1689	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1748	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1807	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1866
Db	1129	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1188	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1247	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1306	TGCACCTGGACATCTTTGTGGACCGCGCTGTGTCTGACACTTGGCTGTGGTCAACGAATGTGG	1365
Qy	1690	T 1690							
Db	1189	T 1189							

RESULT 4

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US-09-925-297-2
; Sequence 2, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Protein
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1691
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1093)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-925-297-2

```

Query Match 4.1%; Score 70.4; DB 10; Length 1691;
Best Local Similarity 68.1%; Pred. No. 1.3e-10;
Matches 98: Conservative 0; Mismatches 46; Indels 0; Gaps 0

Qy	1240	CAGCGTGTGTTGAGCTGTCTACACCCATCATCAGACACGGATCCATCGCTTGCCTGTTCT	1295
Db	448	CAGCTGTGTTGATGCTGTCTCTTCATTAATTCGGAACAGATCCACAGGCTGCAGATTAT	507
Qy	1300	TGACCCGGTGTGAGCAAGTACTCCACATCTCTCACACAAAGCCGTGCTCAAGTTCT	1355
Db	508	TGACCCGAATCATGGCAATACTTTGTATCTCTCCACACAGCGCATTCGAGTTCT	567
Qy	1360	GCACATCTTTGTAAAGCCTGGGCC	1383
Db	568	CAAAATGTTTATCAGTGAGTTCCC	591

```
RESULT 5
US-10-108-605-70
; Sequence 70, Application US/10108605
; Patent No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stan, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; FILE REFERENCE: 31133B
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/10/108,605
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2000-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 11527
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-108-605-70

Query Match          3.9%; Score 68; DB 9; Length 11527;
Best Local Similarity 69.7%; Pred. No. 1e-09;
Matches 92; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1243 CCTGTTTAACTCTTACACCTCATCAAGACGGATCCATCGCTGCCTGTTCTTCA 1302
Db 10193 CCTCATGACGCTCAAAATTTCTATCCACGCGCATATCGCTGCGCGTCATCGA 10252

QY 1303 CCGGTGTGAGGCAAGTACTCCACATCTCTACACACAAAGCGCTGCTCAAGTTCTCTGCA 1362
Db 10253 TCGGGCGACGGCAATCTCTCTACATCTTGACACATAAAGCATCTAGGTCTCTTT 10312

QY 1363 CATCTTTGTAG 1374
Db 10313 CCTATACGTGAG 10324

RESULT 6
US-09-864-761-20146/c
; Sequence 20146, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20146
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009974.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
; OTHER INFORMATION: NT HIT: gill1430152, EVALUE 2.00e-22
; OTHER INFORMATION: EST_HUMAN HIT: BE32467.1, EVALUE 3.00e-06
; OTHER INFORMATION: SWISSPROT HIT: P54619, EVALUE 3.00e-03
US-09-864-761-20146

Query Match          3.8%; Score 65; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGCCCTCAGATCAAGAAGGCTTCTTGTCTGTGGCCACGCTGTGGGGCAGC 60
Db 65 CCTGGCCCTCAGATCAAGAAGGCTTCTTGTCTGTGGCCACGCTGTGGGGCAGC 6

QY 61 CCCTC 65
Db 5 CCCTC 1

RESULT 7
US-09-804-682-29/c
; Sequence 29, Application US/09804682
; Patent No. US20020106765A1
; GENERAL INFORMATION:
; APPLICANT: Kinders, Robert
; APPLICANT: Corey, Michael J.
; TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE SAME AND METHODS FOR SCREENING FOR OR
; TITLE OF INVENTION: MODULATING THE SAME
; FILE REFERENCE: 130001.406
; CURRENT APPLICATION NUMBER: US/09/804,682
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 29
```

```

; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5, 6, 16, 21, 24, 25, 33, 39, 72, 110, 209, 214, 231, 232,
; LOCATION: 235, 237, 238, 244, 245, 246, 256, 282, 292, 297, 306, 319,
; LOCATION: 321, 323, 330, 334, 340, 349, 354, 355, 363, 372, 376, 378,
; LOCATION: 397, 405, 432, 437, 454, 455, 457, 458, 459, 468, 470
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: 485, 487, 488
; LOCATION: 583, 600, 611, 613, 623, 624, 652, 654, 674, 681, 687, 691,
; LOCATION: 694, 701, 713, 716, 720, 721, 725, 731, 734, 735, 739, 743,
; LOCATION: 744, 781, 782, 785, 789, 799, 803, 821, 823, 847, 852
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: 858, 878, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948,
; LOCATION: 957, 961, 965, 981, 991, 993, 1001, 1002, 1005, 1011, 1018,
; LOCATION: 1043, 1047, 1049, 1051, 1054, 1056
; OTHER INFORMATION: n = A,T,C or G
;
US-09-804-682-29

Query Match          2.6%; Score 44.2; DB 10; Length 1064;
Best Local Similarity 47.8%; Pred. No. 0.0058;
Matches 85; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 777 GGAGGGTGAGTGGGAGAGGACCCGGAAGGGGCTGTGTTGATGGTGGCCAGGGCT 836
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 865 GGAGGAGNGGNGGAGGGGNGGAAGGGGGAGGAGGAGGGGNGGNGGGGGGGGG 806
GGAGGAGNGGNGGAGGGGNGGAAGGGGGGAGGAGGAGGGGNGGNGGGGGGGGGGGGG
QY 837 TAAGGTGAGGTGGCAGTGGGATGTCCTGGAGTGAACAGGGAGGAGCAATAGGAGC 896
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 805 GNGGGNGGGGGGANGGNGGNGGNGGGGGGAGGAGGAGGGGGGTAGGGGGGGAA 746
GNGGGNGGGGGGGGANGGNGGNGGNGGGGGGAGGAGGAGGGGGGGGTAGGGGGGGAA
QY 897 CTCGGTGCCTGACGGAAGGAGGCTGCTGGGACTCCAAAGGTGAGGCAGGTGACCG 954
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 745 GNGGGNGGNGGNGGAGGGAGNGGNGGNGAGGTGAGGGGGGNGGNGANAGG 688
GNGGGNGGNGGNGGAGGGAGNGGNGGNGGNGGNGAGGTGAGGGGGGNGGNGANAGG

RESULT 8
US-10-123-155-112
; Sequence 112, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 112
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-123-155-112
Query Match          2.5%; Score 43; DB 9; Length 910;
Best Local Similarity 13.2%; Pred. No. 0.013;
Matches 48; Conservative 93; Mismatches 224; Indels 0; Gaps 0;

QY 71 GACACCAAGAAGCAGAGCTTTGGGTGAGGAGAGGCTGGGAGGTGAAGGAGATGGAG 130
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 536 GVVLPDPQSPQSGDCVWGVHVEKRILLQVEILLNVREGDMLTFLDGDSPSARVLAQ 595
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 131 GAGGTGAGGGGAGATCTTGACGGTTGTCGCGGCTGATCTGTATATACCAAGCT 190
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 596 LRGPQRRRLSSPDLTLOFQAPPNPGPLGQGFVLFHFEKVRNDTCPELPPPEWGR 655
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 191 TGGCTTCAGGCCAGCCAGCCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 250
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 656 TASHGDLIRGLVLYQCEPGYELLGSDILTCQMDLSAAPPACQKIMTCADPBIANGH 715
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 251 TGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTGTGGAGCGCTATGACGACT 310
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 716 RTASDAGFPVGVSHVYRCLPGYSLEGAAMTCYSYSDTGTPKWSDRVPKALKYECPLNPG 775
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 311 GACACCTTTCACCTCCCTACTCATGTCGCGCTGTGCCATAGGTGCTAGGAGGACAAATGGG 370
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 776 VPENGYQTLVYKHQAGESLRFYEGFELIGEVITTCVPGHPSQMTSOPPLCKVTQTTD 835
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 371 GGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 430
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 836 PSRQLEGNLALAILLPLGLVIVLGSVYIYTKQKSLFPGFSGSHSYPTVBSDFSN 895
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 431 TQCCA 435
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 896 PLYEA 900
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 9
US-10-184-644-346/c
; Sequence 346, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-184-644-346
Query Match          2.5%; Score 42.4; DB 9; Length 671;
Best Local Similarity 5.3%; Pred. No. 0.018;
Matches 20; Conservative 151; Mismatches 206; Indels 0; Gaps 0;

QY 924 CTGCGGAGTGCAGGTGAGGAGGAGTACCGGCTCCCTGGCGCTGACCTGCTCTTCTG 983
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 515 M....SAB..AC....TN.GYMBH.SHBM.T.N..SD.M.M..BS..MMM.BMYHKS.C 456
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 984 CAGAGATCTACCTGCAAGGCTGCTTCAAGGCTCTGGTCTCCATCTCTCTTAATGATAGT 1043
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
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```
Db 455 .SWYAY.BMB.MT..M...YBYM.M.C.MYT..ASSS..MNTSMNT.Y...T...SHSS 396
QY 1044 GGGTGTCTCTGCTCACTTACCTGAGCCTCTCTCCACAGTTCCTCCCTTCCCCAGTCCAC 1103
Db 395 S..CYCYMYCYMB..HH.Y..HCSSCCSY.T.CYHY.YYY.M.M..Y.YY....336
QY 1104 TCAGCTCTGAACCTCACTCTTCATCCTAGCGGCACACAGAGGAGCCTGGTGCC 1163
Db 335 .YYYYT...YYT.HYTM.S.YHB.HSHSHSSSS..Y..M.MYC.M...M.T.MYC 276
QY 1164 TGCCCTCTTTTAGGCGCTGGAGTGTCTCTCCCTAGGCTGCCCGAGGCTC 1223
Db 275 Y..MBSBHSBSSSSSSSTSTYKTB...MCHSHMNSHSHSTS.TMMMYTCC..CY 216
QY 1224 ACTGCTCCCATCTCTGACGCTGTGAAGCTGTCTACACCTCATCAAGAACCGGATCC 1283
Db 215 .TYBTMM..A.H.HSAM.S.SSS.SN...S.SBST.H.HSSTMYTMSBSKM.T.AMYM 156
QY 1284 ATCGCTGCTCTTCTT 1300
Db 155 .CSNHSSMNSHSHS.KY 139

RESULT 10
US-10-184-634-346/c
; Sequence 346, Application US/10184634
; Publication No. US20030068641
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-346

Query Match 2.5%; Score 42.4; DB 9; Length 671;
Best Local Similarity 5.3%; Pred. No. 0.018;
Matches 20; Conservative 151; Mismatches 206; Indels 0; Gaps 0;

QY 924 CTTGGAGTCAAGGTGAGGAGGTGACCGGCTCCCTGCGCTGACTCTGCTCTTCTG 983
Db 515 M....SAB..AC....TN.GYMBH.SHEM.T.M..SD.M..M..BS..MM.BMYHKS.C 456
QY 984 CAGAGATCTACCTGACGAGCTCTCAAGCTCTGTCTCCATCTCTCTCTATGATAGT 1043
Db 455 .SYMYAY.BMB.MT..M...YBYM.M.C.MYT..ASSS..MNTSMNT.Y...T...SHSS 396
QY 1044 GGGTGTCTCTGCTCACTTACCTGAGCCTCTCTCCACAGTTCCTCCCTCCCGAGTCCAC 1103
Db 395 S..CYCYMYCYMB..HH.Y..HCSSCCSY.T.CYHY.YYY.M.M..Y.YY....336
QY 1104 TCAGCTCTGAACCTCACTCTTCATCCTAGCGGCACACAGAGGAGCCTGGTGCC 1163
Db 335 .YYYYT...YYT.HYTM.S.YHB.HSHSHSSSS..Y..M.MYC.M...M.T.MYC 276
```

RESULT 12

```
QY 1164 TGCCCTCTTTTAGGCGCTGGAGTGTCTCTCTCCCTAGGCTGCCCGAGGCTC 1223
Db 275 Y..MBSBHSBSSSSSSSTSTYKTB...MCHSHMNSHSHSTS.TMMMYTCC..CY 216
QY 1224 ACTGCTCCCATCTCTGACGCTGTGAAGCTGTCTACACCTCATCAAGAACCGGATCC 1283
Db 215 .TYBTMM..A.H.HSAM.S.SSS.SN...S.SBST.H.HSSTMYTMSBSKM.T.AMYM 156
QY 1284 ATCGCTGCTCTTCTT 1300
Db 155 .CSNHSSMNSHSHS.KY 139

RESULT 11
US-09-984-271-18/c
; Sequence 18, Application US/09984271
; Publication No. US20030040088A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/984,271
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (207)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (209)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (521)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-984-271-18

Query Match 2.4%; Score 40.8; DB 9; Length 1512;
Best Local Similarity 49.1%; Pred. No. 0.062;
Matches 105; Conservative 1; Mismatches 108; Indels 0; Gaps 0;

QY 386 RAGAGCCCCACTTCTCAGSCCTGGGGGCTGCCCCACTGCTCTCTTCCACAGTCCCCAC 445
Db 1286 AAGTGTGCGACAGACAGAGGAGGAGGAGGCTCTGCTGCTGCGCCAGCTTTRGG 1227
QY 446 TGTGTCTCAGACACAGACACTGCGAGGCTGGGAGGGAGTCTGACCTCAACCTGCTT 505
Db 1226 GAGGGGAAGGGCTAGAAACTCCACAGAGAGGGGGTTCGACCCACTATGGACAGT 1167
QY 506 CCACCCAAAGCCCGGGCTGACCTCTCCCTCCCGCCCCCTCCCTGCGAGGATGCTGACCAT 565
Db 1166 CTTACACAGCCACGAGGTTCACCCCGCTTTCCACCACTCTGCTGCTGCGCTGGGCCCC 1107
QY 566 CACTGACTTCTATCTGCTGCTGCATCGCTACTAC 599
Db 1106 CACACTCTCTCATATATACATCTCATCTCC 1073
```



```
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3430R1C217  
; CURRENT APPLICATION NUMBER: US/10/184,634  
; CURRENT FILING DATE: 2002-06-28  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 346  
; LENGTH: 671  
; TYPE: PRF  
; ORGANISM: Homo Sapien  
US-10-184--634-346
```

```
Query Match          2.4%; Score 40.6; DB 9; Length 671;  
Best Local Similarity    7.5%; Pred.No. 0.059;  
Matches   25; Conservative 135; Mismatches 173; Indels      0; Gaps     0;
```

```
QY       644 CAGAGGGCGGCGGAGGGAGTGCTTCTGTGGACCTGTGCCTAGAACCAGTCGT 703  
         :|::: |::: ||::: |: :::: |::: |::: |::: |::: |::: |:::  
Db        89 HASYSADPPVSSSDSPEAFNPADGSDADEDDRCGVMAVTAVATAASDRMESDSDK 148  
  
QY       704 TTC TGACTCTCGAGTCCTGCGATGCTCTAGTCCAGATCTATGAGATTGAACAACAT 763  
         :||::: |::: |::: |::: |::: |::: |::: |::: |::: |:::  
Db       149 SSDNSGLKRTPALKMSVKRKARKASSDLLDAQSVSPSEENSESESSEKTISDQTTPKE 208  
  
QY       764 AAGATTGAGACCTGGAGGGGTGAGTTGGGGAGAGAACCCGGAAAGGGCTGTTGGTGATG 823  
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QY       884 GGCAANTAGCACGCTCGGTGCTTGACGGAAGGAAGCTGCTGGGACTCGAAGGTGAGG 943  
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RESULT 14  
US-10-123-155-394/c  
Sequence 394, Application US/10123155  
Publication No. US20030068794A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini,Maureen  
APPLICANT: DeForge,Laura  
APPLICANT: Desnoyers,Luc  
APPLICANT: Filvaroff,Ellen  
APPLICANT: Gao,Wei-Qiang  
APPLICANT: Gerritsen,Mary E.  
APPLICANT: Goddard,Audrey  
APPLICANT: Godowski,Paul J.  
APPLICANT: Gurney,Austin L.  
APPLICANT: Sherwood,Steven  
APPLICANT: Smith,Victoria  
APPLICANT: Stewart,Timothy A.  
APPLICANT: Tumas,Daniel  
APPLICANT: Watanabe,Colin K  
APPLICANT: Wood,William  
APPLICANT: Zhang,Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C30  
CURRENT APPLICATION NUMBER: US/10/123,155  
CURRENT FILING DATE: 2002-04-15  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 394  
LENGTH: 1184
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 01:49:14 ; Search time 192.613 seconds
(without alignments)
9216.782 Million cell updates/sec
Title: US-09-826-581-3_COPY_612_672
Perfect score: 61
Sequence: 1 gtgaggagtgctgggaat.....gggggggagggagtcctc 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
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- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
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- 23: em.pat.*
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- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pin.*
- 35: em.htg_rod.*
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- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	1722	6	AX281580 Sequence
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c 3	59.4	97.4	152129	2	AC027416 Homo sapi
c 4	30.4	49.8	91247	2	AC106624 Rattus no
c 5	29.8	48.9	127181	2	AC118404 Rattus no
c 6	29.2	47.9	281000	10	MMU276505 Mus muscu
c 7	29	47.5	140819	10	AC121886 Mus muscu
c 8	28.8	47.2	117082	2	AC126076 Rattus no
c 9	28.8	47.2	155645	2	AC094964 Rattus no
c 10	28.6	46.9	899	11	G75185
c 11	28.6	46.9	945	11	G74939
c 12	28.6	46.9	215046	2	AF354168 Ovis arie
c 13	28.4	46.6	184454	2	AC128911 Rattus no
c 14	28.2	46.2	164800	2	AC113756 Rattus no
c 15	27.8	45.6	170476	2	AC111883 Rattus no
c 16	27.8	45.6	191720	2	AC109982 Rattus no
c 17	27.6	45.2	653	11	PM7F7B
c 18	27.6	45.2	127794	9	AL138688 Human DNA
c 19	27.6	45.2	214971	2	AC094543 Rattus no
c 20	27.4	44.9	48489	8	AC091776 Chlamydom
c 21	27.4	44.9	65932	8	AP004938 Lotus jap
c 22	27.4	44.9	68736	2	AC090435 Chlamydom
c 23	27.4	44.9	69660	2	AC106670 Rattus no
c 24	27.4	44.9	134366	2	AC119661 Rattus no
c 25	27.4	44.9	161951	2	CNS078PU
c 26	27.4	44.9	166007	2	AP004862 Oryza sat
c 27	27.4	44.9	183450	2	AC115443 Rattus no
c 28	27.4	44.9	207374	9	CNS078PU
c 29	27.4	44.9	292136	2	AC103544 Rattus no
c 30	27.4	44.9	300605	2	AC098460 Rattus no
c 31	27.2	44.6	36582	2	AC103128 Rattus no
c 32	27.2	44.6	113633	2	AC094512 Rattus no
c 33	27.2	44.6	116239	2	AC117323 Rattus no
c 34	27.2	44.6	143899	2	AC013606 Homo sapi
c 35	27.2	44.6	143899	6	AX411543 Sequence
c 36	27.2	44.6	154126	2	AC010758 Homo sapi
c 37	27.2	44.6	157437	2	AC021669 Homo sapi
c 38	27.2	44.6	164290	2	AC096454 Rattus no
c 39	27.2	44.6	165314	2	AC103081 Rattus no
c 40	27.2	44.6	165434	2	AC087505 Homo sapi
c 41	27.2	44.6	177107	2	AC109908 Rattus no
c 42	27.2	44.6	177433	9	AC011747 Homo sapi
c 43	27.2	44.6	178000	9	AP002893 Homo sapi
c 44	27.2	44.6	178744	2	AC117508 Homo sapi
c 45	27.2	44.6	184668	2	AC096340 Rattus no

ALIGNMENTS

RESULT 1	AX281580	Sequence 3 from Patent WO0177305.	1722 bp	DNA	linear	PAT 03-NOV-2001
AX281580	AX281580	Sequence 3 from Patent WO0177305.				
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DEFINITION	AX281580					
ACCESSION	AX281580					
VERSION	AX281580.1	GI:16608831				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Andersson, L., Luthman, H. and Marklund, S.					
TITLE	Varianants of the human amp-activated protein kinase gamma 3 subunit					
JOURNAL	Patent: WO 0177305-A 3 18-OCT-2001;					

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                    /db_xref="taxon:9606"
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Db 612 GTGACAGTGGCTGGGAATCTTATGGCACCACGAGCGGGCGGAGGGAGTCCCT 671
QY 61 C 61
Db 672 C 672

RESULT 2
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DEFINITION Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
ACCESSION AC009974
VERSION AC009974.9 GI:16799058
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 206854)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
9847074
REFERENCE 2 (bases 1 to 206854)
AUTHORS Harris,A. and Cotton,M.
TITLE The sequence of Homo sapiens BAC clone RP11-459119
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 206854)
Waterston,R.H.
TITLE Direct Submission
Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 206854)
Waterston,R.H.
TITLE Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 206854)
Waterston,R.
TITLE Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 8, 2001 this sequence version replaced gi:13431203.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
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Center project name: H_NH0459119

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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://dcpac.med.buffalo.edu>)

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

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misc_feature 684..763 /note="match to EST EG992568 (NID:g14396638)"
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Qy 61 C 61
Db 166027 C 166027
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LOCUS Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
DEFINITION unordered pieces.
ACCESSION AC027416
VERSION AC027416.2 GI:8317289
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 152129)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL Unpublished
TITLE Homo sapiens, clone RP11-504G11
REFERENCE 2 (bases 1 to 152129)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F., Boguslavsky,L., Bouckgalter,B., Brown,A., Burkett,G., Campiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lenocky,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenda,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7458
Center clone name: 504_G.11
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads

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 DEFINITION *** 52 unordered pieces.
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 VERSION AC106624.2 GI:21734702
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 SOURCE Norway rat.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 91247)
 AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amarutunge,H.C., Are,J.R., Ayele,M., Banks,T.,
 Barbara,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
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 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 Delaney,K.R., Deigado,O., Denna,A.L., Ding,Y., Dinh,H.H.,
 Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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 Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
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 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
 Homsai,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
 Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
 Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
 Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
 Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
 Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
 Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
 Massey,E., Mahoney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
 Miner,C., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
 Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
 Nguyen,N., Nickerson,E., Nwokkwo,S., Ogih,M., Okunoda,G.,
 Oquanyine,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
 Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
 Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
 Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstock,G. and Gibbs,R.
 Direct Submission

TITLE
 JOURNAL
 REFERENCE 2 (bases 1 to 91247)
 AUTHORS Worley,K.C.

TITLE
JOURNALREFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Direct Submission
 Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 91247)
 Worley, K.C.
 Direct Submission
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 11, 2002 this sequence version replaced gi:18139148.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information

 Center project name: GLSC
 Center clone name: CH230-22513
 ----- Summary Statistics

Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye: 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 46677 bases at least Q40
 Consensus quality: 50328 bases at least Q30
 Consensus quality: 53862 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 52 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1038: contig of 1038 bp in length
 * 1039 1138: gap of unknown length
 * 1139 2313: contig of 1175 bp in length
 * 2314 2413: gap of unknown length
 * 2414 3595: contig of 1182 bp in length
 * 3596 3595: gap of unknown length
 * 3596 4800: contig of 1105 bp in length
 * 4801 4900: gap of unknown length
 * 4901 6042: contig of 1142 bp in length
 * 6043 6142: gap of unknown length
 * 6143 7321: contig of 1179 bp in length
 * 7322 7421: gap of unknown length
 * 7422 8609: contig of 1188 bp in length
 * 8610 8709: gap of unknown length
 * 8710 9839: contig of 1130 bp in length
 * 9840 9939: gap of unknown length
 * 9940 11449: contig of 1510 bp in length
 * 11450 11549: gap of unknown length
 * 11550 12574: contig of 1025 bp in length
 * 12575 12674: gap of unknown length
 * 12675 13944: contig of 1270 bp in length
 * 13945 14044: gap of unknown length
 * 14045 15767: contig of 1723 bp in length
 * 15768 15867: gap of unknown length
 * 15868 17437: contig of 1570 bp in length
 * 17438 17537: gap of unknown length
 * 17538 18647: contig of 1110 bp in length
 * 18648 18747: gap of unknown length
 * 18748 20307: contig of 1560 bp in length
 * 20308 20407: gap of unknown length
 * 20408 22599: contig of 2192 bp in length
 * 22600 23714: contig of 1015 bp in length
 * 23715 23814: gap of unknown length
 * 23815 25593: contig of 1779 bp in length
 * 25594 25693: gap of unknown length

JOURNAL

Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Jul 14, 2002 this sequence version replaced gi:20162777.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GUIR

Center clone name: CH230-150Q18

----- Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap: version 0.990329

Consensus quality: 65762 bases at least Q40

Consensus quality: 72462 bases at least Q30

Consensus quality: 77125 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 56 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 1248: contig of 1248 bp in length

* 1249 1348: gap of unknown length

* 1349 2555: contig of 1207 bp in length

* 2556 2656: gap of unknown length

* 2657 4350: contig of 1695 bp in length

* 4351 4450: gap of unknown length

* 4451 5648: contig of 1198 bp in length

* 5649 5749: gap of unknown length

* 5749 7177: contig of 1428 bp in length

* 7177 8374: contig of 1098 bp in length

* 8375 8474: gap of unknown length

* 8475 9627: contig of 1153 bp in length

* 9628 9728: gap of unknown length

* 9728 11358: contig of 1630 bp in length

* 11358 12463: gap of unknown length

* 12463 12562: contig of 1005 bp in length

* 12563 13840: contig of 1278 bp in length

* 13841 13940: gap of unknown length

* 13941 15505: contig of 1565 bp in length

* 15506 15605: gap of unknown length

* 15606 17068: contig of 1462 bp in length

* 17068 17168: gap of unknown length

* 17168 19112: contig of 1945 bp in length

* 19112 19212: gap of unknown length

* 19213 20573: contig of 1361 bp in length

* 20574 20674: gap of unknown length

* 20674 21860: contig of 1187 bp in length

* 21861 21960: gap of unknown length

* 21961 23467: contig of 1507 bp in length

* 23468 23508: gap of unknown length

* 23508 25009: contig of 1941 bp in length

* 25009 25609: gap of unknown length

* 25609 27138: contig of 1529 bp in length

* 27138 27237: gap of unknown length

* 27237 28297: contig of 1060 bp in length

* 28298 28398: gap of unknown length

* 28398 29810: contig of 1412 bp in length

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* 32167 32168: gap of unknown length

* 32168 34176: contig of 2009 bp in length

Query Match 48.9% Score 29.8; DB 2; Length 127181;

Best Local Similarity 70.2%; Pred. No. 13;

Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 GTGAGGAGTGGCTGGGAATCTTATGGCACCCAGAGGGGGGGGGAGT 57

DB 33643 GGGAGGTGCGGGGGGGGGTGGATCCCGAGGGGGGGGGCGCT 33587

RESULT 6

MMU276505

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

carls gene; Cdkn1c gene; cyclin-dependent kinase inhibitor 1C;

cysteinyl-L-tyrosine synthetase; IPI gene; Itm gene; Nap114 gene;

nucleosome assembly protein 1-like 4 protein; Obphi gene; oxysterol

binding protein; Tnfrh1 gene; Tnfrh2 gene; tumor necrosis factor

receptor p60 homologue 1; tumor necrosis factor receptor p60

homologue 2; tumor suppressing subtransferable candidate 5.

western European house mouse.

SOURCE

ORGANISM

Mus musculus domesticus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

Engemann, S., Strodicke, M., Paulsen, M., Franck, O., Reinhardt, R.,

Lane, N., Reik, W. and Walter, J.

Sequence and functional comparison in the Beckwith-Wiedemann

region: implications for a novel imprinting centre and extended

imprinting

Hum. Mol. Genet. 9 (18), 2691-2706 (2000)

20519229

11063728

REFERENCE

AUTHORS

Engemann, S.

Direct Submission

Submitted (17-MAR-2000) Engemann S., Dep. Trautner,

Max-Planck-Institut fuer Molekulare Genetik, Innestrasse 73, 14195

Berlin, GERMANY

Revised by author 22-MAY-2000

3 (bases 1 to 281000)

Engemann, S.

Direct Submission

Submitted (22-NOV-2000) Engemann S., Dep. Trautner,

Max-Planck-Institut fuer Molekulare Genetik, Innestrasse 73, 14195

Berlin, GERMANY

4 (bases 1 to 281000)

Engemann, S.

Direct Submission

Submitted (24-JAN-2001) Engemann S., Dep. Trautner,

Max-Planck-Institut fuer Molekulare Genetik, Innestrasse 73, 14195

Berlin, GERMANY

On Jan 27, 2001 this sequence version replaced gi:11191799.

related accession numbers AJ300452-AJ300460

has a 1000 bp overlap with AJ271885.

FEATURES

Location/Qualifiers

1..281000

/organism="Mus musculus domesticus"

/strain="129 SV"

/sub_species="domesticus"

/db_xref="taxon:10092"

/chromosome="7"

/cell_line="CJ7"

1431..28364

/gene="Obphi"

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7906..8110,9688..9772,11978..12149,12416..12608,

13783..13967,14347..14428,15828..15926,16308..16404,

17790..17888,21514..21610,21996..22086,22181..22317,

22743..22928,23228..23354,24142..24268,25136..25238,

27169..28364)

/gene="Obphi"

join(1432..1455,3536..3622,7265..7345,7478..7578,

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22743..22928,23228..23354,24142..24268,25136..25238,

27169..27307)

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SWAYKPKGVSQSIQTQPLPSSYLIFRAASESDGRCWDALEALRCSSLLSLSTCK

QGDQGGSSPDASPSLYGLPTSATIPDDLFPLNGSALENDAFSDKSERENABDS

AETQDRKTNESDLDSPGGPWGTTTYVQVEGELDETSQVETVSEENKSLM

WLLRLRFGMDLSRVLPFTVLEPRSFGLKSDYYHGDLLSRAAEDDPYCRMKLV

LRWYLSGFYKPKGKIPNPILGETFCRWLHPOTNSHTFYIAEOVSHHPVPSAFYV

SNKDGCMGSGSITAKSKFYGNSLSALLDGKAKLFLNKEEYTLMPYAHGEGULYG

TYTMELGKYNIECEKNNLQAEIDFKLFFGSSANINQISGKIMSGEEVYARLGGHW

DRDVFTESSGGTEKFWTPEEVRORLKRHTVLLLEQSELERIWOHVTRAREG

DQKATQKESYLEEAQRARHQSLTPWKQLFLDPLDTQEWRYEDLSFMDPLK

DIAYQDQDILHTLQRTMSGQTTFLGSPDSRHKRPDRRLRKASQPSGHSQVLES

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/gene="Obphi"

/number=4

7906..8110

/gene="Obphi"

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/gene="Obphi"

/number=18

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	/codon_start=1 /product="tumor necrosis factor receptor p60 homologue" /protein_id="CAC27352.1" /db_xref="GI:12583597" /db_xref="SPTREMBL:Q9ER63" /translation="WPEYSVFNCPDGFYQSDNVCKTCGTFVKAPCKIPIHTQGQCE KCHRGFTTKDNGLHDHCLSTCDKDNNVADCSDRKECCOIGLYYYDKPFPESC RPTKCQQGPVPVLQEENCTANTVCSSVSNPNWLFLMLLVFCI"
exon	35584..35662 /gene="Tnfrhl" /number=1 37049..37176 /gene="Tnfrhl"
exon	/number=2 46179..46291 /gene="Tnfrhl"
exon	/number=3 47068..47141 /gene="Tnfrhl"
exon	/number=4 48531..48580 /gene="Tnfrhl"
gene	/number=5 join(67525..67596,72244..72334,73711..73838,76251..76363, 77140..77213,77826..77868,78677..78828) /gene="Tnfrh2"
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Query Match 47.98; Score 29.2; DB 10; Length 281000;	
Best Local Similarity 69.0%; Pred.No.18;	
Matches 40; Conservative 0; Mismatches 18; Indels 0; Gaps 0;	
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RESULT 7	
AC121886/c	
LOCUS	AC121886 140819 bp DNA linear ROD 16-JUL-2002
DEFINITION	Mus musculus clone RP24-14IK3, complete sequence.
ACCESSION	AC121886
VERSION	AC121886.2 GI:21844658

KEYWORDS	HTG.
SOURCE	House mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 140819)
TITLE	McPherson,J.D. and Waterston,R.H.
JOURNAL	The sequence of Mus musculus clone
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 140819)
TITLE	McPherson,J.D. and Waterston,R.H.
JOURNAL	Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	3 (bases 1 to 140819)
AUTHORS	McPherson,J.D. and Waterston,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT	On Jul 16, 2002 this sequence version replaced gi:21040003.
FEATURES	<p>----- Genome Center -----</p> <p>Center: Washington University Genome Sequencing Center</p> <p>Center code: WUGSC</p> <p>Web site: http://genome.wustl.edu/gsc/index.shtml</p> <p>Contact: submissions@watson.wustl.edu</p> <p>----- Project Information -----</p> <p>Center project name: W.BB0141K03</p> <p>-----</p> <p>Location/Qualifiers</p> <p>1..140819</p> <p>/organism="Mus musculus"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="RP24-141K3"</p> <p>35774 a 34391 c 35026 g 35628 t</p>
BASE COUNT	
ORIGIN	
Query Match	47.5%; Score 29; DB 10; Length 140819;
Best Local Similarity	77.8%; Pred. No. 23;
Matches	35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY	2 TGAGGAGTGGCTGGGAATCTATTGGCAGCCAGCGGGGGG 46
Db	109529 TGGGGAGGGGCTGGCAGAGTCCTCAGGAGCCAGAGGGCTGGAG 109485
RESULT 8	
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LOCUS	AC126076 117082 bp DNA linear HTG 24-JUL-2002
DEFINITION	Rattus norvegicus clone CH230-143P6, *** SEQUENCING IN PROGRESS
ACCESSION	***, 63 unordered pieces.
VERSION	AC126076.2 GI:21699142
KEYWORDS	HTG; HTGS_PHASE1.
SOURCE	Rattus norvegicus.
ORGANISM	Rattus norvegicus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AUTHORS	1 (bases 1 to 117082)
	Murny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Ayele,M., Banks,T., Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouack,J., Bowles,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Byrrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chaves,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinsh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,

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Gabisl,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haviak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsso,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mahoney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenwo,S., Oguh,M., Okwundu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
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Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Teifrod,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 117082)
Worley,K.C.
Direct Submission
Submitted (03-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 117082)
Worley,K.C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 5, 2002 this sequence version replaced gi:21686820.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GZTG
Center Clone name: CH230-143p6
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 55139 bases at least Q40
Consensus quality: 61060 bases at least Q30
Consensus quality: 64630 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 63 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1055: contig of 1055 bp in length
* 1056 1155: gap of unknown length
* 1156 2165: contig of 1010 bp in length
* 2166 2265: gap of unknown length
* 2266 3314: contig of 1049 bp in length
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3315 3414: gap of unknown length
3415 5018: contig of 1604 bp in length
5018 5118: gap of unknown length
5118 6243: contig of 1125 bp in length
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7662 9164: contig of 1402 bp in length
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9264 10352: contig of 1088 bp in length
10352 10452: gap of unknown length
10452 11637: contig of 1185 bp in length
11637 13085: contig of 1348 bp in length
13085 13186: contig of 1432 bp in length
13186 14717: gap of unknown length
14717 16407: contig of 1690 bp in length
16407 16507: gap of unknown length
16507 17676: contig of 1169 bp in length
17676 17776: gap of unknown length
17776 19207: contig of 1431 bp in length
19207 19307: gap of unknown length
19307 21017: contig of 1710 bp in length
21017 21117: gap of unknown length
21117 22172: contig of 1055 bp in length
22172 23366: contig of 1094 bp in length
23366 23466: gap of unknown length
23466 24549: contig of 1083 bp in length
24549 24649: gap of unknown length
24649 25665: contig of 1016 bp in length
25665 25766: gap of unknown length
25766 27421: contig of 1656 bp in length
27421 28564: contig of 1043 bp in length
28564 28665: gap of unknown length
28665 29755: contig of 1091 bp in length
29755 29855: gap of unknown length
29855 31657: contig of 1802 bp in length
31657 31757: gap of unknown length
31757 33595: contig of 1838 bp in length
33595 33696: gap of unknown length
33696 35198: contig of 1503 bp in length
35198 35298: gap of unknown length
35298 36466: contig of 1168 bp in length
36466 36566: gap of unknown length
36566 37640: contig of 1074 bp in length
37640 37740: gap of unknown length
37740 39003: contig of 1263 bp in length
39003 39103: gap of unknown length
39103 41305: contig of 2202 bp in length
41305 41405: gap of unknown length
41405 42620: contig of 1215 bp in length
42620 42720: gap of unknown length
42720 43940: contig of 1220 bp in length
43940 44040: gap of unknown length
44040 45996: contig of 1956 bp in length
45996 46096: gap of unknown length
46096 47529: contig of 1433 bp in length
47529 47629: gap of unknown length
47629 49451: contig of 1822 bp in length
49451 49551: gap of unknown length
49551 50801: contig of 1250 bp in length
50801 50901: gap of unknown length
50901 52881: contig of 1980 bp in length
52881 52981: gap of unknown length
52981 54499: contig of 1518 bp in length
54499 54599: gap of unknown length
54599 55934: contig of 1335 bp in length
55934 56034: gap of unknown length
56034 58138: contig of 2104 bp in length
58138 58238: gap of unknown length
58238 58139

```

```

* 58239 59732: contig of 1494 bp in length
* 59733 59832: gap of unknown length
* 59833 61285: contig of 1453 bp in length
* 61286 61385: gap of unknown length
* 61386 62880: contig of 1495 bp in length
* 62881 62980: gap of unknown length
* 62981 64930: contig of 1950 bp in length
* 64931 65030: gap of unknown length
* 65031 66998: contig of 1968 bp in length
* 66999 67098: gap of unknown length
* 67099 69768: contig of 2670 bp in length
* 69769 69868: gap of unknown length
* 69869 72122: contig of 2254 bp in length
* 72123 72222: gap of unknown length
* 72223 74144: contig of 1922 bp in length
* 74145 74244: gap of unknown length
* 74245 75957: contig of 1713 bp in length
* 75958 76057: gap of unknown length
* 76058 78577: contig of 2520 bp in length
* 78578 80255: gap of unknown length
* 80256 80355: contig of 1578 bp in length
* 80356 82593: gap of unknown length
* 82594 82693: contig of 2238 bp in length
* 82694 84685: gap of unknown length
* 84686 84785: contig of 1992 bp in length
* 84786 86448: gap of unknown length
* 86449 86548: contig of 1663 bp in length
* 86549 87884: gap of unknown length
* 87884 88549: contig of 1336 bp in length

Query Match
Best Local Similarity 47.2%; Score 28.8; DB 2; Length 117082;
Matches 39; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GTGAGGAGTGGGTGGGAATCTTATGGCCACCGAGGGCGGGCGGAGGGGAG 56
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 45287 GGGGGGGGGGGGGGGGGCGTATTATGGCCCCCGGGGGGGGGGGGAG 45342

RESULT 9
AC094964 155645 bp DNA linear HTG 24-AUG-2002
LOCUS Rattus norvegicus clone CH230-6L21, *** SEQUENCING IN PROGRESS ***
DEFINITION 79 unordered pieces.
ACCESSION AC094964
VERSION AC094964.3 GI:22450519
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 155645)
Muzny,D,Marle,, Metzker,M, Lee,, Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,Y., Ayogaji,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswallo,K., Blair,J.J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
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Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Unpublished
JOURNAL 2 (bases 1 to 155645)
AUTHORS Worley,K.C.
DIRECT SUBMISSION
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 155645)
Rat Genome Sequencing Consortium.
DIRECT SUBMISSION
Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 23, 2002 this sequence version replaced gi:21716685.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: G80Z
Center clone name: CH230-6L21
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 96145 bases at least Q40
Consensus quality: 105750 bases at least Q30
Consensus quality: 111678 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 79 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1071: contig of 1071 bp in length
* 1072 1171: gap of unknown length
* 1172 2289: contig of 1118 bp in length
* 2290 2389: gap of unknown length

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sequence does not necessarily represent the entire amplicon.

1. .945

<1. >945

Query Match

Sequence	Matches	Mismatches	Indels	Gaps
Sequence 1	40	0	19	0
Sequence 2	40	0	19	0
Sequence 3	40	0	19	0
Sequence 4	40	0	19	0
Sequence 5	40	0	19	0
Sequence 6	40	0	19	0
Sequence 7	40	0	19	0
Sequence 8	40	0	19	0
Sequence 9	40	0	19	0
Sequence 10	40	0	19	0
Sequence 11	40	0	19	0
Sequence 12	40	0	19	0
Sequence 13	40	0	19	0
Sequence 14	40	0	19	0
Sequence 15	40	0	19	0
Sequence 16	40	0	19	0
Sequence 17	40	0	19	0
Sequence 18	40	0	19	0
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Sequence 20	40	0	19	0
Sequence 21	40	0	19	0
Sequence 22	40	0	19	0
Sequence 23	40	0	19	0
Sequence 24	40	0	19	0
Sequence 25	40	0	19	0
Sequence 26	40	0	19	0
Sequence 27	40	0	19	0
Sequence 28	40	0	19	0
Sequence 29	40	0	19	0
Sequence 30	40	0	19	0
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Sequence 32	40	0	19	0
Sequence 33	40	0	19	0
Sequence 34	40	0	19	0
Sequence 35	40	0	19	0
Sequence 36	40	0	19	0
Sequence 37	40	0	19	0
Sequence 38	40	0	19	0
Sequence 39	40	0	19	0
Sequence 40	40	0	19	0
Sequence 41	40	0	19	0
Sequence 42	40	0	19	0
Sequence 43	40	0	19	0
Sequence 44	40	0	19	0
Sequence 45	40	0	19	0
Sequence 46	40	0	19	0
Sequence 47	40	0	19	0
Sequence 48	40	0	19	0
Sequence 49	40	0	19	0
Sequence 50	40	0	19	0
Sequence 51	40	0	19	0
Sequence 52	40	0	19	0
Sequence 53	40	0	19	0
Sequence 54	40	0	19	0
Sequence 55	40	0	19	0
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Sequence 80	40	0	19	0
Sequence 81	40	0	19	0
Sequence 82	40	0	19	0
Sequence 83	40	0	19	0
Sequence 84	40	0	19	0
Sequence 85	40	0	19	0
Sequence 86	40	0	19	0

1 GTGAGGAGTGGGCTGG

RESULT 12

AF354168.1 GI:139

ORGANISM Ovis aries

AUTHORS Charlier, C., Seger

TITLE	Human-ovine compar
1. <i>Human-ovine compar</i>	

encompassing the c

FOBMED
II337473
2 bases 1 to 215
REFERENCE

* consists of 30 c

★ This sequence wi

★ 1 1205

* 12055 1207

Consensus quality: 151052 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 70 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1106: contig of 1006 bp in length
* 1007: gap of unknown length
* 1107: contig of 1054 bp in length
* 2161: gap of unknown length
* 2261: contig of 1447 bp in length
* 3707: gap of unknown length
* 3807: contig of 1097 bp in length
* 4904: gap of unknown length
* 5004: gap of unknown length
* 6398: contig of 1394 bp in length
* 6499: gap of unknown length
* 7523: contig of 1025 bp in length
* 7524: gap of unknown length
* 7624: contig of 1165 bp in length
* 8788: gap of unknown length
* 8888: gap of unknown length
* 10114: contig of 1226 bp in length
* 10214: gap of unknown length
* 10215: contig of 1165 bp in length
* 11379: gap of unknown length
* 11479: gap of unknown length
* 11380: contig of 1065 bp in length
* 12544: gap of unknown length
* 12644: gap of unknown length
* 12645: contig of 2062 bp in length
* 14706: gap of unknown length
* 14806: gap of unknown length
* 17063: contig of 2257 bp in length
* 17064: gap of unknown length
* 17163: gap of unknown length
* 17164: contig of 1085 bp in length
* 18248: gap of unknown length
* 18348: gap of unknown length
* 19912: contig of 1564 bp in length
* 18349: gap of unknown length
* 19913: gap of unknown length
* 20012: contig of 1543 bp in length
* 20013: gap of unknown length
* 21555: gap of unknown length
* 21556: contig of 1312 bp in length
* 21562: gap of unknown length
* 22967: gap of unknown length
* 23067: gap of unknown length
* 23068: gap of unknown length
* 24534: gap of unknown length
* 24634: gap of unknown length
* 25905: contig of 1271 bp in length
* 26005: gap of unknown length
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* 27235: contig of 1230 bp in length
* 27335: gap of unknown length
* 29168: contig of 1833 bp in length
* 29169: gap of unknown length
* 29288: gap of unknown length
* 30590: contig of 1322 bp in length
* 30591: gap of unknown length
* 30691: contig of 1933 bp in length
* 32624: gap of unknown length
* 32723: gap of unknown length
* 32724: gap of unknown length
* 33865: contig of 1142 bp in length
* 33866: gap of unknown length
* 33966: contig of 1122 bp in length
* 35087: gap of unknown length
* 35188: contig of 1370 bp in length
* 36557: gap of unknown length
* 36558: gap of unknown length
* 36658: contig of 1548 bp in length
* 38205: gap of unknown length
* 38305: gap of unknown length
* 40591: contig of 2286 bp in length
* 40592: gap of unknown length
* 40692: contig of 1012 bp in length
* 41703: gap of unknown length
* 41704: gap of unknown length
* 44051: contig of 2248 bp in length
* 44052: gap of unknown length
* 44152: contig of 1014 bp in length
* 45166: gap of unknown length
* 45265: gap of unknown length
* 45266: contig of 1300 bp in length

* 45566: gap of unknown length
* 45666: contig of 2409 bp in length
* 49075: gap of unknown length
* 49174: contig of 1721 bp in length
* 50895: gap of unknown length
* 50995: contig of 1670 bp in length
* 52665: gap of unknown length
* 52765: contig of 2123 bp in length
* 54888: gap of unknown length
* 54889: contig of 1354 bp in length
* 56342: gap of unknown length
* 56442: contig of 1416 bp in length
* 57858: gap of unknown length
* 57859: contig of 2069 bp in length
* 60027: gap of unknown length
* 60127: contig of 2439 bp in length
* 62566: gap of unknown length
* 62666: contig of 2273 bp in length
* 64939: gap of unknown length
* 65039: contig of 2363 bp in length
* 67402: gap of unknown length
* 67502: contig of 2673 bp in length
* 70175: gap of unknown length
* 70275: contig of 2653 bp in length
* 72928: gap of unknown length
* 73028: contig of 2426 bp in length
* 73229: gap of unknown length
* 73454: contig of 3072 bp in length
* 75554: gap of unknown length
* 75555: contig of 4590 bp in length
* 78626: gap of unknown length
* 78727: contig of 2680 bp in length
* 83116: gap of unknown length
* 83117: gap of unknown length
* 83417: contig of 2706 bp in length
* 86097: gap of unknown length
* 86197: contig of 3098 bp in length
* 88902: gap of unknown length
* 89003: contig of 3329 bp in length
* 92101: gap of unknown length
* 92201: contig of 3057 bp in length
* 95529: gap of unknown length
* 95629: gap of unknown length
* 98686: contig of 3104 bp in length
* 98687: gap of unknown length
* 98787: contig of 4115 bp in length
* 101891: gap of unknown length
* 101892: contig of 4238 bp in length
* 101991: gap of unknown length
* 106105: contig of 3124 bp in length
* 106205: gap of unknown length
* 108205: contig of 3759 bp in length
* 108982: gap of unknown length
* 109083: contig of 3759 bp in length
* 113321: gap of unknown length
* 113322: contig of 3759 bp in length
* 113421: gap of unknown length
* 115445: gap of unknown length
* 115645: contig of 3759 bp in length
* 120404: gap of unknown length

Query Match 46.6%; Score 28.4; DB 2; Length 184454;
Best Local Similarity 76.1%; Pred. No. 34;
Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 8 GTGGCTGGGAATCTTATGGCACACAGAGGGCGGGCGGAGGG 53

Db 7049 GCGGTTGGATAGTCATGGCGCGTGTAGGGCGGGCGGGTGGG 7094

RESULT 14
AC113756/c

LOCUS

DEFINITION Rattus norvegicus clone CH230-195D20, *** SEQUENCING IN PROGRESS

ACCSSION AC113756

VERSION AC113756.3

KEYWORDS HTGS_PHASE1

SOURCE Norway rat

ORGANISM Rattus norvegicus

164800 bp DNA linear HTG 17-JUL-2002

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE AUTHORS

1 (bases 1 to 164800)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunga, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbieri, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouay, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,
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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
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Usmani, K., Vazquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 164800)
Worley, K.C.

Direct Submission
Submitted (05-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 164800)
Worley, K.C.

Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Jul 13, 2002 this sequence version replaced gi:19525921.

COMMENT

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GSES
Center clone name: CH230-195D20

Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 96892 bases at least Q40
Consensus quality: 103381 bases at least Q30

Consensus quality: 108963 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 79 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1648: contig of 1648 bp in length
* 1649 1748: gap of unknown length
* 1749 2082: contig of 1234 bp in length
* 2083 3082: gap of unknown length
* 3083 4545: contig of 1463 bp in length
* 4546 4645: gap of unknown length
* 4646 5832: contig of 1187 bp in length
* 5833 5932: gap of unknown length
* 5933 7111: contig of 1179 bp in length
* 7112 8227: contig of 1016 bp in length
* 8228 9534: contig of 1207 bp in length
* 9535 9635: gap of unknown length
* 9635 11086: contig of 1452 bp in length
* 11087 12505: contig of 1319 bp in length
* 12506 12605: gap of unknown length
* 12606 13936: contig of 1331 bp in length
* 13937 14036: gap of unknown length
* 14037 15243: contig of 1207 bp in length
* 15244 17223: contig of 1880 bp in length
* 17224 17323: gap of unknown length
* 17324 18400: contig of 1077 bp in length
* 18401 19843: contig of 1343 bp in length
* 19844 19943: gap of unknown length
* 19944 21185: contig of 1242 bp in length
* 21186 22817: contig of 1532 bp in length
* 22818 22917: gap of unknown length
* 22918 24380: contig of 1463 bp in length
* 24381 24880: gap of unknown length
* 24881 25864: contig of 1384 bp in length
* 25865 27030: contig of 1066 bp in length
* 27031 27130: gap of unknown length
* 27131 28270: contig of 1140 bp in length
* 28271 28370: gap of unknown length
* 28371 29967: contig of 1597 bp in length
* 29968 30067: gap of unknown length
* 30068 32158: contig of 2091 bp in length
* 32159 32258: gap of unknown length
* 32259 33379: contig of 1121 bp in length
* 33380 33479: gap of unknown length
* 33480 34945: contig of 1466 bp in length
* 34946 35045: gap of unknown length
* 35046 36947: contig of 1902 bp in length
* 36948 37047: gap of unknown length
* 37048 38123: contig of 1076 bp in length
* 38124 38223: gap of unknown length
* 38224 39818: contig of 1595 bp in length
* 39819 39918: gap of unknown length
* 39919 41249: contig of 1331 bp in length
* 41250 41349: gap of unknown length
* 41350 43061: contig of 1712 bp in length
* 43062 43161: gap of unknown length
* 43162 44775: contig of 1614 bp in length
* 44776 44875: gap of unknown length
* 44876 46481: contig of 1606 bp in length

* 46482 46581: gap of unknown length
 * 46592 48396: contig of 1815 bp in length
 * 48397 48496: gap of unknown length
 * 48497 49592: contig of 1096 bp in length
 * 49593 49692: gap of unknown length
 * 49693 51037: contig of 1345 bp in length
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 * 52744 52843: gap of unknown length
 * 52844 54540: contig of 1697 bp in length
 * 54541 54640: gap of unknown length
 * 54641 56806: contig of 2166 bp in length
 * 56807 56906: gap of unknown length
 * 56907 58706: contig of 1700 bp in length
 * 58707 59848: contig of 1142 bp in length
 * 59849 59948: gap of unknown length
 * 59949 61308: contig of 1360 bp in length
 * 61309 61408: gap of unknown length
 * 61409 62678: contig of 1270 bp in length
 * 62679 62778: gap of unknown length
 * 62779 64805: contig of 2027 bp in length
 * 64806 64905: gap of unknown length
 * 64906 67563: contig of 2658 bp in length
 * 67564 67663: gap of unknown length
 * 67664 69361: contig of 1598 bp in length
 * 69362 69461: gap of unknown length
 * 69462 71666: contig of 2205 bp in length
 * 71667 71766: gap of unknown length
 * 71767 73763: contig of 1997 bp in length
 * 73764 73863: gap of unknown length
 * 73864 76437: contig of 2574 bp in length
 * 76438 76537: gap of unknown length
 * 76538 78086: contig of 1549 bp in length
 * 78087 78186: gap of unknown length
 * 78187 80560: contig of 2374 bp in length
 * 80561 80660: gap of unknown length
 * 80661 82392: contig of 1732 bp in length
 * 82393 82492: gap of unknown length
 * 82493 84861: contig of 2369 bp in length
 * 84862 84961: gap of unknown length
 * 84962 86733: contig of 1772 bp in length
 * 86734 86833: gap of unknown length
 * 86834 88701: contig of 1868 bp in length
 * 88702 88801: gap of unknown length
 * 88802 91014: contig of 2213 bp in length

Query Match 46.2%; Score 28.2; DB 2; Length 164800;
 Best Local Similarity 68.4%; Pred. No. 40;
 Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Oy 1 GTGAGGAGTGGCTGGGAATCTTTATGGCACCCAGAGCGGGCGGAGGGGAGT 57
 ||| ||||| ||||| | | | | | ||||| ||| ||||| |||||
 Db 9180 GTGGGAGTGGTGGCGGTGAGTGGATCGAGAGGGGGGTGGGGGGGAGT 9124

RESULT 15

AC111883

LOCUS

DEFINITION Rattus norvegicus clone CH230-26L15, *** SEQUENCING IN PROGRESS

*** 94 unordered pieces.

AC111883

VERSION AC111883.2 GI:21743819

KEYWORDS HTG; HTGS-PHASE1.

SOURCE Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 170476)

AUTHORS

Muzny D.M., Adams C., Adio-Oduola B., Ali-Osman F.R., Allen C.,

Alsbrooks S.L., Anaratunge H.C., Are J.R., Ayele M., Banks T.,

Barbaria J., Benton J., Bimaga K., Blankenburg K., Bonnin D.,

Bouck J., Bowler S., Brieva M., Brown E., Brown M., Bryant N.P.,
 Burch P., Burch P., Burrell C., Burrell K.L., Byrd N.C.,
 Carron F.P., Carter M., Cavazos S.R., Chacko J., Chavez D.,
 Chen G., Chen R., Chen Z., Chowdhry I., Christopoulos C.,
 Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R.,
 Davila M.L., Davis C., Davy-Carroll L., Dederich D.A.,
 Delaney K.R., Delgado O., Denn A.L., Ding Y., Dinh H.H.,
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 Falls T., Ferraguto D., Flagg N., Ford J., Foster P., Frantz P.,
 Gabisi A., Gao J., Garcia A., Garner T., Garza N., Gill R.,
 Gorrell J.H., Guevara W., Gunaratne P., Hale S., Hamilton K.,
 Harris C., Harris K., Hart M., Havlak P., Hayes A., Hernandez J.,
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 Wang S., Ward-Moore S., Warren R., Washington C., Watlington S.,
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 Weinstein G. and Gibbs R.

Direct Submission
 Unpublished
 2 (bases 1 to 170476)
 Worley K.C.

Direct Submission
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

On Jul 13, 2002 this sequence version replaced gi:18701729.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GOKO
 Center clone name: CH230-26L15
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 103990 bases at least Q40
 Consensus quality: 112822 bases at least Q30
 Consensus quality: 119677 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 consists of 94 contigs. The true order of the pieces
 is not known and their order in this sequence record is

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 01:37:39 ; Search time 22.1613 Seconds
(without alignments)
6198.732 Million cell updates/sec

Title: US-09-826-581-3_COPY_612_672

Perfect score: 61

Sequence: 1 gtgaggagtggtggaat.....ggggggcggaggagtcctc 61

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

- 1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
- 2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
- 4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
- 5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
- 6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
- 7: /SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
- 8: /SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
- 9: /SID52/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
- 10: /SID52/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
- 11: /SID52/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
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- 22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	1722	22	AAH43683
2	27.2	44.6	143899	24	AAH38336
3	26	42.6	17761	22	AAK79415
4	26	42.6	17761	23	ABK42709
5	25.8	42.3	112414	24	ABL59091
6	25.6	42.0	14070	22	AAK70465
7	25.2	41.3	886	22	AAH08414
8	25.2	41.3	1030	21	AAK77940
9	25.2	41.3	1105	22	AAK77880

C	10	25.2	41.3	1374	22	AAH18673	Human CDNA sequenc
C	11	25.2	41.3	5938	23	ABK42266	Genomic sequence #
C	12	25.2	41.3	9305	24	ABL54634	Human p53AIP1 asso
	13	25	41.0	275	24	ABN96428	Gene #2926 used to
	14	25	41.0	303	21	AAA14998	cDNA encoding a hu
C	15	25	41.0	541	20	AAK37383	Human secreted pro
	16	25	41.0	1351	24	AAK99401	DNA of APP related
	17	24.8	40.7	563	24	ABL93040	Rat metastatic tum
	18	24.8	40.7	1727	23	AAK83596	DNA encoding novel
	19	24.8	40.7	1991	22	ABA46174	Human breast cell
	20	24.8	40.7	1991	22	ABA26334	Probe #4800 for ge
	21	24.8	40.7	1991	22	AAK04847	Human brain expres
	22	24.8	40.7	1991	22	AAK30374	Human bone marrow
	23	24.8	40.7	1991	22	AAI36331	Probe #5017 used t
	24	24.8	40.7	1991	24	ABS04972	Human genome-deriv
	25	24.8	40.7	2837	22	ABA51286	Human breast cell
	26	24.8	40.7	2837	22	ABA36219	Probe #14685 for g
	27	24.8	40.7	2837	22	AAK17578	Human brain expres
	28	24.8	40.7	2837	22	AAK43391	Human bone marrow
	29	24.8	40.7	2837	22	AAI49460	Probe #18146 used
	30	24.8	40.7	2837	24	ABS17483	Human genome-deriv
C	31	24.8	40.7	5849	24	ABK17335	Human RB-interacti
C	32	24.8	40.7	5868	17	AAH18020	Human RIZ allele D
C	33	24.8	40.7	5868	21	AAA60104	Human RIZ allele D
C	34	24.8	40.7	5868	21	AAA60123	Human RIZ allele E
C	35	24.8	40.7	5868	21	AAA60124	Human mutant RIZ a
C	36	24.8	40.7	5868	24	AAK18781	DNA sequence encod
C	37	24.6	40.3	498	15	AAQ78112	Hepatitis C virus
C	38	24.6	40.3	573	17	AAH16646	Hepatitis C virus
C	39	24.6	40.3	573	17	AAH16647	Hepatitis C virus
C	40	24.6	40.3	24843	24	AAK17764	Human Genomic DNA
	41	24.4	40.0	231	22	ABA37353	Human foetal liver
	42	24.4	40.0	231	22	ABA38943	Probe #17409 for g
	43	24.4	40.0	231	22	AAK22202	Human brain expres
	44	24.4	40.0	231	22	AAK48368	Human bone marrow
	45	24.4	40.0	231	22	AAI26223	Probe #16156 for g

ALIGNMENTS

RESULT 1

AAH43683

ID AAH43683 standard; DNA: 1722 BP.

XX

AC AAH43683;

XX

DT 21-JAN-2002 (first entry)

DE PRKAG3 intron 4 - intron 10.

XX

KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;

KW metabolic disease; diabetes; obesity; substitution; ds.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT intron 1..13

FT /*tag= a

FT /number= "Intron 4"

FT /note= "3' portion of intron 4"

FT 14..95

FT /*tag= b

FT /number= "Exon 5"

FT 96..552

FT /*tag= c

FT /number= "Intron 5"

FT 553..611

FT /*tag= d

FT /number= "Exon 6"

FT 612..736

FT /*tag= e

FT /number= "Intron 6"

FT

FT	exon	737..782	
FT		/*tag= f	
FT		/number= "Exon 7"	
FT	intron	783..986	
FT		/*tag= g	
FT		/number= "Intron 7"	
FT	exon	987..1041	
FT		/*tag= h	
FT		/number= "Exon 8"	
FT	intron	1042..1242	
FT		/*tag= i	
FT		/number= "Intron 8"	
FT	exon	1243..1369	
FT		/*tag= j	
FT		/number= "Exon 9"	
FT	intron	1370..1522	
FT		/*tag= k	
FT		/number= "Intron 9"	
FT	exon	1523..1688	
FT		/*tag= l	
FT		/number= "Exon 10"	
FT	intron	1689..1722	
FT		/*tag= l	
FT		/number= "Intron 10"	
FT		/note= "5' portion of intron 10"	
XX	WO200177305-A2.		
PN			
PD	18-OCT-2001.		
XX			
XX	06-APR-2001; 2001WO-S500765.		
XX			
XX	07-APR-2000; 2000US-195665P.		
PR	(AREX-) AREXIS AB.		
PA			
XX			
PI	Andersson L, Luthman H, Marklund S;		
XX	WPI; 2001-657170/75.		
DR			
PT	New variants of human AMP-activated protein kinase		
PT	associated with a metabolic disease e.g. diabetes		
PT	for determining a risk estimate of diseases in s		
PT	variant -		
XX			
PS	Example 1; Fig 3; 25pp; English.		
XX			
CC	The sequences given in AAH43681-84 represents ggs		
CC	encoding the human AMP-activated protein kinase		
CC	(PRAG3). Detecting the presence of the PRKAG3 D		
CC	is useful in determining a risk estimate of a me		
CC	such as diabetes or obesity, in a subject. The		
CC	in exons 3, 4 or 10. In exon 3 variation may be		
CC	a G for a C at nucleotide 320, resulting in the		
CC	substitution p71A; in exon 4 variation may be a		
CC	T for a C at nucleotide 550; and in exon 10 vari		
CC	substitution of a T for a C at nucleotide 1037,		
CC	amino acid substitution R340W. There may also b		
CC	in intron 6.		
XX			
SQ	Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0		
	Query Watch	100.0%;	Score 61; DB 22;
	Best Local Similarity	100.0%;	Pred. No. 5.1e-10
	Matches 61; Conservative 0; Mismatches		
QY	1 GTGAGCAGTGGCGTGGGAATCTTATGGCACCCACGAGG		
Db	612 GTGAGCAGTGGCGTGGGAATCTTATGGCACCCACGAGG		
QY	61 C 61		
Db	672 C 672		

RESULT 2
AAL38336
ID AAL38336 standard; DNA: 143899 BP.
XX
AC AAL38336;
DT
DT DT
XX 15-AUG-2002 (first entry)
XX Genomic sequence encoding a human Ngr2 protein.
DE
XX
KW Cerebroprotective; neuroprotective; cytosstatic; Nogo receptor homologue;
KW Ngr3; axonal growth; central nervous system; CNS; cerebral injury;
KW spinal cord injury; stroke; demyelinating disease; multiple sclerosis;
KW monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;
KW multifocal leukoencephalopathy; panencephalitis; Spongy degeneration;
KW Alexander's disease; Canavan's disease; metachromatic leukodystrophy;
KW Krabbe's disease; immune; bait protein; genetic mapping; gene therapy;
KW transgenic animal; unregulated cellular growth; cancer; tumour; human;
KW gene; ds.
OS
XX Homo sapiens.
OS
XX
PN WO200229059-A2.
XX
PD 11-APR-2002.
XX
XX 06-OCT-2001; 2001WO-US31488.
XX
XX 06-OCT-2000; 2000US-238361P.
PR
XX (UYVY) UNIV YALE.
PA (BIOJ) BIOGEN INC.
PA
PI Strittmatter SM, Cate RL, Sah DWY;
PI WPI; 2002-416677/44.
DR
XX
XX Novel Nogo receptor homolog polypeptide, Ngr2 or Ngr3, useful for
PT treating central nervous system disorder, cerebral injury, spinal cord
PT injury, stroke, and demyelinating diseases -
XX
XX Example 2; Page 176-214; 277pp; English.
PS
XX
CC The invention relates to a Nogo receptor homologue polypeptide, Ngr2 or
CC Ngr3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NLRRCCT
CC sequence, or a 420, 461 or 392 amino acid sequence, all given in the
CC specification. The Ngr3 protein or its binding antibody is useful for
CC decreasing inhibition of axonal growth of a central nervous system (CNS)
CC neuron, by contacting the neuron Ngr3 or its antibody, and for treating
CC CNS disease, disorder or injury. Ngr3 or a vector comprising Ngr3 is
CC useful for treating cerebral injury, spinal cord injury, stroke,
CC demyelinating diseases, e.g. multiple sclerosis, monophasic
CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,
CC panencephalitis, Marchiafava-Bignami disease, Spongy degeneration,
CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy and
CC Krabbe's disease. Ngr3 is useful for inducing an immune response in a
CC mammal against Ngr3, as a bait protein in a two-hybrid or three-hybrid
CC assay, and as a research tool for identification, characterisation and
CC purification of interacting, regulatory proteins. The nucleotide
CC sequences of the invention are useful for screening for RFP associated
CC with certain disorders, for genetic mapping, and for gene therapy. The
CC vector containing Ngr3 is useful for producing non-human transgenic
CC animals. The Ngr3 binding antibody is useful for isolating and purifying
CC Ngr3, for localisation and/or quantitation of Ngr3, and for diagnostic
CC and therapeutic purposes. The sequences of the invention, vectors and
CC antibodies are useful for treating or preventing unregulated cellular
CC growth such as cancer and tumour growth. This polynucleotide sequence
CC represents the genomic sequence encoding a human Ngr2 protein of the
CC invention.
XX
SQ Sequence 143899 BP: 36346 A; 35277 C; 35318 G; 35657 T; 1301 other;

Query Match 44.6%; Score 27.2; DB 24; Length 143899;
Best Local Similarity 67.9%; Pred. No. 25;
Matches 38; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGGAATCTTATGGCCACCCAGAGGGGGGGGGAGGAG 56
Db 121203 GAGAGGGCGGGAAGAAATTTAGGGGCGACAGAGAGGCTGGGGGGCGGAGAAG 121258

RESULT 3
AAK79415
ID AAK79415 standard; DNA; 17761 BP.
XX
AC AAK79415;
XX
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34227.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX
PN WO200157182-A2.
XX
PD
PP
XX 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
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PR 14-AUG-2000; 2000US-0225758.
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PR 17-NOV-2000; 2000US-0249217.

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PR 05-DEC-2000; 2000US-0251988.
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PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
PI WPI; 2001-483426/52.
DR
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 34227; 307lpp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 17761 BP; 3197 A; 5132 C; 5595 G; 3837 T; 0 other;

Query Match 42.6%; Score 26; DB 22; Length 17761;
Best Local Similarity 65.5%; Pred. No. 50;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 GTGACAGTGGCTGGGAATCTATGCGCACCCAGAGGGCGGGCGGAGGGGAGTC 58
Db 1563 GTGAGGTGCGGTGGTATTGTCGGGTTCCAGAAAGCGCTGTCGCTGGAGTC 1620

RESULT 4
ABK42709
ID ABK42709 standard; DNA; 17761 BP.
XX
AC ABK42709;
XX
DT 21-MAY-2002 (first entry)
XX
DE Genomic sequence #608 encoding novel human connective tissue polypeptide.
XX
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```
KW Human; connective tissue related disorder; cancer; gene therapy;
KW cytostatic; gene; ds.
XX
XX Homo sapiens.
XX
XX WO200155343-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01322.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
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XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
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XX 11-JUL-2000; 2000US-0217487.
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XX 14-SEP-2000; 2000US-0233063.
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XX 21-SEP-2000; 2000US-0234223.
XX 21-SEP-2000; 2000US-0234274.
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Human; connective tissue related disorder; cancer; gene therapy; cytostatic; gene; ds.

Homo sapiens.

WO200155343-A1.

02-AUG-2001.

17-JAN-2001; 2001WO-US01322.

31-JAN-2000; 2000US-0179065.

04-FEB-2000; 2000US-0180628.

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02-MAR-2000; 2000US-0186350.

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18-APR-2000; 2000US-0198123.

19-MAY-2000; 2000US-0205515.

07-JUN-2000; 2000US-0209467.

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14-AUG-2000; 2000US-0225758.

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PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
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PR 11-DEC-2000; 2000US-0254097.

PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-565190/63.
XX Nucleic acid encoding novel connective tissue associated polypeptides,
PT used in diagnosing, preventing, treating or ameliorating a disorder
PT such as cancer or rheumatoid arthritis -
XX Disclosure; SEQ ID No 1596; 673pp; English.
XX The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
CC (cDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s). Including
CC cancer. The polynucleotide sequences of the invention are also useful
CC in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding
CC the novel human connective tissue related polypeptides.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 17761 BP; 3197 A; 5132 C; 5595 G; 3837 T; 0 other;

Query Match 42.6%; Score 26; DB 23; Length 17761;
Best Local Similarity 65.5%; Pred. No. 50;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GTGAGGAGTGGCTGGGAATCTATGGCCACCCAGAGGGGGGGGGAGGAGTC 58
DB 1563 GTGAGGTGTGGCTGGGTAATTGTCGGGGTTCAGAAAGCCTGTGCCGTGGAGTC 1620
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RESULT 5
ABL59091/c
ID ABL59091 standard; DNA; 112414 BP.
XX
AC ABL59091;
XX
DT 20-AUG-2002 (first entry)
XX
DE Nucleotide sequence of Ehime-1 strain of Red sea bream Iridovirus.
XX
KW Neutralisation; Chrysothryps major Iridovirus; antigen; kSIV; ss.
XX
OS Red sea bream Iridovirus.
XX
PN JF2002101885-A.
XX
PD 09-APR-2002.
XX
PF 27-SEP-2000; 2000JP-0294991.
XX
PR 27-SEP-2000; 2000JP-0294991.
XX
PA (NORQ) NORINSUISANSHO YOSHOKU KENKYU.
XX (KURI/) KURITA J.
XX
DR WPI; 2002-440455/47.
XX
PT A DNA encoding a protein related to neutralization and infection
PT prevention of Chrysothryps major Iridovirus -
XX
PS Example 1; Page 13-51; 65pp; Japanese.
XX
CC The specification describes proteins related to neutralisation and
CC infection prevention of Chrysothryps major Iridovirus. The protein
CC encoded by the DNA is useful as an antigen for preventing infection
CC of Chrysothryps major Iridovirus. The present sequence represents the

CC nucleotide sequence of the Ehime-1 strain of Red sea bream iridovirus
CC (RSIV).

SQ Sequence 112414 BP; 26205 A; 29684 C; 30351 G; 26174 T; 0 other;
Query Match 42.3%; Score 25.8; DB 24; Length 112414;
Best Local Similarity 73.3%; Pred. No. 67;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 10 GGGTGGGAATCTTATGACACCCAGAGGGCGGGCGGAGGGG 54
Db 18391 GGGGTGGGATCTGATGGGTGACAAGAGGGGCTTAGCGCAGGG 18347

RESULT 6

AAK70465
ID AAK70465 standard; DNA; 14070 BP.

XX AC AAK70465;

XX DT 06-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25277.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX OS Homo sapiens.

XX WC200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01354.

XX PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214866.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 11-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 14-JUL-2000; 2000US-0217496.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

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PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

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PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

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PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

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PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

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PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246529.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.

XX	08-FEB-2001	(first entry)
XX	Human cancer associated gene sequence SEQ ID NO:334.	
XX		
XX	Human: cancer associated gene; cancer antigen; detection; cancer;	
KW	diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;	
KW	antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;	
KW	kernitammatory; antihypertensive; antiallergic; antibacterial; cardiant;	
KW	dermatological; neuroprotective; thrombolytic; coagulant; neotropic;	
KW	vastotropic; antipsoriatic; angiogenic; gene therapy; inflammation;	
KW	immune disorder; haematopoietic cell disorder; autoimmune disorder;	
KW	allergic reaction; graft versus host disease; organ rejection;	
KW	haemostatic; thrombolytic; cardiovascular disorder; infection;	
KW	neurological disease; drug screening; ss.	
OS	xx	
OS	Homo sapiens.	
XX	WO200055350-A1.	
PN	21-SEP-2000.	
PD	xx	
PF	08-MAR-2000; 2000WO-US05682.	
PE	xx	
PR	12-MAR-1999; 99US-012470.	
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Ruben SM;	
PT	WPI; 2000-587533/55.	
DR	P-PSDB; AAB43731.	
DR	Novel isolated nucleic acids comprising sequences encoding peptides	
PT	useful for treating or diagnosing e.g. cancer -	
PT	Claim 1; Page 886; 2352pp; English.	
PS	xx	
XX	AAC77607 to AAC78448 encode the human cancer associated proteins given	
CC	in AAB43398 to AAB44239. The proteins can have activities based on the	
CC	tissues and cells the genes are expressed in. Example of activities	
CC	include: cytostatic; proliferative; vulnerable; immunomodulator;	
CC	antiasthmatic; antiasthmatic; antirheumatic; antiarthritic;	
CC	antidiabetic; antihypertensive; antiallergic; antibacterial; coagulant;	
CC	dermatological; neuroprotective; cardiant; thrombolytic; coagulant;	
CC	neotropic; vasotrophic; antipsoriatic and antiangiogenic. The	
CC	polynucleotides and polypeptides can be used for preventing, treating or	
CC	ameliorating medical conditions and diagnosing pathological conditions.	
CC	Polynucleotides, polypeptides, antibodies, agonists and antagonists from	
CC	the present invention may be used to treat immune disorders by activating	
CC	or inhibiting the proliferation, differentiation or mobilisation of	
CC	immune cells, to treat disorders of haematopoietic cells, autoimmune	
CC	disorders, allergic reactions, graft versus host disease and organ	
CC	rejection, modulate haemostatic or thrombolytic activity, modulate	
CC	inflammation, cancers, cardiovascular disorders, neurological disease and	
CC	bacterial or viral infections. The peptides, nucleotides, antibodies,	
CC	agonists and antagonists may be also be used in drug screens. AAC78449 to	
CC	AAC78457 and AAB44240 represent sequences used in the exemplification of	
CC	the present invention.	
XX	Sequence 1030 BP; 175 A; 362 C; 287 G; 195 T; 11 other;	
SQ	xx	
Query Match	41.3%; Score 25.2; DB 21; Length 1030;	
Best Local Similarity	66.7%; Pred. No. 72;	
Matches	36; Conservative 0; Mismatches 18; Indels 0; Gaps 0	
QY	4 AGGAGTGGCTCGGAATCTTTATGGCACACCAGAGGGGGGGGGAGGGAGT 57	
Ddb	418 AGGCTCCCCCAAGGACTCATAGGAGCAGGGGGGGGGGGGGGGAGT 365	
RESULT 9		
AAF77880/c		

ID	AAF77880 standard; cDNA; 1105 BP.
XX	
AC	AAF77880;
AC	
DT	30-MAY-2001 (first entry)
XX	
XX	Human ATFx coding sequence with 5' extension.
DE	
XX	
XX	Human; ATFx; gamma aminobutyric acid B receptor; GABA B receptor;
KW	transcription factor; ss.
KW	
XX	
OS	Homo sapiens.
XX	
PN	WO200116596-A2.
XX	
PD	08-MAR-2001.
XX	
PF	31-AUG-2000; 2000WO-GB03361.
XX	
PR	31-AUG-1999; 99GB-0020569.
PR	12-JAN-2000; 2000GB-0000516.
XX	
XX	(GLAX) GLAXO GROUP LTD.
PA	
PI	White J, Wise A, Marshall F;
XX	
DR	WPI; 2001-265904/27.
DR	P-PSDB; AAB80896.
XX	
PT	Identifying modulators of gamma aminobutyric acid(GABA)-B receptor
PT	mediated activity by monitoring the interaction between GABAB receptor
PT	and the CREB/ATF transcription factors in the presence of a test
XX	substance
XX	
PS	Claim 17; Fig 9; Tipp; English.
XX	
CC	The present invention relates to a method for identifying a modulator of
CC	gamma aminobutyric acid_B (GABA_B) receptor-mediated activity, by
CC	monitoring the interaction between a CREB/ATF transcription factor
CC	capable of binding to GABA_B receptor. The present sequence is the coding
CC	sequence for human ATFx, which was used in the method of the present
CC	invention. ATFx is a member of the CREB/ATF family of transcription
CC	factors. ATFx contains a bZIP domain, by which it interacts with the
CC	coiled coil domain of GABA_B receptor. Modulators of GABA_B receptor
CC	activity are useful for treating central nervous system or peripheral
CC	nervous system disorders. The present sequence encodes an ATFx protein
CC	with a N-terminal extension (compared to AAB80892).
XX	
XX	
SQ	Sequence 1105 BP; 198 A; 399 C; 308 G; 200 T; 0 other;
	Query Match 41.3%; Score 25.2; DB 22; Length 1105;
	Best Local Similarity 66.7%; Pred. No.72;
	Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0
QY	4 AGGAGTGGGTGGGAATCTTATGGCACCCAGAGGGCGGGCGAGGGGAGT 57
Db	190 AGGGCTCCCCCAAGGACCTCATAGGAGCCAGGGGCGAGGGCGGGGAGT 137
RESULT 10	
AAH18673/c	
ID	AAH18673 standard; cDNA; 1374 BP.
XX	
AC	AAH18673;
XX	
DT	26-JUN-2001 (first entry)
XX	
DE	Human cDNA sequence SEQ ID NO:18921.
XX	
KW	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX	
OS	Homo sapiens.
XX	

```
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
PR Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 18921; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 1374 BP; 225 A; 516 C; 365 G; 268 T; 0 other;
XX
Query Match 41.3%; Score 25.2; DB 22; Length 1374;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 4 AGCAGTGGCTGGGAATCTTATGGCCACGAGGGCGGGCGGGGAGT 57
DB 459 AGGGCTCCCCCAAGGACCTCATAGGAGCCAGGGGGCGGGGGGAGT 406
RESULT 11
ABK42266/c
ID ABK42266 standard; DNA; 5938 BP.
XX
AC ABK42266;
XX
DT 21-MAY-2002 (first entry)
XX
DE Genomic sequence #165 encoding novel human connective tissue polypeptide.
XX
KW Human; connective tissue related disorder; cancer; gene therapy;
KW cytostatic; gene; ds.
XX
```

```
OS Homo sapiens.
XX
PN WO200155343-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01322.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0218680.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
```


XX SQ Sequence 303 BP; 67 A; 85 C; 110 G; 41 T; 0 other;

Query Match 41.0%; Score 25; DB 21; Length 303;
Best Local Similarity 64.9%; Pred No. 75;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 5 GGATGGGCTGGGAATCTTATTGGCACCCAGAGGGCGGGCGAGGGGAGTCCTC 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 99 GGAGCGGATGCGAAGGAGCGGCACCATTAAGGAGGAGCGGCGGCGGAGTTCTC 155

RESULT 15
AA337383/c

ID AA337383 standard; cDNA; 541 BP.
AC AC
XX AAX37383;
DT 06-JUL-1999 (first entry)
XX Human secreted protein cDNA fragment containing gene 15.

DE XX
KW Human; secreted protein; prevention; cancer; tumour; treatment; protein therapy:
KW gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder;
KW developmental abnormality; foetal deficiency; blood disorder; lymphoma;
KW leukemia; immune system disorder; autoimmune disease; hepatic disease;
KW renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS;
KW Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;
KW arthritis; psoriasis; digestive; endocrine; infection; ss.
XX OS Homo sapiens.
XX HO Homo sapiens.
PN WO9909155-A1.
PD 25-FEB-1999.
XX PF 18-AUG-1998; 98W0-USI7044.
XX 16-JUN-1998; 98US-0092956.
PR 15-JUL-1998; 98US-0092956.
PR 19-AUG-1997; 97US-0056368.
PR 19-AUG-1997; 97US-0056369.
PR 19-AUG-1997; 97US-0056535.
PR 19-AUG-1997; 97US-0056555.
PR 19-AUG-1997; 97US-0056556.
PR 19-AUG-1997; 97US-0056628.
PR 19-AUG-1997; 97US-0056629.
PR 19-AUG-1997; 97US-0056726.
PR 19-AUG-1997; 97US-0056728.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Brewer LA, Duan R, Ebner R, Endress GA, Feng P;
PI Florence C, Florence KA, Komatsoulis GA, Lafleur DW;
PI Moore PA, Olsen HS, Rosen CA, Ruben SW, Shi Y, Soppet DR;
PI Young PE;
XX WPI; 1999-190160/16.
DR P-PSDB; AAY07758.
XX New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
PS Claim la; Page 198; 280pp; English.
XX This invention describes novel isolated human secreted proteins and
CC their encoding nucleic acid sequences. The products of the invention
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also pathological conditions can be
CC diagnosed by determining the presence or amount of expression of
CC the new polypeptides in a sample or by determining the presence or
CC absence of mutations in the new polynucleotides. Specific uses are

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CC described for each of the 70 polynucleotides, based on which tissues
CC they are most highly expressed in, and include developing products for
CC the diagnosis or treatment of cancer, tumors, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC asthma, sepsis, diabetes, Alzheimer's and cognitive disorders,
CC schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine
CC disorders, infections and AIDS. The human secreted proteins of the
CC invention are represented in AAY07744-X707850 and the encoding nucleic
CC acids are represented in AAX37369-X37441.
xx
SQ Sequence 541 BP; 118 A; 135 C; 131 G; 155 T; 2 other;

Query Match          41.0%; Score 25; DB 20; Length 541;
Best Local Similarity 69.4%; Pred. No. 79;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 12 GCTGGGAATCTTATGGGCACCCAGAGGGCGGGCGGAGGGAGTCTCT 60
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 62 CATGGCTTAAGATCTCTGACAGACATGCTGGGGGGGGGGGGGGGATTCCT 14

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Job time : 23.1613 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 13, 2003, 02:37:44 ; Search time 151.839 Seconds
(Without alignments)
6506.409 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- EST:*
1: em_estba:*
2: em_esthum:*
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8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
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26: em_gss_pro:*
27: em_gss_fod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32.2	52.8	354	10 AW026388	AW026388 wv12f05.x
C 2	30.4	49.8	1208	14 BQ433885	BQ433885 AGENCOURT
C 3	29.8	48.9	1056	14 BM800472	BM800472 AGENCOURT
C 4	29.2	47.9	688	9 AL514251	AL514251 AL514251
C 5	28.8	47.2	1084	14 BQ708179	BQ708179 AGENCOURT
C 6	28.4	46.6	872	9 AL530561	AL530561 AL530561

C 7	28.2	46.2	735	12 BG309093	BG309093 HVSME000
C 8	28.2	46.2	1729	14 BM909483	BM909483 AGENCOURT
C 9	28	45.9	403	14 BQ521472	BQ521472 NISC_nll1
C 10	28	45.9	530	14 BQ038856	BQ038856 pgnlc.pk0
C 11	27.8	45.6	653	17 AG122806	AG122806 Pan trogl
C 12	27.8	45.6	712	17 AG090162	AG090162 Pan trogl
C 13	27.8	45.6	1434	14 BQ648687	BQ648687 AGENCOURT
C 14	27.6	45.2	493	17 BH756447	BH756447 SALK_0356
C 15	27.6	45.2	1242	13 B1489045	B1489045 603021030
C 16	27.6	45.2	1293	14 BM912901	BM912901 AGENCOURT
C 17	27.4	44.9	272	10 BB195192	BB195192 BB195192
C 18	27.4	44.9	576	12 BF430892	BF430892 OG05G0673
C 19	27.4	44.9	740	13 B1955582	B1955582 HVSME002
C 20	27.4	44.9	901	17 A2200974	A2200974 SP_00555A
C 21	27.4	44.9	1386	12 B5963498	B5963498 601657281
C 22	27.2	44.6	212	9 AU256222	AU256222 AU256222
C 23	27.2	44.6	733	17 AG180340	AG180340 Pan trogl
C 24	27.2	44.6	883	17 A2527770	A2527770 ENTDA487F
C 25	27.2	44.6	886	12 BF272027	BF272027 GA_Eb001
C 26	27.2	44.6	894	13 B1953428	B1953428 HVSME001
C 27	27.2	44.6	912	12 BG191779	BG191779 RST10875
C 28	27.2	44.6	926	12 BB890765	BB890765 601431204
C 29	27.2	44.6	997	14 BQ675584	BQ675584 AGENCOURT
C 30	27.2	44.6	1097	14 BM801525	BM801525 AGENCOURT
C 31	27.2	44.6	1101	17 CNS00DDA	AL067198 Drosoph11
C 32	27.2	44.6	1327	13 BM464195	BM464195 AGENCOURT
C 33	27	44.3	211	10 BB379140	BB379140 BB379140
C 34	27	44.3	442	13 BM116323	BM116323 L0834C09-
C 35	27	44.3	833	10 BE559614	BE559614 601347308
C 36	27	44.3	1015	12 BF215427	BF215427 601880953
C 37	27	44.3	1066	14 BQ066683	BQ066683 AGENCOURT
C 38	26.8	43.9	282	9 AA872225	AA872225 oh71b02.s
C 39	26.8	43.9	443	10 BB858755	BB858755 BB858755
C 40	26.8	43.9	943	12 BE744657	BE744657 601577506
C 41	26.8	43.9	1099	14 BQ878976	BQ878976 AGENCOURT
C 42	26.8	43.9	1555	14 BM923470	BM923470 AGENCOURT
C 43	26.6	43.6	243	10 BB038623	BB038623 BB038623
C 44	26.6	43.6	392	10 AW081866	AW081866 XB56C05.X
C 45	26.6	43.6	659	13 B1954751	B1954751 HVSME001

ALIGNMENTS

RESULT 1
AW026388/c 354 bp mRNA linear EST 09-MAR-2000
LOCUS wv12f05.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529345 3'
DEFINITION similar to contains element MSR1 repetitive element ;, mRNA
sequence.

ACCESSION AW026388
VERSION AW026388.1 GI:5879918
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 354)

NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGP), Tumor Gene Index

Unpublished (1998)

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CNA Library Arrayed by: Greg Lennon, Ph.D.

CNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1245 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 338.

Location/Qualifiers

1..354

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NCI-CGAP_Brn23"

/tissue_type="glioblastoma (pooled)"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT7n3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7n3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaudo."

72 a 104 c 89 g 88 t 1 others

BASE COUNT

ORIGIN

Query Match 52.8%; Score 32.2; DB 10; Length 354;

Best Local Similarity 74.1%; Pred. No. 19;

Matches 40; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 8 GTGGCGTGGGAATCTTATGGCCACCCAGAGCGGGCGGAGGGAGTCTCTC 61

Db 213 GGGGGGGGGATCTTTTGAACCCCGGGGGGGGGGGGGAGAGCCCC 160

RESULT 2

BQ433885/c

LOCUS

DEFINITION BQ433885 1208 bp mRNA linear EST 24-MAY-2002

AGENCOURT 7751176 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6062177

5', mRNA sequence.

ACCESSION BQ433885

VERSION BQ433885.1

GI:21172961

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1208)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC/DCIB/PTP

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Cloning Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13333 row: d column: 18

High quality sequence stop: 135.

Location/Qualifiers

1..1208

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6062177"

/clone_lib="NIH_MGC_72"

/tissue_type="melanotic melanoma"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life

Technologies."

182 a 536 c 129 g 360 t 1 others

BASE COUNT

ORIGIN

ORIGIN

Query Match

Best Local Similarity

Matches

40; Conservative

0; Mismatches

16; Indels

0; Gaps

0;

QY

2 TGAGGAGTGGCTGGGATCTTATGGCACCACAGAGGGGGGGGGGGAGT 57

Db

1118 TGAGGAGGGTCTGGGGAGATCAAGGGGGGAATAGAGGGGGGGGGAGAGAAT 1063

RESULT 3

BQ433885/c

LOCUS

DEFINITION BQ433885 1056 bp mRNA linear EST 05-MAR-2002

AGENCOURT 6419113 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534991

5', mRNA sequence.

ACCESSION BQ433885

VERSION BQ433885.1

GI:19117295

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1056)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Cloning Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12222 row: f column: 16

High quality sequence stop: 635.

Location/Qualifiers

1..1056

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5534991"

/clone_lib="NIH_MGC_71"

/tissue_type="leiomyosarcoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2.1 kb.

238 a 334 c 277 g 207 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

40; Conservative

0; Mismatches

17; Indels

0; Gaps

0;

QY

1 GTGAGGAGTGGCTGGGAACTTATGGCACCACAGAGGGGGGGGGGGAGT 57

Db

983 GAGGGGGGAGGCTTGGAACTTATGGTGAACATGAGGGGGGGGGCGCGGTAT 927

RESULT 4

AL514251

LOCUS

DEFINITION AL514251 LPI_NFL006_PL2 Homo sapiens cDNA clone CLOBB006202 3

prime, mRNA sequence.

ACCESSION AL514251

VERSION AL514251.1

GI:12777745

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

688 bp mRNA linear EST 13-FEB-2001

AL514251

LOCUS

DEFINITION

prime, mRNA sequence.

ACCESSION

VERSION

GI:12777745

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 688)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source 1..688
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 201 a 99 c 163 g 145 t 80 others
ORIGIN

Query Match 47.9%; Score 29.2; DB 9; Length 688;
Best local Similarity 55.7%; Pred. No. 1.4e+02;
Matches 34; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGAATCTTATGGCACCAGCGGGGGGGGGGGAGTCT 60
DB 379 GGGGGGGGGGGGGGAAAAAANNWTTKSCCCSSGGGGGGGGGGGGGGG 438

QY 61 C 61
DB 439 C 439

RESULT 5
LOCUS BQ708179/c 1084 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8292191 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280902
5', mRNA sequence.
ACCESSION BQ708179
VERSION BQ708179.1 GI:21847078
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1084)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA library Preparation: Rubin Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2472 row: n column: 07
High quality sequence stop: 415.
Location/Qualifiers
1..1084
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6280902"

/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life technologies). Note: this is a NIH_MGC Library."

BASE COUNT 139 a 421 c 311 g 213 t
ORIGIN

Query Match 47.2%; Score 28.8; DB 14; Length 1084;
Best local Similarity 69.6%; Pred. No. 1.9e+02;
Matches 39; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGAATCTTATGGCACCAGCGGGGGGGGGGGAG 56
DB 834 GTGAGAGGGGTCGGGAGCGACGTCACAGCGGAGGGGGCGGCGG 779

RESULT 6
LOCUS AL530561 LTI_NFL001_NBC4 872 bp mRNA linear EST 13-FEB-2001
DEFINITION AL530561 prime, mRNA sequence.
ACCESSION AL530561
VERSION AL530561.1 GI:12794054
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 872)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source 1..872
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD007Y022"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 195 a 189 c 337 g 38 t 113 others
ORIGIN

Query Match 46.6%; Score 28.4; DB 9; Length 872;
Best local Similarity 55.2%; Pred. No. 2.4e+02;
Matches 32; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGAATCTTATGGCACCAGCGGGGGGGGGAGTCT 58
DB 379 GGGAGGAGGGAAGAAKKCKGCKGCCAACAGAGGCGGCGKAGGCGCC 436

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QY      1 GTGAGGAGTGGCGCTGGGAATCTTATGGCACCACCCAGAGGGCGGGCGGAGGGGAGT 57
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      562 GTGGCGAGGGGTGGGGAGGGGAGGGAACCCACCGGGCGGTGAGCGAAGGAGT 618

RESULT 8
BM909483/c
LOCUS   BM909483               1729 bp     mRNA       linear    EST 12-MAR-2002
DEFINITION AGENCOURT_6640847 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5434071
          5', mRNA sequence.
ACCESSION BM909483
VERSION   BM909483.1 GI:19359862
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1729)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-re@mail.nih.gov
          Tissue Procurement: Lou Staudt
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LECMI910 row: 1 column: 16
          High quality sequence stop: 136.
          Location/Qualifiers
            1..1729
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone_image="IMAGE:5434071"
              /clone_lib="NIH_MGC_99"
              /tissue_type="lymphoma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /note="Organ: lymph. Vector: pOTB7; Site_1: XhoI; Site_2:
              EcoRI; cDNA made by oligo-dT priming. Directionally cloned
              into EcoRI/XhoI sites using the following 5' adaptor:
              GGCACGAG(G). Size-selected >500bp for average insert size
              1.8kb. Library constructed by Ling Hong in the laboratory
              of Gerald M. Rubin (University of California, Berkeley)
              using ZAP-cDNA synthesis kit (Stratagene) and Superscript
              II RT (Life Technologies). Note: this is a NIH_MGC
              Library."
BASE COUNT 359 a 788 c 184 g 392 t        6 others
ORIGIN

Query Match         46.2%; Score 28.2; DB 14; Length 1729;
Best Local Similarity 68.4%; Pred. No. 2.9e+02;
Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY      1 GTGAGGAGTGGCGCTGGGAATCTTATGGCACCCAGAGGGCGGGCGGAGGGGAGT 57
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      205 GGGAGGGGGTGTTGGGGATGTGATGGCGACGCGAGGTAAAGAGGGGGGGGGTGT 149

RESULT 9
BM9521472/c
LOCUS   BQ521472             403 bp     mRNA       linear    EST 10-JUN-2002
DEFINITION NISC_nllci01.xl NICHD_XGC_Emb7 Silurana tropicalis cdna clone
          IMAGE:5336064 3', mRNA sequence.
ACCESSION BQ521472
VERSION   BQ521472.1 GI:21380341
KEYWORDS  EST.
SOURCE    western clawed frog.
ORGANISM  Silurana tropicalis
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


<p>Tissue Procurement: CGAP (Stanford) cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov High quality sequence stop: 438. Location/Qualifiers 1..1434 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6270062" /clone_lib="NIH_MGC_100" /tissue_type="hepatocellular carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /notes="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size of Gerard M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." BASE COUNT 313 a 552 c 293 g 273 t 3 others ORIGIN</p>		<p>Query Match 45.6%; Score 27.8; DB 14; Length 1434; Best Local Similarity 69.1%; Pred. No. 3.7e+02; Matches 38; Conservative 17; Indels 0; Gaps 0;</p>	
QY	3	GAGCAGTGGCGTGGGAATCTTATGGCACCCAGCGGGGGCGGAGGAGT	57
Db	1081	GGGTGGGGGGGGGAATATAACCGCCCCCGGGGGGTGGGGGAGGAGT	1027
RESULT 14			
BH756447/c			
LOCUS	BH756447	493 bp	DNA linear GSS 01-MAR-2002
DEFINITION	SALK_053697.52.05.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_053697.52.05.n. DNA sequence.		
ACCESSION	BH756447		
VERSION	GSS		
KEYWORDS	thale cress.		
SOURCE	Arabidopsis thaliana		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eumariophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.		
REFERENCE	1 (bases 1 to 493)		
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Email: ecker@salk.edu This is single pass sequence recovered from the left border of TDNA. Class: TDNA tagged, Location/Qualifiers 1..493 /organism="Arabidopsis thaliana" /strain="Columbia 0"		
FEATURES			
source			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:39:09 ; Search time 4.64516 Seconds
(without alignments)
4027.262 Million cell updates/sec

Title: US-09-826-581-3_COPY_612_672
Perfect score: 61
Sequence: 1 9tagagagtggtgctgggaat.....ggggcgagggaggtcttc 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2.6/prodata/1/ina/5A.COMB.seq.*
2: /cgn2.6/prodata/1/ina/5B.COMB.seq.*
3: /cgn2.6/prodata/1/ina/6A.COMB.seq.*
4: /cgn2.6/prodata/1/ina/6B.COMB.seq.*
5: /cgn2.6/prodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2.6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24.8	40.7	5183	1 US-08-459-568-3	Sequence 3, Appli
C 2	24.8	40.7	5183	2 US-08-399-411-3	Sequence 3, Appli
C 3	24.8	40.7	5868	3 US-08-516-859A-3	Sequence 3, Appli
C 4	24.8	40.7	5868	4 US-09-586-472-3	Sequence 3, Appli
C 5	24.8	40.7	5868	4 US-09-528-706-3	Sequence 3, Appli
C 6	24.6	40.3	573	2 US-08-290-665A-139	Sequence 139, App
C 7	24.6	40.3	573	2 US-08-290-665A-140	Sequence 139, App
C 8	24.6	40.3	573	5 PCT-US95-10398-139	Sequence 139, App
C 9	24.6	40.3	573	5 PCT-US95-10398-140	Sequence 140, App
C 10	24.4	40.0	957	4 US-08-836-075A-17	Sequence 17, Appli
C 11	24.4	40.0	4403765	4 US-09-103-840A-2	Sequence 2, Appli
C 12	24.4	40.0	4411529	4 US-09-103-840A-1	Sequence 1, Appli
C 13	24.2	39.7	31571	1 US-08-323-443B-1	Sequence 1, Appli
C 14	24.2	39.7	53526	3 US-08-658-136-2	Sequence 2, Appli
C 15	24.2	39.7	53577	3 US-08-658-136-1	Sequence 1, Appli
C 16	24	39.3	739	4 US-08-943-731-136	Sequence 136, App
C 17	24	39.3	24183	4 US-08-943-731-3	Sequence 3, Appli
C 18	23.4	38.4	393	3 US-09-188-930-26	Sequence 26, Appli
C 19	23.4	38.4	601	4 US-09-336-536-74	Sequence 74, Appli
C 20	23.4	38.4	728	4 US-09-336-536-2	Sequence 2, Appli
C 21	23.4	38.4	1001	3 US-09-188-930-218	Sequence 218, App
C 22	23.4	38.4	1015	3 US-09-188-930-30	Sequence 30, Appli
C 23	23.4	38.4	1338	4 US-09-336-536-1	Sequence 1, Appli
C 24	23.4	38.4	1347	4 US-09-140-804-1	Sequence 1, Appli
C 25	23.4	38.4	2543	1 US-08-555-669-11	Sequence 11, Appli
C 26	23.4	38.4	2543	3 US-09-073-663-11	Sequence 11, Appli
C 27	23.2	38.0	1701	3 US-09-264-737-3	Sequence 3, Appli

C 28	23.2	38.0	1866	1 US-08-336-408B-1	Sequence 1, Appli
C 29	23.2	38.0	1866	5 PCT-US91-00399-1	Sequence 1, Appli
C 30	23	37.7	573	2 US-08-290-665A-135	Sequence 135, App
C 31	23	37.7	573	2 US-08-290-665A-136	Sequence 136, App
C 32	23	37.7	573	2 US-08-290-665A-137	Sequence 137, App
C 33	23	37.7	573	2 US-08-290-665A-138	Sequence 138, App
C 34	23	37.7	573	2 US-08-290-665A-144	Sequence 144, App
C 35	23	37.7	573	5 PCT-US95-10398-135	Sequence 135, App
C 36	23	37.7	573	5 PCT-US95-10398-136	Sequence 136, App
C 37	23	37.7	573	5 PCT-US95-10398-137	Sequence 137, App
C 38	23	37.7	573	5 PCT-US95-10398-138	Sequence 138, App
C 39	23	37.7	573	5 PCT-US95-10398-144	Sequence 144, App
C 40	23	37.7	803	1 US-08-157-335-3	Sequence 3, Appli
C 41	22.6	37.0	46	1 US-08-171-389-85	Sequence 85, Appli
C 42	22.6	37.0	46	1 US-08-123-936-85	Sequence 85, Appli
C 43	22.6	37.0	46	2 US-08-475-228A-85	Sequence 85, Appli
C 44	22.6	37.0	46	3 US-08-482-080A-85	Sequence 85, Appli
C 45	22.6	37.0	46	4 US-09-354-947-85	Sequence 85, Appli

ALIGNMENTS

RESULT 1
US-08-459-568-3/C
; Sequence 3, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..5158

US-08-459-568-3
Query Match 40.7%; Score 24.8; DB 1; Length 5183;
Best Local Similarity 67.3%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;


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; FILING DATE: 06-MAR-1995
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Campbell, Cathryn A.
;   REGISTRATION NUMBER: 31,815
;   REFERENCE/DOCKET NUMBER: P-LJ 4130
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 535-9001
;   TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 5868 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 121..5278
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-586-472-3

Query Match          40.7%; Score 24.8; DB 4; Length 5868;
Best Local Similarity 67.3%; Pred. No. 13;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 GAGGAGTGGGCTGGGATCTTATGGCACCCAGAGGGGGGGCGGAGGGG 54
Db 3122 GAAGAGGGGGCTGGAGAGGTACGGTAGGAAGGAGGGGGGGCGGAGTGG 3071

RESULT 5
US-09-528-706-3/C
; Sequence 3, Application US/09528706
; Patent No. 6468985
; GENERAL INFORMATION:
;   APPLICANT: Huang, Shi
;   TITLE OF INVENTION: Retinoblastoma Protein - Interacting
;   TITLE OF INVENTION: Zinc Finger Proteins
;   NUMBER OF SEQUENCES: 106
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Campbell & Flores LLP
;     STREET: 4370 La Jolla Village Drive, Suite 700
;     CITY: San Diego
;     STATE: California
;     COUNTRY: USA
;     ZIP: 92122
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/528,706
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/516,859
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/292,683
;     FILING DATE: 18-AUG-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Campbell, Cathryn A.
;     REGISTRATION NUMBER: 31,815
;     REFERENCE/DOCKET NUMBER: P-LJ 1776
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (619) 535-9001
;     TELEFAX: (619) 535-8949
;   INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 5868 base pairs
;       TYPE: nucleic acid
```

```
;
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 121..5278
; US-09-528-706-3

Query Match          40.7%; Score 24.8; DB 4; Length 5868;
Best Local Similarity 67.3%; Pred. No. 13;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 GAGGAGTGGGCTGGGATCTTATGGCACCCAGAGGGGGGGCGGAGGGG 54
Db 3122 GAAGAGGGGGCTGGAGAGGTACGGTAGGAAGGAGGGGGGGCGGAGTGG 3071

RESULT 6
US-08-290-665A-139/C
; Sequence 139, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
;   APPLICANT: BURK, J., MILLER, R.H. AND
;   APPLICANT: PURCELL, R.H.
;   TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
;   TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
;   TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
;   TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
;   NUMBER OF SEQUENCES: 263
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: MORGAN & FINNEGAN
;     STREET: 345 PARK AVENUE
;     CITY: NEW YORK
;     STATE: NEW YORK
;     COUNTRY: USA
;     ZIP: 10154
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: FLOPPY DISK
;     COMPUTER: IBM PC COMPATIBLE
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: WORDPERFECT 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/290,665A
;     FILING DATE: 15-AUG-1994
;     CLASSIFICATION: 435
;     ATTORNEY/AGENT INFORMATION:
;       NAME: RICHARD W. BORK
;       REGISTRATION NUMBER: 36,459
;       REFERENCE/DOCKET NUMBER: 2026-4116
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212) 758-4800
;       TELEFAX: (212) 751-6849
;       TELEX: 421792
;     INFORMATION FOR SEQ ID NO: 139:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 573 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;       ORIGINAL SOURCE:
;         ORGANISM: homosapiens
;         INDIVIDUAL ISOLATE: 24
;   US-08-290-665A-139

Query Match          40.3%; Score 24.6; DB 2; Length 573;
Best Local Similarity 70.2%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 12 GCTGGGAATCTTATGGCACCCAGAGGGGGGGCGGAGGGGAGTC 58
Db 340 GCCGGGGATCATTTGGGCCCAAGATGGCGGAGAGCCGCGAGGAGAC 294
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RESULT 7
US-08-290-665A-140/c
; Sequence 140, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R. H. AND
; APPLICANT: PURCELL, R. H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: Z8
US-08-290-665A-140
Query Match 40.3%; Score 24.6; DB 2; Length 573;
Best Local Similarity 70.2%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
OY 12 GCTGGGAATCTTATGGCCACCCAGAGGGCGGGCGGAGGGAGTC 58
DB 340 GCCGGGGATCATTTGGCCCCCAAGCGTCCGAGAGCCGCGGGGGAC 294

RESULT 8
PCT-US95-10398-139/c
; Sequence 139, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R. H. AND
; APPLICANT: PURCELL, R. H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
```

```
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10398
; FILING DATE: 15-AUG-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29 JUNE 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290/665
; FILING DATE: 15 AUGUST 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: Z4
PCT-US95-10398-139
Query Match 40.3%; Score 24.6; DB 5; Length 573;
Best Local Similarity 70.2%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
OY 12 GCTGGGAATCTTATGGCCACCCAGAGGGCGGGCGGAGGGAGTC 58
DB 340 GCCGGGGATCATTTGGCCCCCAAGATGCGCCGAGAGCCGCGGGAGAC 294

RESULT 9
PCT-US95-10398-140/c
; Sequence 140, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R. H. AND
; APPLICANT: PURCELL, R. H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10398
; FILING DATE: 15-AUG-1995
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; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 957 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-836-075A-17

Query Match 40.0%; Score 24.4; DB 4; Length 957;
Best Local Similarity 68.0%; Pred.No.14;
Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 9 TGGCGTGGGAATCTATTATGGCACCCAGAGGGCGGGCGGAGGGGAGTC 58
   || || || || || || || || || || || || || || || || || ||
Db 343 TGTGCCGGGGTGCCTTTGGGCCCCACGAGGGGCGAGAGCCCCGGGGGAC 294

RESULT 11
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 40.0%; Score 24.4; DB 4; Length 4403765;
Best Local Similarity 63.8%; Pred.No.30;
Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 3 GAGAGCTGGCGTGGGAATCTATTATGGCACCCAGAGGGCGGGCGGAGGGGAGTCCT 60
   || || || || || || || || || || || || || || || || || ||
Db 3958304 GAAGGTGGTGCACGAAGTTGTGGCGCCAGATCGGTGCGGACGATGGACACT 3958247

RESULT 12
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

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; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          40.0%; Score 24.4; DB 4; Length 4411529;
Best Local Similarity 63.8%; Pred. No. 30;
Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 3 GAGGAGTGGCTGGGAATCTTTATGGCACCACCGAGGGCGGGCGGAGGGAGTCCT 60
   || |||| | || |||| | |||| | |||| | |||| | |||| | |||| |
Db 3966215 GAAGGCTGTCGACGAGATTTCTGGGCCGCCAGATCGTCCGACCCGATGCACACT 3966158

RESULT 13
US-08-323-443B-1
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0372/0A462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match          39.7%; Score 24.2; DB 1; Length 31571;
Best Local Similarity 62.3%; Pred. No. 24;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGAATCTTTATGGCACCACCGAGGGCGGGCGGAGGGAGTCCT 60
   || |||| | || |||| | |||| | |||| | |||| | |||| | |||| |
Db 16436 GTCACTCGTGGGAGGTGACACCTTGGGCAAGTAGAGCCCGCTGGCAGAGGTGAGGCT 16495
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QY 61 C 61
Db 16496 C 16496

RESULT 14
US-08-658-136-2
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match          39.7%; Score 24.2; DB 3; Length 53526;
Best Local Similarity 62.3%; Pred. No. 26;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGAATCTTTATGGCACCACCGAGGGCGGGCGGAGGGAGTCCT 60
   || |||| | || |||| | |||| | |||| | |||| | |||| | |||| |
Db 17422 GTCACTCGTGGGAGGTGACACCTGGGCAAGTAGAGCCCGCTGGCAGAGGTGAGGCT 17481

QY 61 C 61
Db 17482 C 17482

RESULT 15
US-08-658-136-1
; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
```

```

; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

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Query Match      39.7%; Score 24.2; DB 3; Length 53577;
Best local Similarity 62.3%; Pred. No. 26;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      1 GTGAGGAGTGCGCTGGGAATCTATTGGGCACCCAGAGGGCGGGGGGAGGGGAGTCCT 60
Db      17421 GTACATCGTGGGAGGGTGACACCTGGGGAAGTAGAGCCCGTGGCAGGAGGTGAGGCCT 17480

QY      61 C 61
Db      17481 C 17481

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Search completed: June 13, 2003, 06:00:55
Job time : 13.6452 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
(without alignments)
4579.068 Million cell updates/sec

Title: US-09-826-581-3_COPY_612_672
Perfect score: 61
Sequence: 1 gtgaggagtggctggaat.....ggggggaggaggagtcctc 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Published Applications_NA:*
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 - 2: /cgn2_6/ptodata/1/pubpna/PTCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 - 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
 - 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 - 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	1722	10	US-09-826-581-3
2	26	42.6	17761	9	US-10-092-154-1596
3	26	42.6	17761	10	US-09-764-847-1596
4	25.2	41.3	1030	10	US-09-925-301-334
5	25.2	41.3	5938	9	US-10-092-154-1153
6	25.2	41.3	5938	10	US-09-764-847-1153
7	25	41.0	275	10	US-09-880-107-2925
8	25	41.0	541	9	US-10-144-929-25
9	25	41.0	1351	9	US-09-964-899-30
10	25	41.0	1847	12	US-10-044-090-338
11	24.8	40.7	1991	10	US-09-864-761-4800
12	24.8	40.7	2837	10	US-09-864-761-21539
13	24.8	40.7	5868	9	US-10-024-450-3
14	24.6	40.3	498	9	US-09-899-046-193
15	24.6	40.3	498	9	US-09-878-281-193
16	24.4	40.0	231	10	US-09-864-761-24263
17	24.4	40.0	550	10	US-09-864-761-7558
18	24.4	40.0	957	9	US-09-851-138-17
19	24.4	40.0	1155	9	US-10-126-279-14

c 20	24.4	40.0	3367	9	US-10-223-085-33	Sequence 33, Appl
c 21	24.4	40.0	3367	9	US-10-223-084-33	Sequence 33, Appl
c 22	24.4	40.0	3367	9	US-10-223-088-33	Sequence 33, Appl
c 23	24.4	40.0	3367	9	US-10-223-090-33	Sequence 33, Appl
c 24	24.4	40.0	3889	9	US-10-037-270-400	Sequence 400, App
c 25	24.4	40.0	174566	9	US-10-020-141-1	Sequence 1, Appli
c 26	24.2	39.7	53522	9	US-09-904-968A-1	Sequence 1, Appli
c 27	24	39.3	13862	9	US-09-764-891-5477	Sequence 5477, Ap
c 28	24	39.3	13862	9	US-09-764-891-10204	Sequence 10204, A
c 29	23.8	39.0	606	9	US-09-738-626-1796	Sequence 1796, Ap
c 30	23.8	39.0	1074	9	US-09-738-626-1795	Sequence 1795, Ap
c 31	23.8	39.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
c 32	23.6	38.7	383	10	US-09-867-701-10278	Sequence 10278, A
c 33	23.6	38.7	540	9	US-09-822-846-553	Sequence 553, App
c 34	23.6	38.7	4241	9	US-10-171-581-213	Sequence 213, App
c 35	23.6	38.7	4711	12	US-10-044-090-210	Sequence 210, App
c 36	23.6	38.7	4720	9	US-09-822-846-158	Sequence 158, App
c 37	23.6	38.7	22452	9	US-09-764-868-1487	Sequence 1487, Ap
c 38	23.6	38.7	22452	9	US-09-764-868-1489	Sequence 1489, Ap
c 39	23.4	38.4	100	10	US-09-969-373-114	Sequence 114, App
c 40	23.4	38.4	393	9	US-10-152-661-26	Sequence 26, Appl
c 41	23.4	38.4	393	9	US-09-866-050A-26	Sequence 26, Appl
c 42	23.4	38.4	1001	9	US-10-152-661-218	Sequence 218, App
c 43	23.4	38.4	1001	9	US-09-866-050A-218	Sequence 218, App
c 44	23.4	38.4	1015	9	US-10-152-661-30	Sequence 30, Appl
c 45	23.4	38.4	1015	9	US-09-866-050A-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-09-826-581-3
; Sequence 3, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SU
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3

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Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 612 GTGAGAGTGGCTGGGAATCTTATGGGCACCCAGAGGGGGGGGAGGGAGTCTT 671
QY 61 C 61
Db 672 C 672

RESULT 2

US-10-092-154-1596
; Sequence 1596, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

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; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1596
; LENGTH: 17761
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1596

Query Match      42.6%; Score 26; DB 9; Length 17761;
Best Local Similarity 65.5%; Pred. No. 2.3;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCGTGGGAATCTTATGGCACCCAGAGGGCGGGGGCGAGGGGAGTC 58
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Db 1563 GTGAGGTGGCGTGGGTATTGCTGGGGTTCCAGAAAGCCTGTGCCGTGCTGGAGTC 1620

RESULT 3
US-09-764-847-1596
; Sequence 1596, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1596
; LENGTH: 17761
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1596

Query Match      42.6%; Score 26; DB 10; Length 17761;
Best Local Similarity 65.5%; Pred. No. 2.3;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCGTGGGAATCTTATGGCACCCAGAGGGCGGGGGCGAGGGGAGTC 58
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Db 1563 GTGAGGTGGCGTGGGTATTGCTGGGGTTCCAGAAAGCCTGTGCCGTGCTGGAGTC 1620

RESULT 4
US-09-925-301-334/c
; Sequence 334, Application US/09925301
; Patent No. US2002052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 334
; LENGTH: 1030
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59)
; OTHER INFORMATION: n equals a.t,g, or c
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; NAME/KEY: misc_feature
; LOCATION: (989)
; OTHER INFORMATION: n equals a.t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1006)
; OTHER INFORMATION: n equals a.t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1023)
; OTHER INFORMATION: n equals a.t,g, or c
US-09-925-301-334

Query Match      41.3%; Score 25.2; DB 10; Length 1030;
Best Local Similarity 66.7%; Pred. No. 5.3;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 4 AGGAGTGGGCTGGGAATCTTATGGCACCCAGAGGGCGGGGGCGAGGGGAGT 57
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Db 418 AGGGCTCCCCAAGACCTCATAGGAGCCAGGGGGGACGAGGGCGGGGAGT 365

RESULT 5
US-10-092-154-1153/c
; Sequence 1153, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1153
; LENGTH: 5938
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1153

Query Match      41.3%; Score 25.2; DB 9; Length 5938;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCGTGGGAATCTTATGGCACCCAGAGGGCGGGGGCGAGGGG 54
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1855 GAGGGACAGAGCTAGGAGAGGGAGGCGAGCCAGAGGCGAGGGGTGCAGGG 1802

RESULT 6
US-09-764-847-1153/c
; Sequence 1153, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1153
; LENGTH: 5938
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1153

Query Match      41.3%; Score 25.2; DB 10; Length 5938;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCGTGGGAATCTTATGGCACCCAGAGGGCGGGGGCGAGGGG 54
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1855 GAGGGACAGAGCTAGGAGAGGGAGGCGAGCCAGAGGCGAGGGGTGCAGGG 1802
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Query Match 41.0%; Score 25; DB 9; Length 541;

Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4800
LENGTH: 1991
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL031277.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.98
US-09-864-761-4800

Query Match 40.7%; Score 24.8; DB 10; Length 1991;
Best Local Similarity 67.3%; Pred. No. 7;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 GAGGAGTGGCTGGGAACTCTATGGCACCAGAGGGCGGGCGGAGGGG 54

DB 1022 GAAGAGGGGCTGGGAAAGGAGGTACGGTAGGAGGAGGGCGGGCGGAGTGG 1073

RESULT 12

US-09-864-761-21539
Sequence 21539, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
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PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 21539
LENGTH: 2837
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL031277.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.98
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OTHER INFORMATION: EST_HUMAN HIT: BE885438.1, EVALUE 0.00e+00
US-09-864-761-21539

Query Match 40.7%; Score 24.8; DB 10; Length 2837;
Best Local Similarity 67.3%; Pred. No. 6.9;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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; LOCATION: 1..49

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

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- 9: gb.pr.*
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- 32: em.htg_other.*
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- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1453	88.2	2115	6	AX098002	AX098002 Sequence	
4	1453	88.2	2115	9	AF214519	AF214519 Homo sapi	
5	1447	87.9	2109	6	AX099776	AX099776 Sequence	
6	1172.8	71.2	2022	6	AX099804	AX099804 Sequence	
7	1142	69.3	1873	6	AX398333	AX398333 Sequence	
8	1140.4	69.2	1873	4	AF214520	Sus scrofa	
9	1140.4	69.2	1873	6	AX099800	AX099800 Sequence	
10	1140.4	69.2	1873	6	AX398331	AX398331 Sequence	
11	1138.8	69.1	1873	6	AX398335	AX398335 Sequence	
12	1138.8	69.1	1873	6	AX398337	AX398337 Sequence	
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14	1134.4	68.9	1867	6	AX099774	AX099774 Sequence	
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18	396.8	24.1	1623	10	AF036535	Mus musculus	
19	395.4	24.0	3132	10	BC015283	BC015283 Mus musculus	
c	20	395.2	24.0	206854	9	AC009974	AC009974 Homo sapi
21	393.4	23.9	1578	9	HSU42412	U42412 Human 5'-AM	
22	393.4	23.9	1677	9	BC000358	BC000358 Homo sapi	
23	367.2	22.3	1774	6	AX364914	AX364914 Sequence	
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25	366.6	22.3	2194	9	AF139104	AF139104 Sequence	
26	366.6	22.3	2194	9	AF087875	AF087875 Homo sapi	
27	366.6	22.3	2203	9	BC020540	BC020540 Homo sapi	
28	366.6	22.3	2223	9	AK001887	AK001887 Homo sapi	
29	363.4	22.1	2062	9	HS2424976	AJ2424976 Homo sapi	
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31	300.8	18.3	2082	3	AF094764	AF094764 Drosophila	
32	299.2	18.2	1905	6	AX482695	AX482695 Sequence	
33	299.2	18.2	3210	3	AY084138	AY084138 Drosophila	
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35	278.8	16.9	1014	6	AX281581	AX281581 Sequence	
36	278.8	16.9	152129	2	AC027416	AC027416 Homo sapi	
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38	267.4	16.2	227724	2	AF336381	AF336381 Mus musculus	
39	254.6	15.5	146577	2	AC128070	AC128070 Rattus norvegicus	
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ALIGNMENTS

RESULT 1
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LOCUS AX281582 1647 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 5 from Patent WO0177305.
ACCESSION AX281582
VERSION AX281582.1 GI:16608833
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Andersson,L., Luthman,H. and Marklund,S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 5 18-OCT-2001;

FEATURES	Aresis AB (SE)			
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QY	61	CTGGAGCAGCCTTGGGGTTCGAGCATCAAGAGATGAGCTTCTTAGACGAAGAACAAG	120	
DB	61	CTGGAGCAGCCTTGGGGTTCGAGCATCAAGAGATGAGCTTCTTAGACGAAGAACAAG	120	
QY	121	CAGCTCATGGCCATCACCAGCTGTGACCAGCAGCTCAGAAAGATCCGTGGGAAACGGAG	180	
DB	121	CAGCTCATGGCCATCACCAGCTGTGACCAGCAGCTCAGAAAGATCCGTGGGAAACGGAG	180	
QY	181	GGCCAAAGCCTTGAGATGGACAGGCAAGAGTCGTTGGAGGAGGGGACCCACAGGTCA	240	
DB	181	GGCCAAAGCCTTGAGATGGACAGGCAAGAGTCGTTGGAGGAGGGGACCCACAGGTCA	240	
QY	241	GGGGGAAGTCCCGGTCACAGGCGAGCTGTGAGTCCACCGGGCTGGAGGCCACATTC	300	
DB	241	GGGGGAAGTCCCGGTCACAGGCGAGCTGTGAGTCCACCGGGCTGGAGGCCACATTC	300	
QY	301	CAAGACACACCTTGGCTCAAGCTGATCTGCGGGGTGGGCACTCCACCAACAGGGTG	360	
DB	301	CAAGACACACCTTGGCTCAAGCTGATCTGCGGGGTGGGCACTCCACCAACAGGGTG	360	
QY	361	GGACTGCTCCCTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGGA	420	
DB	361	GGACTGCTCCCTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGGA	420	
QY	421	GCTGGCCAGGAGTCCACGACAGAGGCGCTGGGAGTGTGAGCTAAGAGGCTGCTGGA	480	
DB	421	GCTGGCCAGGAGTCCACGACAGAGGCGCTGGGAGTGTGAGCTAAGAGGCTGCTGGA	480	
QY	481	AGAGAGGCTGTGCTGTGCTGTCCCGCAGGCCCCCATTTCCCAAGCTGGGCTGGGATGA	540	
DB	481	AGAGAGGCTGTGCTGTGCTGTCCCGCAGGCCCCCATTTCCCAAGCTGGGCTGGGATGA	540	
QY	541	CGAACTGCGGAAACCCGGGCCGAGATCTACATGGCTTCATGCGAGGACACACCTTGCTA	600	
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QY	601	CGATGCCATGGCACTAGCTCCAAAGCTAGTCACTCTCGACACCATGCTGGAGATCAAGAA	660	
DB	601	CGATGCCATGGCACTAGCTCCAAAGCTAGTCACTCTCGACACCATGCTGGAGATCAAGAA	660	
QY	661	GGCTCTTCTTGTCTGTGGCCAAACGGTGTGGGGCAGCCCTCTATGGGACAGCAAGAA	720	
DB	661	GGCTCTTCTTGTCTGTGGCCAAACGGTGTGGGGCAGCCCTCTATGGGACAGCAAGAA	720	

Qy	721	GCAGAGCTTTGTGGGATGCTGACCATCAGTACTTCACTCTGCTGGTGTGTCATPCGCTACTA	780	
Db	721	GCAGAGCTTTGTGGGATGCTGACCATCAGTACTTCACTCTGCTGGTGTGTCATPCGCTACTA	780	
Qy	781	CAGGTCCCGCTGCTCCAGATCTATGAGATTGACACATAGATTGAGACTCGAGGGA	840	
Db	781	CAGGTCCCGCTGCTCCAGATCTATGAGATTGACACATAGATTGAGACTCGAGGGA	840	
Qy	841	GATCTACCTGCAAGGCTGCTTCAAGCCTCTGCTCCATCTCTCCTAATGATGACCTGTT	900	
Db	841	GATCTACCTGCAAGGCTGCTTCAAGCCTCTGCTCCATCTCTCCTAATGATGACCTGTT	900	
Qy	901	TGAAGCTGTCTACACCTCTATCAAGAACCGGATCCATCGCTGCTTCTTGACCCGCT	960	
Db	901	TGAAGCTGTCTACACCTCTATCAAGAACCGGATCCATCGCTGCTTCTTGACCCGCT	960	
Qy	961	GTCAGGCAAGCTACTCTACATCTCCACACAAACGCTGCTCAAGTCTCTGCAACATCTT	1020	
Db	961	GTCAGGCAAGCTACTCTACATCTCCACACAAACGCTGCTCAAGTCTCTGCAACATCTT	1020	
Qy	1021	TGGTTCCTGCTGCCCCGGGCTCTCTCTACCGCACTATCCAAAGATTTGGGATCGG	1080	
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Qy	1081	CACATTCGAGACTTGGCTGTGCTGGAGACAGCACCATCCTGACTGCACTGGACAT	1140	
Db	1081	CACATTCGAGACTTGGCTGTGCTGGAGACAGCACCATCCTGACTGCACTGGACAT	1140	
Qy	1141	CTTTGTGACCGGGTGTGCTGCACCTGCTGCTCAAGAAATGTTGCTGAGTCTGGG	1200	
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Qy	1201	CCTCTATTCCCGCTTGTGATGATTCACCTGGCTGCCACGCAACCTACACACCTGGA	1260	
Db	1201	CCTCTATTCCCGCTTGTGATGATTCACCTGGCTGCCACGCAACCTACACACCTGGA	1260	
Qy	1261	CATGAGTGTGGAGAGCCCTGAGGAGGACACTATGTCTGGAGGAGTCTCTTCTG	1320	
Db	1261	CATGAGTGTGGAGAGCCCTGAGGAGGACACTATGTCTGGAGGAGTCTCTTCTG	1320	
Qy	1321	CCAGCCCCACAGAGCTTGGGGAAGTATGATCAGAGATTTGCTGGGAGCAGGTACACAG	1380	
Db	1321	CCAGCCCCACAGAGCTTGGGGAAGTATGATCAGAGATTTGCTGGGAGCAGGTACACAG	1380	
Qy	1381	GCTGTGCTAGTGACAGACACCATCTCTTGGGCTGCTCTCTCTCGACATCCT	1440	
Db	1381	GCTGTGCTAGTGACAGACACCATCTCTTGGGCTGCTCTCTCTCGACATCCT	1440	
Qy	1441	TCAGGCACTGCTGCTCAGCCCTGCTGGCATGATGCTCGGGGCTCGAGAGATCTGAG	1500	
Db	1441	TCAGGCACTGCTGCTCAGCCCTGCTGGCATGATGCTCGGGGCTCGAGAGATCTGAG	1500	
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Db	1501	TCTTAATCCCAAGCCACCTGACACTTGAAGCCATGAGGGAACCTGGAGAACTCAGC	1560	
Qy	1561	CTTCACTTCCCGCCACCCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1620	
Db	1561	CTTCACTTCCCGCCACCCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1620	
Qy	1621	GGCCATGACACACGCTCTTTAGTCTTC	1647	
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RESULT 2
HSA249977
LOCUS
DEFINITION Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit (AMPK gamma 3 gene).
ACCESSION AJ249977
VERSION AJ249977.1 GI:6688200

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RESULT 3
AX099802
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2115)
Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
Patent: WO 012003-A 29 22-MAR-2002
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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BASE COUNT 460 a 622 c 562 g 471 t
ORIGIN

Query Match 88.2%; Score 1453; DB 6; Length 2115;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 35; Indels 7; Gaps 2;

QY 95 ATGAGCTTCTAGAGCAAGAAACACAGCTCATGGCCATCACAGCTGTGACCAAGCAGC 154
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QY 155 TCAGAAAGAAATCCGTGGGAAACGAGGAGGCAAGCCTTTGAGATGGCAAGGCAAGTCG 214
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QY 215 GTGAGAGAGGGAGCCACACAGGTACAGGGGAGGTCCCGGTCCAGGCCAGCTGCTGAG 274
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QY 275 TCCACCGGCTGAGGGCCACATTCGCCAAGACACACCTTTGGCTCAAGTGTATCCTGCC 334
Db 181 TCCACCGGCTGAGGGCCACATTCGCCAAGACACACCTTTGGCTCAAGTGTATCCTGCC 240

QY 335 GGGGTGGGCACTCCACAAAGGGTGGGACTGCTCCCTCTGACTGTACAGCCTCAGCT 394
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QY 455 GAGTGTGAGCTTAGAAGGCTGCTGGAAGAGAGGCTGCTCCCTGTGCTGTCCCGCAGGCC 514
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QY 755 TTTCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCTATCAAGAACCGGATC 934
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LOCUS Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
DEFINITION mRNA, complete cds.
ACCESSION AF214519
VERSION AF214519.1 GI:8215681
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2115)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
and Andersson,L.
A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle
Science 288 (5469), 1248-1251 (2000)
20280150
MEDLINE 10818001
PUBMED
REFERENCE 2 (bases 1 to 2115)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden

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ALVLSFAGIDALGA"
BASE COUNT 460 a 622 c 562 g 471 t
ORIGIN

Query Match 88.2%; Score 1453; DB 9; Length 2115;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 35; Indels 7; Gaps 2;

Qy 95 ATGAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCATCCACAGCTGTGACACAGC 154
Db 1 ATGAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCATCCACAGCTGTGACACAGC 60
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AX099776
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DEFINITION Sequence 3 from Patent WO0120003.
ACCESSION AX099776
VERSION AX099776.1 GI:13538810
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2109)
AUTHORS Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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Query Match 87.9%; Score 1447; DB 6; Length 2109;
Best Local Similarity 97.3%; Pred. No. 0;
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LOCUS AX099804 2022 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 31 from Patent WO0120003.
ACCESSION AX099804
VERSION AX099804.1 GI:13538838
KEYWORDS .
SOURCE
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS Andersson L., Looft C., Kalm E., Milan D., Robic A.,
Rogel-Galliard C., Iannuccielli N., Gellin J., le Roy P. and
Chardon P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
FEATURES
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1. .2022
Location/Qualifiers
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BASE COUNT 412 a 623 c 593 g 394 t
ORIGIN

Query Match 71.2%; Score 1172.8; DB 6; Length 2022;
Best Local Similarity 85.7%; Pred. No. 9.4e-260;
Matches 1351; Conservative 0; Mismatches 217; Indels 8; Gaps 4;

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RESULT 11
AX398335
LOCUS 1873 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 5 from Patent WO2020850.
ACCESSION AX398335
VERSION AX398335.1 GI:21261110
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1
REFERENCE
AUTHORS Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for

reproductive and meat quality traits
Patent: WO 0220850-A 5 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
FEATURES
Location/Qualifiers
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Query Match 69.1%; Score 1138.8; DB 6; Length 1873;
Best Local Similarity 85.7%; Pred. No. 6.6e-252;
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LOCUS AX398337 1873 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 7 from Patent WO0220850.
ACCESSION AX398337
VERSION AX398337.1 GI:21261112
KEYWORDS
SOURCE plg.
ORGANISM Sus. scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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REFERENCE
AUTHORS Rothschild, M.F., Ciobanu, D.C., Malek, M. and Piastow, G.

TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 7 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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Location/Qualifiers
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ORIGIN
Query Match 69.1%; Score 1138.8; DB 6; Length 1873;
Best Local Similarity 85.7%; Pred. No. 6.6e-252;
Matches 1314; Conservative 0; Mismatches 212; Indels 8; Gaps 4;
Qy 95 ATGAGCTTCTTACGACCAAGAAACAGACGCTCAGGCCATCCAGCTGTGACGACGAGC 154
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DEFINITION
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VERSION X95578.1
KEYWORDS AMP-activated protein kinase; gamma subunit.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus
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REFERENCE
AUTHORS Woods,A., Cheung,P.C., Smith,F.C., Davison,M.D., Scott,J.,
Berl,R.K. and Carling,D.
TITLE Characterization of AMP-activated protein kinase beta and gamma
subunits. Assembly of the heterotrimeric complex in vitro
J. Biol. Chem. 271 (17), 10282-10290 (1996)
JOURNAL 96215327
MEDLINE 8626596
PUBMED
REFERENCE 2 (bases 1 to 1328)
AUTHORS Carling,D.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-1996) D. Carling, MRC Clinical Sciences Centre,
Department of Molecular Medicine, RPMs, Hammersmith Hospital,
DuCane Road, London, W12 0NN, UK
FEATURES
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Best Local Similarity 64.9%; Pred. No. 5.4e-85;
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1 (bases 1 to 1328)

Woods,A., Cheung,P.C., Smith,F.C., Davison,M.D., Scott,J., Berl,R.K. and Carling,D.

Characterization of AMP-activated protein kinase beta and gamma subunits. Assembly of the heterotrimeric complex in vitro

J. Biol. Chem. 271 (17), 10282-10290 (1996)

96215327

8626596

2 (bases 1 to 1328)

Carling,D.

Direct Submission

Submitted (07-FEB-1996) D. Carling, MRC Clinical Sciences Centre, Department of Molecular Medicine, RPMs, Hammersmith Hospital, DuCane Road, London, W12 0NN, UK

Location/Qualifiers

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Query Match 25.2%; Score 414.8; DB 10; Length 1328;

Best Local Similarity 64.9%; Pred. No. 5.4e-85;

Matches 614; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1172.8	71.2	2022	AAD03321	Sus scrofa PRKAG3
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13	407.2	24.7	989	22	AAH43682	PRKAG3 intron 2 -
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16	390.2	23.7	1576	18	AA785927	Mammalian AMPK-gam
17	367.2	22.3	1774	24	ABL39755	Human NS cDNA sequ
18	366.6	22.3	1435	20	AAU06882	Disease associated
19	366.6	22.3	2223	22	AAH14839	Human cDNA sequenc
20	299.2	18.2	3261	23	ABL18857	Drosophila melanog
21	278.8	16.9	1014	22	AAH43684	PRKAG3 intron 10 -
c	252	15.3	3425	22	AAK72740	Human immune/haema
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24	222	13.5	1467	23	AAH84265	Human cDNA clone (
25	213.2	12.9	735	22	AAH07561	Human colon cancer
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27	168.2	10.2	1722	22	AAH43683	DNA encoding novel
28	159.8	9.7	2303	23	AAH84267	Bovine embryonic g
29	144.6	8.8	956	24	ABN74716	Human polynucleoti
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31	127.2	7.7	39651	23	ABL18856	cDNA sequence #559
32	123.6	7.5	1446	24	ABK36168	Human secreted pro
33	120.8	7.3	350	21	AAC01661	Pig PRKAG3 gene 5'
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35	111.8	6.8	808	24	AAD36462	Human prostate exp
36	106.2	6.4	539	23	ABV09172	Human prostate cell
37	106.2	6.4	615	23	ABV33323	Human foetal liver
c	85	5.2	378	22	ABA44706	Probe #3373 for ge
39	85	5.2	378	22	ABA55162	Human brain expres
40	85	5.2	378	22	ABA24907	Human bone marrow
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ALIGNMENTS

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XX 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-SE00765.
XX PR 07-APR-2000; 2000US-195665P.
XX FA (AREX-) AREXIS AB.
XX PI Andersson L, Luthman H, Marklund S;
XX DR MPI: 2001-657170/75.
XX P-PSDB; Q0B47679.
PT New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
PS Disclosure: Fig 5; 25pp; English.
XX
CC This sequence represents the full length cDNA encoding the human
CC AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
CC the presence of the PRKAG3 DNA, or a variant, is useful in determining
CC a risk estimate of a metabolic disease, such as diabetes or obesity,
CC in a subject. The variation may occur in exons 3, 4 or 10. In exon
CC 3 variation may be a substitution of a G for a C at nucleotide 320,
CC resulting in the amino acid substitution P71A; in exon 4 variation may
CC be a substitution of a T for a C at nucleotide 550; and in exon 10
CC variation may be a substitution of a T for a C at nucleotide 1037,
CC resulting in the amino acid substitution R340W. There may also be
CC nucleotide variation in intron 6. The numbering of these
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Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 2
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DT 13-JUN-2001 (first entry)
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KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiac; gene therapy; ss.
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PF 11-SEP-2000; 2000WO-BP09896.
XX
PR 10-SEP-1999; 99EP-0402236.
PR 18-MAY-2000; 2000EP-0401388.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.
PA (LOOF/) LOOFT C.
PA (KALM/) KALM E.
XX
XX Andersson L, Loof C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
PI P-PSDB; AAE00223.
XX
DR WPI; 2001-244810/25.
DR P-PSDB; AAE00223.
XX
XX New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment of disorders
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy -
XX
XX Claim 12; Page 65-68; 71pp; English.
XX
XX The present sequence is a cDNA encoding human adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC complete PRKAG3. Mutation in Prkag3 results in an altered regulation of
CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
CC useful as therapeutic for treating carbohydrate metabolism disorders such
CC as diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a

CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX
SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
Query Match 88.2%; Score 1453; DB 22; Length 2115;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 35; Indels 7; Gaps 2;
QY 95 ATGAGCTTCTAGAGCAAGAAACACAGCAGCTCATGGCCATCACAGCTGTGACCAAGCAGC 154
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QY 1 ATGAGCTTCTAGAGCAAGAAACACAGCAGCTCATGGCCATCACAGCTGTGACCAAGCAGC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 155 TCAGAAAGAAATCCCTGGGAACGGAGGSCCAAGGCTTGAGATGGACAGGCAAGTCG 214
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 TCAGAAAGAAATCCCTGGGAACGGAGGSCCAAGGCTTGAGATGGACAGGCAAGTCG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 215 GTGGAGGAAGGGAGCCACAGGTCAGGGGGAAGGTCGCCGGTCCAGGCGCAGCTGCTGAG 274
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 GTGGAGGAAGGGAGCCACAGGTCAGGGGGAAGGTCGCCGGTCCAGGCGCAGCTGCTGAG 180
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QY 275 TCCACCGGGCTGGAGGCCACATTCGCCAAGACACAGCCTTGCTCAAGCTGATCCTGCC 334
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 TCCACCGGGCTGGAGGCCACATTCGCCAAGACACAGCCTTGCTCAAGCTGATCCTGCC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 335 GGGGTGGGCACTCCACCAACAGGGTGGGACTGCTCCCTCCCTGACTGTACAGCTCAGCT 394
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QY 395 GCAGGCTCCAGCAGATGATGTGGAGCTGGCCAGGAGTTCGCCAGCCACAGAGGCTGG 454
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 GCAGGCTCCAGCAGATGATGTGGAGCTGGCCAGGAGTTCGCCAGCCACAGAGGCTGG 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 455 GAGTGTAGCTAGAGGCTGCTGGAAGAGAGGCTGCCCTGTGCTGCTGCCCGCAGGCC 514
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 GAGTGTAGCTAGAGGCTGCTGGAAGAGAGGCTGCCCTGTGCTGCTGCCCGCAGGCC 420
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QY 515 CCATTTCACAGCTGGGCTGGGATGACGAACTGGGAAACCCGGCGCCAGATCTACATG 574
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 635 TTCGACACCATGCTGGGATCAAGAAAGGCTTCTTTGCTGCTGGTGGCAACGGTGTGGG 694
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 695 GCAGGCGCTTATGGGACAGCAAGAGAGCTTTGTGGGATGTGTGACCACTACTGAC 754
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 601 GCAGGCGCTTATGGGACAGCAAGAGAGCTTTGTGGGATGTGTGACCACTACTGAC 660
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QY 755 TTCATCTGGTGTGCTGCTAGTACAGGTCGCCCTGGTGGTGGTGGTGGTGGTGGTGG 814
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QY 815 CAACATAAGATGTAGAGCTTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGGCTCTGGTC 874
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QY 721 CAACATAAGATGTAGAGCTTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGGCTCTGGTC 780
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QY 935 CATCGCTGCTGCTTCTTTGACCGGGTGCAGGACAGCTACTCCACATCTCTACACACAA 994
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 841 CATCGCTGCTGCTTCTTTGACCGGGTGCAGGACAGCTACTCCACATCTCTACACACAA 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 901 CGCCTGCTCAAGTTCTGACATCTTTGGTTCCCTGTGTCGCCGGCCCTCTCTCTAC 960
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Qy 1535 CAATGAAGGAACTGGAGAACTCAGCCTTCATCTTCCCCACCCCAATTTGCTGTTCAG 1594
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Db 1494 CTATGATTCAGGTCTCTTTCAGCCTTCCAAATTTGCTTGCCT 1536

RESULT 3
AAD03296
ID AAD03296 standard; DNA; 2109 BP.
XX
AC AAD03296;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
XX
KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiact; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
5'UTR 1..471
FT /*tag= a
FT 472..1389
FT CDS /*tag= b
FT /*product= "Human Prkag3 protein"
FT 1390..2109
FT /*tag= c
XX
PN W0200120003-A2.
XX
PD 22-MAR-2001.
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XX 11-SEP-2000; 2000WO-EP09896.
XX
PR 10-SEP-1999; 99EP-0402236.
PR 18-MAY-2000; 2000EP-0401388.
XX
FA (JNRG ) INRA INST NAT RECH AGRONOMIQUE.
FA (ANDE/) ANDERSSON L.
PA (LOOF/) LOOFT C.
PA (KALM/) KALM E.
XX
Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
WPI: 2001-244810/25.
DR P-PSDB; AAE00221.
XX
New variants of the gamma subunit of vertebrate adenosine
monophosphate-activated kinase for diabetes or treatment of disorders
associated with energy metabolism such as diabetes, obesity, and
myopathy -
XX
Claim 12; Fig 2; 71pp; English.
XX
The present sequence is a cDNA encoding human adenosine monophosphate
(BMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
PRKAG3. Mutation in Prkag3 results in an altered regulation of
carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
useful as therapeutic for treating carbohydrate metabolism disorders such
as diabetes, obesity, and disorders associated with muscle metabolism
such as myopathy and cardiovascular diseases, to modulate AMPK
activity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder,
preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRKAG3.
XX
Transgenic animal and host cell transformed with PRKAG3 or a
heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
of PRKAG3 and is useful in gene therapy.
XX
SQ Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
Query Match 87.9%; Score 1447; DB 22; Length 2109;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 35; Indels 7; Gaps 2;
Qy 101 TTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACACGCTGTGACCAAGCTCAGAA 160
Db 1 TTCTTAGAGCAAGAAACAGCAGCTCATGGCCATCACACGCTGTGACCAAGCTCAGAA 60
Qy 161 AGAATCCCTGGAAACGGAGGCCAAAGCCTTGAGATGGACAAAGGAGCAAGTTCGGTGGAG 220
Db 61 AGAATCCCTGGAAACGGAGGCCAAAGCCTTGAGATGGACAAAGGAGCAAGTTCGGTGGAG 120
Qy 221 GAAGGGAGCCACCAAGCTCAGGGGGAAGTCCCGGTCCAGGCCAGCTGCTGAGTCCACC 280
Db 121 GAAGGGAGCCACCAAGCTCAGGGGGAAGTCCCGGTCCAGGCCAGCTGCTGAGTCCACC 180
Qy 281 GGGCTGGAGGCCACATTTCCCAAGACCACACCTTTGGCTCAAGCTGATCCCTGCCGGGTG 340
Db 181 GGGCTGGAGGCCACATTTCCCAAGACCACACCTTTGGCTCAAGCTGATCCCTGCCGGGTG 240
Qy 341 GGCATCTCCACCAACAGGGTGGAGTGCCTCCCTCTGACTGTGTACAGCCTCAAGTCAAGC 400
Db 241 GGCATCTCCACCAACAGGGTGGAGTGCCTCCCTCTGACTGTGTACAGCCTCAAGTCAAGC 300
Qy 401 TCCAGCACAGATGATGTGGAGCTGGCCAGCGAGTTCACGACACAGAGCCTGGAGTGT 460
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XX WO200220850-A2.
XX 14-MAR-2002.
XX 10-SEP-2001; 2001WO-US28283.
XX 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciohanu DC, Malek M, Plastow G;
XX WPI; 2002-393850/42.
DR P-PSDB; AAE22985.
XX
PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene -
XX
XX PS Disclosure; Page 89-91; 109pp; English.
XX
CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX
XX SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
Query Match 69.3%; Score 1142; DB 24; Length 1873;
Best Local Similarity 85.8%; Pred. No. 5.6e-288;
Matches 1316; Conservative 0; Mismatches 210; Indels 8; Gaps 4;
Qy 95 ATGAGCTTCTAGAGCAAGAAACACAGCTCATGSCCATCCACCTGTGACCAAGCAGC 154
Db 1 ATGAGCTTCTAGAGCAAGAGAGAGCGCTTCATGSCCATCCCGAGCTGTAACCAACAGC 60
Qy 155 TCAGAAAGATTCCTGGGAAACGGAGGCCAAAGCCTTGAGATGAGCAAGCAGCAAGTCG 214
Db 61 TCAGAAAGAGCCATGGGACACAGGCGGACCAAGGCTCTAGATGGACAAAGCAGGAGAT 120
Qy 215 GTGAGGAAGGGAGCCACAGGTCAGGGGAAGGTCCTCGGTCCAGGCCAGCTGCTGAG 274
Db 121 GTAGAGGAAGGGGGCTCTGGGGCCCGAGGGAAGTCCCGCAGTCCAGGCCAGTTCGTGAG 180
Qy 275 TCCACGGGGCTGGAGGCCACATATCCCAAGACACACACCTTGCTGCTCAAGCTGATCC--T 331
Db 181 TCCACGGGGCAGGAGGCCACATATCCCAAGGCCACACCTTGSCCAAGCGCTCCCTTG 240
Qy 332 GCGGGGTGGCCACTCCACCAACAGGTGGGACTGCTCCCTCTGACTGTACAGCCCTCA 391
Db 241 GCGGAGTGGACAAACCCCAACAGAGCGGACATCTCCCTCTGACTGTGACGCTCA 300
Qy 392 GCTGAGGCTCCAGCACAGATGATGTGAGCTGGCCACGGAGTTCCAGGCCACAGAGGCC 451
Db 301 GCTCCGACTCCACACAGACCATCTGGATCTGGGATAGAGTTCTCAGCCTCCGGGGCG 360
Qy 452 TGGGAGTGTAGAGTGTAGAGGCTCTGGAAGAGAGGCTGCTCCCTGTGCTGTGCTCCGCGAG 511
Db 361 TCGGGGATGAGCT--TGGGCTGTGGAAGAGAGAGCCAGCCCGTGGCCATCCCCAGAG 417
Qy 512 GCCCATTTCCAAAGCTGGGCTGGGATGACCAATCGCGAAACCCCGGCCACAGATCTAC 571
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Qy 572 ATGGCGTTTCATGCGAGGAGCACACCTGTGATGCATGCATGGAACCTAGCTCAAGCTAGTGC 631
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Db 658 GACTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
Qy 812 GAACAACATAGATGAGACCTGGAGGAGATCTACTGCAAGGCTGCTGCAAGGCTGCTG 871
Db 718 GAAGAACAATAGATGAGACCTGGAGGAGATCTACTTCAAGGCTGCTGCAAGGCTGCTG 777
Qy 872 GTCTCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAAACCGG 931
Db 778 GTCTCCATCTCTCTCAATGACAGCTGTTTGAAGCTGTCTAGCGCTCTCATCAAGAAACCGG 837
Qy 932 ATCCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 991
Db 838 ATCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
Qy 992 AAAGCGCTGCTCAAGTTCCTGACATCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
Db 898 AAGCGCTTCTCAAGTTCCTGACATCTTTGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
Qy 1052 TACGCGACTATCAAGATTTGGGATGCGGACATTCGAGACTTGGCTGTGGTGTGGAG 1111
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Qy 1232 GCTGCCAGCAAACTTACAACTGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1291
Db 1138 GCTGCCCAACAACTTACAACTGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1197
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Db 1438 AAGCCATGAGAGGAGC-CGTGGACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1496
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RESULT 6
 AAD03319
 ID AAD03319 standard; cDNA; 1873 BP.
 XX AC AAD03319;
 XX DT 13-JUN-2001 (first entry)
 XX DE Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
 XX KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
 KW chromosome 15; ss.
 XX OS Sus scrofa.
 XX FH 13-SEP-2000; 2000WO-EP09896.
 XX FT CDS
 XX FT Key Location/Qualifiers
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 XX FT /*tag= a
 XX FT /product= "Sus scrofa complete Prkag3 protein"
 XX PN W0200120003-A2.
 XX PD 22-MAR-2001.
 XX PF 11-SEP-2000; 2000WO-EP09896.
 XX PR 10-SEP-1999; 99EP-0402236.
 XX PR 18-MAY-2000; 2000EP-0401388.
 XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX PA (ANDE/) ANDERSSON L.
 XX PA (LOOF/) LOOFT C.
 XX PA (KALM/) KALM E.
 XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
 XX PI Iannuccelli N, Geilun J, Le Roy P, Chardon P;
 XX DR WPI; 2001-244810/25.
 XX DR P-PSDB; AAE00222.
 XX PT New variants of the gamma subunit of vertebrate adenosine
 XX PT monophosphate-activated kinase for diagnosis or treatment of disorders
 XX PT associated with energy metabolism such as diabetes, obesity, and
 XX PT myopathy -
 XX PS Claim 12; Page 62-64; 71pp; English.
 XX CC The present sequence is a cDNA encoding pig adenosine monophosphate
 XX CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
 XX CC complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome
 XX CC 15. Mutation in Prkag3 results in an altered regulation of carbohydrate
 XX CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
 XX CC therapeutic for treating carbohydrate metabolism disorders such as
 XX CC diabetes, obesity, and disorders associated with muscle metabolism
 XX CC such as myopathy and cardiovascular diseases, to modulate AMPK
 XX CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
 XX CC and its functionally altered mutants are useful for the diagnostic
 XX CC evaluation, genetic testing and prognosis of a metabolic disorder,
 XX CC preferably a carbohydrate metabolism disorder. Primers that can detect
 XX CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
 XX CC useful for detecting a dysfunction of carbohydrate metabolism resulting
 XX CC from the expression of a functionally altered allele of PRKAG3.
 XX CC Transgenic animal and host cell transformed with PRKAG3 or a
 XX CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
 XX CC screening compounds able to modulate AMPK activity. Nucleic acid
 XX CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
 XX CC in a sequence encoding the first cystathione beta synthase (CBS) domain
 XX CC of PRKAG3 and is useful in gene therapy.
 XX SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 69.2%; Score 1140.4; DB 22; Length 1873;
 Best Local Similarity 85.7%; Pred. No. 1.5e-287;
 Matches 1315; Conservative 0; Mismatches 211; Indels 8; Gaps 4;
 QY 95 ATGAGCTTCCTAGAGCAAGAAACAGCAGCTCATGGCCATCACCAGCTGTGACACAGC 154
 DB 1 ATGAGCTTCCTAGAGCAAGAGAGAGCCCTTCATGGCCATCCCGAGCTGTACCACAGC 60
 QY 155 TCAGAAAGATCCGTGGGAAACGGAGGCCAAAGCCTTTAGATGGACAGGAGGAGTCG 214
 DB 61 TCAGAAAGAGCCATGGGGACCAAGGGCTCTAGATGGACAGGAGGAGGAT 120
 QY 215 GTGAGGAGGAGGAGGCCACCAAGCTCAGGGGAGAGTCCCGGTCCAGGCCAGCTGCTGAG 274
 DB 121 GTAGAGGAGGAGGAGGCCCTCCGGGGCCGAGGAGGTCCCCAGTCCAGGGCGTTGCTGAG 180
 QY 275 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACACACCCCTTGGCTCAAGCTGATCC - - - 331
 DB 181 TCCACCGGGCAGGAGGCCACATTCCTCCCAAGGCCACACCCCTTGGCCCAAGCCGCTCCCTTG 240
 QY 332 GCGGGGTGGGCATTCACACAGAGGTGGGACTGCCTCCCTCTGACTGTACAGCCTCA 391
 DB 241 GCGAGGTGGACACACCCGCCAACAGAGCGGGACATCCTCCCTCTGACTGTGACGCTCA 300
 QY 392 GCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCACAGCCACAGAGGCC 451
 DB 301 GCCTCCGACTCCACACAGACCATCTGGATCTGGGGATAGAGTTCTCAGCCTCGGGGGG 360
 QY 452 TGGGAGTGTGAGCTAGAAGGCTCTGTGAAGAGAGGCTTGCCTGTGCTGTGCTGCTGCTG 511
 DB 361 TCGGGGATGAGCT - - - TGGGCTGTGTGAAGAGAGCCAGCCGCTGCCATCCCCAGAG 417
 QY 512 GCGCCATTTCCAAAGCTGGGTGGATGAGAGCAACTGCGGAAACCGGGGCCAGATCTAC 571
 DB 418 GTGCTGTATACCCAGGCTGGGTGGATGATGAGTGCAGAAAGCGGGGGCCAGGTCTAC 477
 QY 572 ATGCGCTTATCAGGAGCACACCTGCTAGATGCCATGGCAACTAGTCCAAAGCTAGTTC 631
 DB 478 ATGCACTTATCAGGAGCACACCTGCTAGATGCCATGGGAGCAGCTCAAACTGGTTC 537
 QY 632 ATCTTCGACACCATGCTGGAGATCAAGAGGCTCTTTTGTCTGTGGTGGCCAAAGGTGTG 691
 DB 538 ATCTTCGACACCATGCTGGAGATCAAGAGGCTCTTTTGTCTGTGGTGGCCAAAGGTGTG 597
 QY 692 CGGGAGCCCCCTATGGGACAGCAAGACAGAGCTTTTGGGGAGTGTGACCATCACT 751
 DB 598 CGAGCGGACCTTTGTGGGACAGCAAGAGAGAGCTTCGTGGGATGCTGACCATCA 657
 QY 752 GACTTCATCTGCTGCTGCTACTACAGTCCCGCTGGTCCAGATCTATGAGATT 811
 DB 658 GACTTCATCTGCTGCTGCTGCTATACAGTCCCGCTGGTCCAGATCTACGAGATT 717
 QY 812 GAACAACATAAGATTGAGACCTTGGAGGAGATCTACTGCAAGGCTGCTTCAAGCCCTCTG 871
 DB 718 GAAGAACATAAGATTGAGACCTTGGAGGAGATCTACTTCAAGGCTGCTTCAAGCCCTCTG 777
 QY 872 GTCTCATCTCTCTTAATGATGAGCTGTTTGAAGCTGTCTACACCTCATCAGAACCGG 931
 DB 778 GTCTCATCTCTCTTCCAATGAGGCTTTCGAAGCTGTCTAGCCCTCATCAGAACCGG 837
 QY 932 ATCCATCGCTGCTGTTCTTTGACCCCGGTGTGAGCAAGCTACTCCACATCTCCACACAC 991
 DB 838 ATCCACCGCTGCGGGTCTTGAGACCTTCTCCGGGGCTGTGCTCCACATCTCCACAT 897
 QY 992 AAACGCTGCTCAAGTTCCTGCACATCTTTGGTTCCTGCTGCCCGGCCCTCTTCTCTC 1051
 DB 898 AAGCGGCTTCTCAAGTTCCTGCACATCTTTGGCACCTCTGCTGCCCGGCCCTCTTCTCTC 957
 QY 1052 TACCGCATATCCAGATTTGGGATCGGCACATTCGAGAGCTTGGCTGTGGTGTGGAG 1111
 DB 958 TACCGCATATCCAGATTTGGGATCGGCACATTCGAGAGCTTGGCGGTGGTGTGGAA 1017

[illegible]

Db	1258	GACCGATTGTCGGGGAAACAGTGCACCGCGCTGGTCTGCTGGATGAGACACGACACCTT	1311
Qy	1412	TTGGGCGTGGTCTCCCTCTCCGACATCCTTCAGGCACTGSGTGTCTAGCCCTGCTGGCATC	1471
Db	1318	CTGGGCGTGGTCTCCCTCTCTGACATCCTTCAGGCTTGGTGTCTAGCCCTGCTGGAATT	1377
Qy	1472	GATCCCTCGGGGCTGAGAAGATCTGAGTCTCAATCCCAAGCCACCT-GCACACCTGG	1530
Db	1378	GATCCCTCGGGGCTGAGAACCTTTGGAACCTTGTCTCTCAGGCCACCTGGCACACCTGG	1437
Qy	1531	AAGCAATGAAGGAACTGGGAAACTCAGCCTTTCATCTTCCCCACCCCATTTGCTGGT	1590
Db	1438	AAGCACTGAAGGGACC-CGTGGACTCAGCTCTCACTTCCCTCAGGCCACTTGTCTGGT	1496
Qy	1591	TCAGCTATGATTCAGGTAGGCTCTGCCCTGGGCC	1624
Db	1497	CTGGCTCTTCTTCAGGTAGGCTCGCGCCGGGCC	1530
RESULT 9			
AAD36459			
ID	AAD36459 standard; DNA; 1873 BP.		
XX	AC		
XX	AAD36459;		
DT	09-AUG-2002 (first entry)		
XX	Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).		
DE	AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;		
KW	screening; meat quality; single nucleotide polymorphism; SNP; pig;		
KW	gene; variant; ds.		
XX	XX		
OS	Sus scrofa.		
XX	XX		
FH	Key		
FT	CDS		
FT	Location/Qualifiers		
FT	1..1395		
FT	/*tag= a		
FT	/product= "Pig PRKAG3 polymorphic variant (PRKAG3-199)"		
FT	replace (595, A)		
FT	/*tag= b		
FT	/standard_name= "Single nucleotide polymorphism (SNP)"		
XX	XX		
PN	W0200220850-A2.		
XX	XX		
PD	14-MAR-2002.		
XX	XX		
PF	10-SEP-2001; 2001WO-US28283.		
XX	XX		
PR	08-SEP-2000; 2000US-231045P.		
PR	08-JAN-2001; 2001US-260239P.		
PR	18-JUN-2001; 2001US-299111P.		
XX	XX		
PA	(IOWA) UNIV IOWA STATE RES FOUND INC.		
XX	XX		
PI	Rothschild MF, Ciobanu DC, Malek M, Plastow G;		
XX	XX		
DR	WPI; 2002-393850/42.		
DR	P-PSDB; AA22987.		
XX	XX		
PT	Screening animals to determine those likely to produce larger litters		
PT	and improved meat quality traits involves assaying for the presence of		
PT	polymorphisms in the AMP activated protein kinase regulatory gamma		
PT	subunit gene .		
XX	XX		
PS	Disclosure; Page 98-100; 109pp; English.		
XX	XX		
CC	The invention relates to a method for screening animals to determine		
CC	those more likely to produce large litters and improved meat quality		
CC	traits. The method involves assaying for the presence of a genotype		
CC	in the sample of genetic material obtained from animal. The genotype		
CC	is characterised by polymorphism(s) in the AMP activated protein		
CC	kinase regulatory gamma subunit (PRKAG3) gene. The method is used		

PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
PA
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
XX WPI; 2002-393850/42.
DR P-PSDB; AAE22988.
XX
XX Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene
XX
XX Disclosure; Page 102-104; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterized by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
XX
SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match 69.1%; Score 1138.8; DB 24; Length 1873;
Best Local Similarity 85.7%; Pred. No. 3.8e-287;
Matches 1314; Conservative 0; Mismatches 212; Indels 8; Gaps 4;

QY 95 ATGAGCTTCCTAGAGCAAGAAACACAGAGCTCATGCGCATACACAGCTGTGACACGAGC 154
Db 1 ATGAGCTTCCTAGAGCAAGAGAGAGCGCTTCATGGCCATCCGAGCTGTAACACCGAGC 60

QY 155 TCAGAAAGATCCGTGGGAACGGAGGCGCCAAAGCCCTTGAGTGGACAGGCGAGAGTCG 214
Db 61 TCAGAAAGAGCATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120

QY 215 GTGGAGGAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 274
Db 121 GTAGAGGAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180

QY 275 TCCACCGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG ---T 331
Db 181 TCCACCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240

QY 332 GCGGGGTGGGCACTCCACCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 391
Db 241 GCGGAGGTGACAAACCCCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300

QY 392 GGTGAGGCTCCAGCAGAGATGATGTGGAGTGGCCAGGAGTTCCTCCAGCCACAGAGGCC 451
Db 301 GCTCCGAGCTCCAGCAGAGATCTGGATCTGGGAGATAGAGTTCCTCAGCCCTCGGCGGCG 360

QY 452 TGGGAGTGTAGCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 511
Db 361 TGGGGGATGAGCT---TGGGCTGGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417

QY 512 GCGCCATTTCCAGAGTGGGAGTACGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 571
Db 418 GTGCTGTATACCGAGCTGGGAGTGGATGATGAGTGGAGAGGAGGAGGAGGAGGAGGAGG 477

QY 572 ATGCGCTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 631
Db 478 ATGCACTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 537

QY 632 ATCTTCGACACCATGCTGGAGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 691
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 597

QY 692 CGGGCAGCCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGATGCTGACCATCACT 751
Db 598 CAAGCGGACCTTTGTGGGACAGCAAGAGCAGAGCTTGTGGGATGCTGACCATCACT 657

QY 752 GACTTCATCTGTGGTGTGATGCTTACAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 811
Db 658 GACTTCATCTGTGGTGTGATGCTTACAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 717

QY 812 GAACAACATAGATGAGAGCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGGCTGCTG 871
Db 718 GAAGAACAATAGATGAGAGCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTGCTG 777

QY 872 GTCTCCATCTCTCTATGATGAGCTGTTGAAGCTGCTTACACCTCTATCAAGAACGG 931
Db 778 GTCTCCATCTCTCTCAATGACAGCTGTTCGAAGCTGCTTACGCGCTCTATCAAGAACGG 837

QY 932 ATCCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Db 838 ATCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897

QY 992 AAAGCGCTGCTCAAGTTCCTGACATCTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
Db 898 AAAGCGCTTCTCAAGTTCCTGACATCTTTGGCACCCTGCTGCTGCTGCTGCTGCTGCTGCT 957

QY 1052 TACCGCATCTCAAGATTTGGGATCGGCATTCGCACATTCGCAGACTTGGCTGTGCTGGAG 1111
Db 958 TACCGCATCTCAAGATTTGGGATCGGCATTCGCAGACTTGGCCTGTGCTGGAA 1017

QY 1112 ACAGCACCATCTGACTGACATGACATGCTTTGAGCGCGGCTGTGCTGCTGCTGCTGCT 1171
Db 1018 ACAGCGCCATCTGACCGGCTGACATCTTCGTTGAGCGCGGCTGTGCTGCTGCTGCTGCT 1077

QY 1172 GTGCTCAAGAGTGTGTGAGTGTGGGCTCTATTTCCCGCTTTGATGTGATTCACCTG 1231
Db 1078 GTGCTCAAGAGTGTGAGAGTGTGGGCTCTACTCTGCTTTGATGTGATTCACCTG 1137

QY 1232 GCTGCCAGCAAACTACAAACCTTGGACATGAGTGTGGGAGAGCCCTGAGGAGGAGG 1291
Db 1138 GCTGCCCAACAACTACAAACCTTGGACATGAGTGTGGGAGAGCCCTGAGGAGGAGG 1197

QY 1292 ACATATGCTGTGAGGAGTTCCTTTCTGCCAGCCCAACGAGAGCTTGGGGAGAGTATC 1351
Db 1198 ACATGTGCTGTGAAGCGTCTCTTCTGCCAGCCCAACGAGAGCTTGGGGAGAGTATC 1257

QY 1352 GACAGATGCTCGGAGAGGATACACAGGCTGTGCTAGTGGACGAGACCCAGCATCTC 1411
Db 1258 GACCGGATTTGCCGGGAACAGGTGCACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317

QY 1412 TTGGGCGTGTCTCCCTCTCCGACATCTTCAAGGAGTGTGCTGCTGCTGCTGCTGCTGCT 1471
Db 1318 CTGGGCGTGTGCTCTCTCTGACATCTTCAAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 1377

QY 1472 GATGCGCTCGGGGCTGAGAAGATCTGAGTCTCTCAATCCCAAGCCACCT- GCACACCTGG 1530
Db 1378 GATGCGCTCGGGGCTGAGAAGCTTGGAACTTTGCTCTCAGGCGCACCTGCGCACACCTGG 1437

QY 1531 AAGCCAAATGAAGGAACTGGAGAGCTCAGGCTTCACTTCCCCACCCCACTTTCCTGCT 1590
Db 1438 AAGCCAGTGAAGGAGGAGC- CGTGGAGTCAAGTCTCACTTCCCCCTCAGGCGCACCTTCTGCT 1496

QY 1591 TCAGCTATGATTCAGTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1624
Db 1497 CTGGCTCTGTTCAAGTGTAGGCTCCGCGCGGCGCC 1530

RESULT 11
AAD03295
ID AAD03295 standard; cDNA; 1867 BP.
XX
AC AAD03295;
XX
DT 13-JUN-2001 (first entry)
XX

DE Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.

XX Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
KW chromosome 15; ss.

XX Sus scrofa.

OS Key Location/Qualifiers

FH 5'UTR 1..471

FT /*tag= a

FT 472..1389

FT /*tag= b

FT /product= "Sus scrofa PRKAG3 protein"

FT 1390..1867

FT /*tag= c

XX WO200120003-A2.

PN 22-MAR-2001.

XX 11-SEP-2000; 2000WO-EP09896.

XX 10-SEP-1999; 99EP-0402236.

PR 18-MAY-2000; 2000EP-0401388.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

PA (ANDE/) ANDERSSON L.

PA (LOOF/) LOOPT C.

PA (KALM/) KALM E.

XX Andersson L, Looft C, Kaim E, Milan D, Robic A, Rogel-Gaillard C;

PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX WPI: 2001-244810/25.

DR P-PSDB; AAE00220.

XX New variants of the gamma subunit of vertebrate adenosine

PT monophosphate-activated kinase for diagnosis or treatment of disorders

PT associated with energy metabolism such as diabetes, obesity, and

PT myopathy -

XX Claim 12; Fig 2; 71pp; English.

PS The present sequence is a cDNA encoding pig adenosine monophosphate

CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,

CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.

CC Mutation in Prkag3 results in an altered regulation of carbohydrate

CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as

CC therapeutic for treating carbohydrate metabolism disorders such as

CC diabetes, obesity, and disorders associated with muscle metabolism

CC such as myopathy and cardiovascular diseases, to modulate AMPK

CC activity, and for restoring a normal AMPK function. PRKAG3 sequence

CC and its functionally altered mutants are useful for the diagnostic

CC evaluation, genetic testing and prognosis of a metabolic disorder,

CC preferably a carbohydrate metabolism disorder. Primers that can detect

CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are

CC useful for detecting a dysfunction of carbohydrate metabolism resulting

CC from the expression of a functionally altered allele of PRKAG3.

CC Transgenic animal and host cell transformed with PRKAG3 or a

CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for

CC screening compounds able to modulate AMPK activity. Nucleic acid

CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or

CC in a sequence encoding the first cystathione beta synthase (CBS) domain

CC of PRKAG3 and is useful in gene therapy.

XX Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;

Query Match

Best Local Similarity 68.9%; Score 1134.4; DB 22; Length 1867;

Matches 1309; Conservative 0; Mismatches 211; Indels 8; Gaps 4;

QY 101 TTCTACGACAAAGAACAGCAGCCTCATGCCATACACAGCTGTGACACAGCAGCTCAGAA 160
|||||
Db 1 TTCTAGACGACGAGAGAGCGCTTCATGCCATCCGAGCTGTAAACACAGCAGCTCAGAA 60
QY 161 AGAATCCGTGGGAAACGGAGGCGCCAAAGCCTTCAGATGGACAAAGCAGAGTCCGTGGAG 220
|||||
Db 61 AGRAGCCATGGGGACAGGGGAAACAAGCCTCTAGATGGACAAGCAGAGAGATGTAGAG 120
QY 221 GAGGGGAGCCACAGGTCAGGGGGAAGTCCCGGTCAGGCCAGCTAGCTGTGAGTCCACC 280
|||||
Db 121 GAAGGGGGCCTCCGGGGCCCGAGGAGGTCCCCAGTCCAGGCCAGTGTGCTGAGTCCACC 180
QY 281 GGGCTGAGGCCACATCCCAAGACACACACCTTCGCTCAAGCTGATCC---TGCGGG 337
|||||
Db 181 GGGCAGGAGGCCACATTCCTCCCAAGGCCACACCTTGGCCCAAGCCGCTCCCTTGGCCGAG 240
QY 338 GTGGGCACCTCCACCAACAGGCTGGGACTGGCTCCCTCTGACTGTACAGCCTCAGCTGCA 397
|||||
Db 241 GTGGACAACCCCAACAGAGCGGACATCTCCCTCTGACTGTGACAGCTCAGCCTCC 300
QY 398 GGCTCAGCAGACAGATGTGGAGCTGGCCACAGGAGTTCAGGCCACAGAGGCTGGGAG 457
|||||
Db 301 GACTCCAAACACAGACCATCTGGATCTGGCATAGAGTTCTCAGCCTCGGGCGCTCGGG 360
QY 458 TGTGAGCTAGAAGGCTGCTGGAAGAGAGGCTGCCCTGTGCTGTGCCCGCAGGCCCA 517
|||||
Db 361 GATGAGCT---TGGGCTGGTGGAGAGAGGCCAGCCCGTGGCCATCCCAAGAGGTGCTG 417
QY 518 TTTCCCAAGCTGGGCTGGGATGACGAATGCGGAAACCCGGGCCAGATTAATACGCG 577
|||||
Db 418 TTACCCAGGCTGGCTGGGATGATGAGTGCAGAAGCCGGGGCCAGGTCTACATGCAC 477
QY 578 TTCATGACGAGACACACCTGCTACGATGCCATGGCACTAGCTCCCAAGCTAGTCACTTC 637
|||||
Db 478 TTCATGACGAGACACACCTGCTACGATGCCATGGCGACCACTCCAACTGGTCACTTC 537
QY 638 GACACCATGCTGGAGATCAAGAGGCTTCTTCTCTGTGGGCCAAAGCTGTGGGGCA 697
|||||
Db 538 GACACCATGCTGGAGATCAAGAGGCTTCTTCTGCTGGTGGGCCAAAGCTGTGGAGCG 597
QY 698 GCGCCTCTATGGACAGCAGAGGATTTGTGGGATGCTGACCATCACTGACTTC 757
|||||
Db 598 GCACCTTTGTGGACAGCAAGAGCAGAGCTTCTGTGGGATGCTGACCATCACAGACTTC 657
QY 758 ATCTGCTGCTGATCGCTACTACAGGTCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 817
|||||
Db 658 ATCTTGTGCTGACCGCTATTACAGTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 717
QY 818 CATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTCAAGGCTGCTGCTGCT 877
|||||
Db 718 CATAAGATTGAGACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTGCTGCTGCT 777
QY 878 ATCTCTCTAATGATAGCCTGTTTGAAGCTGCTACACCTCATCAAGAACCGGATCCAT 937
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Db 778 ATCTCTCCAATGACAGCCTGTTTGAAGCTGCTACGCTGCTCATCAAGAACCGGATCCAC 837
QY 938 GCGCTGCTGCTTGTGACCGGCTGTCAGGACACCTACTTCCACATCTCTACACACAAAGCG 997
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Db 838 GCGCTGCGGCTGCTGGACCTGCTCTCCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
QY 998 CTGCTCAAGTTCCTGGACATCTTGGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1057
|||||
Db 898 CTTCCTCAAGTTCCTGGACATCTTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
QY 1058 ACTATCCAAAGATTGGGCATTCGGACATTCGGAGACTTGGCTGTGCTGCTGCTGCTGCTGCT 1117
|||||
Db 958 ACCATCCAAAGATTGGGCATTCGGGCATTCGGACATTCGGAGACTTGGCTGTGCTGCTGCTGCTGCT 1017
QY 1118 CCATCTCTGACTGCACTGGACATCTTGTGGACCGGGGTGTGTGCTGCTGCTGCTGCTGCTGCT 1177
|||||
Db 1018 CCCATCTCTGACCGCACTGGACATCTTGTGGACCGGGGTGTGTGCTGCTGCTGCTGCTGCTGCT 1077

QY 1178 AACGAATGTGTCAAGTGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCC 1237
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1078 AACGAATGTGTCAAGTGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCC 1137
QY 1238 CAGCAACCTTCAACACCTTGGACATGAGTGTGGGAGAGCCCTGAGGCAGAGGACACTA 1297
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1138 CAACAACATACAACACCTTGGACATGAATGTGGGAGAAGCCCTGAGGCAGGGACACTG 1197
QY 1298 TGTCTGGAGGAGTCTTTCTCTCCAGCCCAAGAGCTTTGGGGGAAGTGAATGCACAGG 1357
||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1198 TGTCTGGAAGGCTCTTTCTCTCCAGCCCAAGAGCTTTGGGGGAAGTGAATGCACAGG 1257
QY 1358 ATTGTCTGGGACGAGGTACACAGCTGTGTAGTGTGACAGAGCCCAAGCATCTCTTGGGC 1417
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1258 ATTTGTCGGGAACAGTGTCAACCGCTTGTCTGTGGATGAGACCCAGCCTTCTTGGGC 1317
QY 1418 GTGGTCTCCCTCTCCGACATCTTTCAGGCACGTGGTGCACGCTCTGTGCATCATGATGC 1477
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1318 GTGGTCTCCCTCTCTGACATCTCTTCAAGGCTCTGGTGTGCTCAGCCCTGTGGAATGATGCC 1377
QY 1478 CTGGGGCTCTGAGAAGATCTGAGTCTCAATCCCAAGCCACT-GCACACCTTGGAGCCA 1536
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1378 CTGGGGCTCTGAGAACCTTGAACCTTTGCTCTCAGGCCCACTGTGSCACACCTTGGAGCCA 1437
QY 1537 ATGAAGGGAACCTGGAGAACTCAGCCTTCTATCTTCCCAACCCCAATTTGCTGTTCAGCT 1596
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1438 GTGAAGGGAGC-CGTGGAGTACGCTCTCACTTCCCTCAGCCCACTTGTGTGTGGCT 1496
QY 1597 ATCATTCAGTGGCTGTCCCTGGGCC 1624
| ||||| ||||| ||||| |||||
Db 1497 CTGTTCAGGTAGGCTCGGCCGGGCC 1524
RESULT 12
ABAO8485
ID ABAO8485 standard; cDNA; 547 BP.
XX ABAO8485;
AC ABAO8485;
XX
XX
XX 11-JAN-2002 (first entry)
XX
XX Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261.
XX
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnary; antiulcer; SS.
XX
XX Homo sapiens.
XX
XX WO200157188-A2.
XX
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US03800.
XX
XX 03-FEB-2000; 2000US-0496914.
XX
XX 27-APR-2000; 2000US-0560875.
XX
XX {HYSE-} HYSEQ INC.
XX
XX Tang Yt, Liu C, Drmanac RT;
XX
XX WPI; 2001-457740/49.
XX
XX

DR P-PSDB; ABB11241.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX Claim 1; Page 429; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis; cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
SQ Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
Query Match 27.2%; Score 448.8; DB 22; Length 547;
Best Local Similarity 99.6%; Pred. No. 3.5e-107;
Matches 450; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 738 TGTGACCATCACTGACCTTCATCTCTGGTGTGCTGCTACTACAGGTCCCGCTGCC 797
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TGTGACCATCACTGACCTTCATCTCTGGTGTGCTGCTACTACAGGTCCCGCTGCC 60
QY 798 AGATCTATGAGATTGAACAACATAGATTGAGACCTTGAGAGGAGATCTACCTGCAAGGCT 857
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AGATCTATGAGATTGAACAACATAGATTGAGACCTTGAGAGGAGATCTACCTGCAAGGCT 120
QY 858 GCTTCAAGGCTCTGGTCTCCATCTCTCTTAATGATAGCTGTTTGAAGCTGTCTACACCC 917
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GCTTCAAGGCTCTGGTCTCCATCTCTCTTAATGATAGCTGTTTGAAGCTGTCTACACCC 180
QY 918 TCATCAAGAACCGGATCCATCGCTGCTGCTTTTGTACCCCGGTGTCAGGCAAGTACTCC 977
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 TCATCAAGAACCGGATCCATCGCTGCTGCTTTTGTACCCCGGTGTCAGGCAAGTACTCC 240
QY 978 ACATCTCTCACACACAAACCGCTGCTCAAGTTCCTGCACATCTTTGGTTCCTGTGCCCC 1037
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ACATCTCTCACACACAAACCGCTGCTCAAGTTCCTGCACATCTTTGGTTCCTGTGCCCC 300
QY 1038 GSCCCTCCTCTCTACCGCACTATCCAAGATTGGGCATCGGCACATTCGGAGACTTGG 1097

|||||
301 GGCCTCTCTTCTACCGCACTATCCAGATTTGGCATCGGCACATTCGAGACTGG 360
|||||
1098 CTGTGCTGTGGAGACAGACCCATCCTGACTGGACATCTTTTGTGGACCGCGTG 1157
|||||
361 CTGTGCTGTGGAGACAGACCCATCCTGACTGGACATCTTTTGTGGACCGCGTG 420
|||||
1158 TGCTGCACTGCCCTGTGGTCAAGGAATGCTGGT 1189
|||||
421 TGCTGCACTGGCTGTGGTCAAGGAATGCTGGT 452
|||||
RESULT 13
AAH43682 standard; DNA; 989 BP.
XX AC AAH43682;
XX XX
XX 21-JAN-2002 (first entry)
XX XX
XX PRKAG3 intron 2 - Intron 4.
XX XX
XX Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
XX KW metabolic disease; diabetes; obesity; substitution; ds.
XX OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
XX FT intron 1..21
XX FT /tag= a "Intron 2"
XX FT /number= "3' portion of intron 2"
XX FT /note= "3' portion of intron 2"
XX FT 22..177
XX FT /tag= b
XX FT /number= "Exon 3"
XX FT 178..541
XX FT /tag= c
XX FT /number= "Intron 3"
XX FT 542..945
XX FT /tag= d
XX FT /number= "Exon 4"
XX FT 946..989
XX FT /tag= e
XX FT /number= "Intron 4"
XX FT /note= "5' portion of intron 4"
XX XX
XX WO200177305-A2.
XX PN
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-SE00765.
XX PR
XX PR 07-APR-2000; 2000US-195665P.
XX XX
XX PA (AREX-) AREXIS AB.
XX XX
XX PI Andersson L, Luthman H, Marklund S;
XX XX
XX WPI; 2001-657170/75.
XX XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
XX PT associated with a metabolic disease e.g. diabetes or obesity and method
XX PT for determining a risk estimate of diseases in subject by detecting the
XX PT variant -
XX XX
XX Example 1; Fig 2; 25pp; English.
XX PS
XX CC The sequences given in AAH43681-84 represents genomic fragments
XX CC encoding the human AMP-activated protein kinase gamma 3 subunit
XX CC (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
XX CC is useful in determining a risk estimate of a metabolic disease,
XX CC such as diabetes or obesity, in a subject. The variation may occur
XX CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of

a G for a C at nucleotide 320, resulting in the amino acid
substitution P71a; in exon 4 variation may be a substitution of a
T for a C at nucleotide 550; and in exon 10 variation may be a
substitution of a T for a C at nucleotide 1037, resulting in the
amino acid substitution R340W. There may also be nucleotide variation
in intron 6.
XX CC
SQ Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
Query Match 24.7%; Score 407.2; DB 22; Length 989;
Best Local Similarity 99.3%; Pred. No. 3.2e-96;
Matches 409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 247 AGSTCCCCGGTCCAGGCCAGCTCTGAGTCCACCGGGTGGAGGCCACATTCGCCAAGAC 306
|||||
DB 540 AGSTCCCCGGTCCAGGCCAGCTCTGAGTCCACCGGGTGGAGGCCACATTCGCCAAGAC 599
|||||
QY 307 CACACCCCTTGGCTCAAGCTGATCCTGCCGGGTGGGCCTCCACACAGGGTGGGACTG 366
|||||
DB 600 CACACCCCTTGGCTCAAGCTGATCCTGCCGGGTGGGCCTCCACACAGGGTGGGACTG 659
|||||
QY 367 CFTCCCTCTGACTGTACAGCTCAGCTCAGGCTCCAGCTCCAGATGATGTGGAGTGGC 426
|||||
DB 660 CCTCCCTCTGACTGTACAGCTCAGCTCAGGCTCCAGCTCCAGATGATGTGGAGTGGC 719
|||||
QY 427 CACGGAGTTCCACGACAGAGGCTGGAGTGTGAGCTAGAGGCTGCGAAGAGAG 486
|||||
DB 720 CACGGAGTTCCACGACAGAGGCTGGAGTGTGAGCTAGAGGCTGCGAAGAGAG 779
|||||
QY 487 GCCTGCCCTGTGCTGTCCCGCAGGCCCATTTCCCAAGCTGGCTGGGATGAGCAACT 546
|||||
DB 780 GCCTGCCCTGTGCTGTCCCGCAGGCCCATTTCCCAAGCTGGCTGGGATGAGCAACT 839
|||||
QY 547 GCGGAAACCCGGCGCCAGATCTACATGCGCTTCATGCGAGGACACACCTGTCTAGATGC 606
|||||
DB 840 GCGGAAACCCGGCGCCAGATCTACATGCGCTTCATGCGAGGACACACCTGTCTAGATGC 899
|||||
QY 607 CATGGCAACTAGCTCCCAAGCTAGTTCATCTCGACACCATGCTGGAGATCAAG 658
|||||
DB 900 CATGGCAACTAGCTCCCAAGCTAGTTCATCTCGACACCATGCTGGAGGTGAGG 951
|||||
RESULT 14
ABK84324
ID ABK84324 standard; cDNA; 1578 BP.
XX AC ABK84324;
XX XX
XX 14-AUG-2002 (first entry)
XX DE Human cDNA differentially expressed in granulocytic cells #895.
XX XX
XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
XX KW viral infection; parasitic infection; protozoal infection;
XX KW fungal infection; sterile inflammatory disease; psoriasis;
XX KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
XX KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
XX KW adult respiratory distress syndrome; inflammatory bowel disease;
XX KW Crohn's disease; ulcerative colitis; periodontal disease;
XX KW granulocyte activation; chronic inflammation; allergy.
XX OS Homo sapiens.
XX XX
XX WO200228999-A2.
XX PN
XX 11-APR-2002.
XX PD
XX XX
XX PF 03-OCT-2001; 2001WO-US30821.
XX PR
XX PR 03-OCT-2000; 2000US-237189P.
XX XX
XX PA (GENE-) GENE LOGIC INC.
XX XX

PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -

XX Claim 1; SEQ ID NO 895; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA) by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulation (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;

CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating Gs; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection, and
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1578 BP; 400 A; 377 C; 379 G; 422 T; 0 other;

Query Match 23.9%; Score 393.4; DB 24; Length 1578;

Best Local Similarity 65.1%; Pred. No. 1.5e-92;

Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0;

QY 567 TCTACATCGCTTCATGCAGGACGACACCTGCTACGATGCCATGCAACTAGCTCCCAAGC 626

DB 177 TGTATATCTCCTCATGAAGTCTCATCGCTGCTATGACCTGATCCCAAGCTCCAAAT 236

QY 627 TAGTCATCTTCGACACCATCTGGAGATCAAGAAGCCCTTCTGCTGCTGGTGGCCAAAG 686

DB 237 TGGTGTATTTGATAGCTGCTCCGTCAGGTGAAGAAAGCTTTTCTGCTTGGTACTAAGC 296

QY 687 GTGTCGGGCGAGCCCTCTATGGGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 746

DB 297 GTGTACGAGCTGCCCCCTTTATGGGATAGTAGAGAGCAAAAGTTTGTGGGCGATGCTGACCA 356

QY 747 TCATGACTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806

DB 357 TCATGATTTTCATCAATATCCCTGACCCGCTACTATATAATCAAGCCCTTGGTACAGATCATG 416

QY 807 AGATTGAACACATAAGATTGAGACTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGC 866

DB 417 AGCTAGAGAGACAGATAGAACTTGGAGAGAGGTGATCTCCAGGACTCCCTTAAAC 476

QY 867 CTCTGGTCTCCATCTCTCTCTAAATGATAGCCTGTTTGAAGCTGTCTACACCCCTCATCAAA 926

DB 477 CGCTTGTCTGCAATCTCTCTAAATGATAGCCTGTTTGAAGCTGTCTACACCCCTCATCAAA 536

QY 927 ACCGATCCATCGCTGCTGCTTGTGACCCGCTGTGACGCAACGTAAGTCTCCACATCCCTCA 986

DB 537 ACAGATCCACAGGCTGCCAGTATTGACCCAGAAATCAGGCAATACTTGTACATCTCTCA 596

QY 987 CACACAAAGCCCTGCTCAAGTTCCTGCAATCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCT 1046

DB 597 CCCAAGAGCATCTCTGAAGTTCCTCAAAATGTTTATCTAGTTCCTCCCAAGCCAGAGT 656

QY 1047 TCCTTACCGCATATCAAGATTTGGCATCGGCATTCGAGACTTGGCTGTGGTGC 1106

DB 657 TCATGTCCCAAGTCTCTGGAGAGAGCTACAGATTTGGCACCTATGCCAATATTGCTATGGTTC 716

QY 1107 TGGAGACAGCACCACCTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1166

DB 717 GCATACACCCCGCTCTATGTGGCTCTGGGATTTTGTACAGCATCGAGTCTCAGCCC 776

QY 1167 TGCTGTGGTCAACGAATTTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 1226

DB 777 TGCCAGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 836

QY 1227 ACCTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 1286

DB 837 ATCTGGGACGAGAAAGACCTTACACACACCTTACATGATGATGATGATGATGATGATGAT 896

QY 1287 AGAGGACATATCTCTGGAGGAGTCTCTTCTGCCAGCCGCCAGAGAGCTTGGGGGAAG 1346

DB 897 ATGATCACATTTCTTGGAGGTGTCTCAAGTGTCTACCTGATGAGACTCTGGAGACCA 956

QY 1347 TGATCGACAGGATTTCTGGGAGGAGGTACACAGGCTGGTGTGTGTGTGTGTGTGTGTGT 1406

DB 957 TCATCAACAGGCTAGTGGAGAGAGGTTCCAGGCTTGTGTGTGTGTGTGTGTGTGTGTGT 1016

QY 1407 ATCTTTGGGCTGTCTCTCTCTCCGACATCTTTCAGGACTGTGTGTGTGTGTGTGTGTGT 1457

DB 1017 TGGTCAAGGAGATTTGATCCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCA 1067

RESULT 15

AAC98774

ID AAC98774 standard; cDNA; 1691 BP.

XX AAC98774;

XX 09-MAR-2001 (first entry)

XX Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:2.

DE Human; pancreas; pancreatic cancer; pancreatic cancer antigen;

XX detection; diagnosis; identification; cytostatic; neuroprotective;

XX neotropic; immunomodulatory; relaxant; contraceptive; gynaecological;

XX antiinflammatory; cardiant; gene therapy; chromosome mapping;

XX linkage analysis; tissue identification; tissue typing; forensic;

XX neural; immune system; muscular; reproductive; gastrointestinal;

XX pulmonary; cardiovascular; renal; proliferative; ss.

XX Homo sapiens.

XX WO200055320-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05989.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX	WPI: 2000-579444/54.
DR	P-PSDB; AAB54009.
XX	
PT	New nucleic acid that is a pancreatic cancer antigen for preventing,
XX	treating, or ameliorating a medical condition, particular pancreatic
PT	cancer, or for use in assays for diagnosing a pathological condition -
XX	
XX	Claim 1; Page 498-499; 1379pp; English.
XX	
CC	AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC	proteins, called pancreatic cancer antigens, given in AAB54008 to
CC	AAB54466. The human pancreatic cancer antigens have cytostatic,
CC	neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
CC	gynaecological, cardiant and antiinflammatory activities, and can be used
CC	in gene therapy. The polynucleotide and proteins can be used for
CC	preventing, treating, or ameliorating a medical condition or in assays
CC	for diagnosing a pathological condition or a susceptibility to one in a
CC	subject. Binding partners to the proteins and the activity of the
CC	proteins can be identified. The pancreatic cancer antigens can be used to
CC	detect, treat or prevent pancreatic disorders, especially cancer.
CC	Agonists and antagonists to the antigens can be screened for. The
CC	pancreatic cancer antigen polynucleotides can be used to design nucleic
CC	acid hybridisation probes that can be used in chromosome mapping, linkage
CC	analysis, tissue identification and/or typing and a variety of forensic
CC	and diagnostic methods. The proteins can be used to generate antibodies
CC	which are used to purify, detect and target the polypeptides, including
CC	both in vivo and in vitro diagnostic and therapeutic methods. The
CC	proteins can be used to treat or prevent neural, immune system, muscular,
CC	reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC	proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC	sequences used in the exemplification of the present invention.
XX	
SQ	Sequence 1691 BP: 458 A; 382 C; 401 G; 449 T; 1 other:
	Query Match 23.9%; Score 393.4; DB 21; Length 1691;
	Best Local Similarity 65.1%; Pred. No. 1.6e-92;
	Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0;
QY	567 TCATCATGGCTTCATGCGAGCAGCACACCTGTAGCATGCCATGGCAAAATAGTCCCAAGC 626
DB	
	123 TGTATATTCCCTTCATGAAGTCTCATCGTGCTATGACCTGATTTCCCACAGCTCCAAT 182
QY	627 TAGTCATCTTGACACCATGCTGAGATCAAGAAGCGCTCTTTTGGTCTGGTGGCCAACG 686
DB	
	183 TGGTGTGTAATTGATACGTCCTCGAGTCAAGAAAGAGCTTTTTTGGTGTGGTAGCTAAGC 242
QY	687 GTGTGGGGCAGGCCCTCTATGGCAGCAGCAAGACAGAGCTTTGTGGGGATGCTGACCA 746
DB	
	243 GTGTACAGCTGCCTCTTATGGGATAGTAAAGACAAGTTTGTGGGGCATGCTGACCA 302
QY	747 TCATGACTTTCATCTGCTGGTCTGATCGCTACTACAGGTGCCCTGGTGGTCAGATCTATG 806
DB	
	303 TCACTGATTTTCATCAATAATCTCGACCGCTACTAATAATCAGCTTGGTACAGATCTATG 362
QY	807 AGATTGAACACAAATGAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGC 866
DB	
	363 AGCTAGAAGAACAAGATAGAACTTTGGAGAGGTGTATCTCCAGGACTCTCTTTAAAC 422
QY	867 CTCGTGCTCCATCTCTCTTAATCATAGCCTGTTTGAAGCTGTCTACACCTTCATCAAGA 926
DB	
	423 CGCTGTGTCATTTCTCTTAATCCACAGCTGTGTTTGTATCTCTTCAATTAATTCGGA 482
QY	927 ACCGGATCCATGCTGCTGTCTTTCACCCGGTGTCAGGCAAGGTACTCCATCTCTCA 986
DB	
	483 ACAAGATCCACAGCTGGCAGTATTGACCCAGATCAGGCAATACTTGTATCATCTCTCA 542
QY	987 CACACAAAGCCCTGCTCAAGTTCCTGCACATCTTTTGGTTCCTCGCCGCCGCTCTCT 1046
DB	
	543 CCCACAGCGCATCTGAAGTTCCTCAAATTTGTTATCACTGAGTTCCTCCACAGCCAGAGT 602
QY	1047 TCCTCTACCGCACTATCCAAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGC 1106

Db 176 TGTATATCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCACAAAGCTCAAAAT 235
QY 627 TAGTCATCTCGACACATGCTGGAGATCAAGAGCGCTTCTTTCGCTCTGGTGGCCACAG 686
Db 236 TGGTTCTATTGATACGCTCCCTCAGGTGAAGAAAGCTTTTTCGCTTTGGTGAAGTAAAG 295
QY 687 GTCTGGGGGAGCCCTCTATGGAGCAGCAAGCAAGCAGAGCTTTGTGGGATGCTGACCA 746
Db 296 GTCTAGAGCTGCCCCCTTATGGGATAGTAAAGCAAGAGTTTGTGGGATGCTGACCA 355
QY 747 TCAGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 806
Db 356 TCAGTCACTCAATCAATCTGACCGCTACTTAATCAATCAAGCTTGTGTACAGTCTAG 415
QY 807 AGATTGAACAACATAAGATGAGACCTGGAGGAGATCACTCTCAAGGCTGTTCAAGC 866
Db 416 AGCTAGAACAAACAGATGAGAACTTGGAGAGAGTGTATCTCCAGGACTCCTTTAAAC 475
QY 867 CTCTGCTCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCTCAAGA 926
Db 476 CGTTGCTGCAATTTCTCTAATGCCAGCTTGTGTATGCTGTCTCTTCAATTAATTCGCA 535
QY 927 ACCGGATCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 986
Db 536 ACAGATCCACAGGCTGCCAGTATTGACCCAGATCAGCAACTTTGTATCATCTCA 595
QY 987 CACACAAAGCGCTGCTCAAGTCTGACATCTTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCTG 1046
Db 596 CCCACAAAGGCAATTCGAAGTCTCTCAAAATGTTTATCATCTGAGTTCCTCCCAAGAGAT 655
QY 1047 TCCTCTACCGCACTATCCAGATTTGGGATCGGCACATCCGAGACTTGGCTGTGGTGC 1106
Db 656 TCATGTCCAAAGTCTCTGGAAGAGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC 715
QY 1107 TGGAGACAGCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1166
Db 716 GCATACAGACCCCGTCTATGTGCTCTGGGATTTTGTACAGCATCGAGTCTCAGCC 775
QY 1167 TGCTGTGTGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1226
Db 776 TGCCAGTGTGATGAGAAGGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 835
QY 1227 ACCTGCTGCCAGCAACCTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1286
Db 836 ATCTGCGACGAGAAAGACCTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 895
QY 1287 AGAGACATATGCTGAGGAGCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1346
Db 896 ATCGATCACATTAATTTGAGGGTGTCTCAAGTGTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTG 955
QY 1347 TGATGACAGAGATTCCTGGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1406
Db 956 TCATCAACAGGCTAGTGAAGCAGAGGTTTACCCGACTTGTATGCTGCTGCTGCTGCTGCTGCTGCTG 1015
QY 1407 ATCTCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1457
Db 1016 TGGTCAAGGAAATGTATCACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1066

RESULT 2

US-08-878-989-14
; Sequence 14, Application US/08878989
; Patent No. 5685803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES

; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
; US-08-878-989-14

Query Match 22.3%; Score 366.6; DB 2; Length 1435;
Best Local Similarity 62.9%; Pred. No. 3.3e-87;
Matches 567; Conservative 0; Mismatches 334; Indels 0; Gaps 0;
QY 567 TCATACATGCGCTTCATGTCAGGAGCACACCTGCTACCATGCCATGCCACTAGCTTCAAGC 626
Db 183 TTTACATGCGGATTCATGAGGTCACACAAGTGTATGATCGTTCACACCAAGTTTCAAGC 242
QY 627 TAGTCATCTTCGACACCATGCTGGAGATCAAGAGCGCTTCTTTCGCTCTGGTGGCCACAG 686
Db 243 TTGTTGCTTGTACTACTACATTAAGTTAAAGGCGCTTCTTTCGCTTGTGAGCCACAG 302
QY 687 GTGTGGGGGAGCGCCCTCTATGGGACAGCAAGAGCAGAGCTTGTGGGATGCTGACCA 746
Db 303 GTGTCCGAGCAGCGCCACTGTGGGAGAGTAAAAAAGAGTTTGTAGGAATGCTAACAA 362
QY 747 TCATGACTTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 806
Db 363 TTACATGATTTCATAAATACTACTACATATATAAATCAACCTATGCTGCTGCTGCTGCTGCTG 422
QY 807 AGATTGAACAACATTAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGC 866
Db 423 AATTAGAGGACATATAAATTGAACATGGAGGAGGCTTTATTATACAGAAACATTTAAGC 482
QY 867 CTCTGCTTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTTACACCTCATCAAGA 926
Db 483 CTTTGTAGTATATATCTCCAGATCAAGCCTCTTCGATGCTGTATGCTTCTGCTGCTGCTGCTG 542
QY 927 ACCGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 986
Db 543 ATAAATCCACAGATTGCGGCTTATGACCTATCAAGTGGGAAATGCACTTTATATACTTAA 602
QY 987 CACACAAAGCGCTGCTCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1046

Db 603 CCCACAAAGAACTCCTCAAGTTCCTCCAGCTTTTATGTCGTGATATGCCAAAGCCCTGGCT 662
QY 1047 TCCTCTACCGCACTATCCAGATTTTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGC 1106
Db 663 TATGAGCAGAACTGGATGAGCTTGGAAATAGGAACGTACCAACATTTGCCCTTCATAC 722
QY 1107 TGGAGACAGCACCCACTGCTGACTGCCACTGGACATCTTTGTGGACCGCGCTGTCTGGCAC 1166
Db 723 ATCCAGACACTCCCATCATCAAGCCTTGAACATATTTGTGGAAGACGAATATCAGCTC 782
QY 1167 TGCTGTGGTCAAGCAATGTGGTCAGGTGCTGGGCTCTATTCGCCGTTTGTGATGTATTC 1226
Db 783 TGCTGTGGTGTGATCAGTCAGCAAGAAAGTTGTAGATATTTATTCACAAATTTGTGTAATTA 842
QY 1227 ACCTGGCTGCCAGCAACCTACAAACCTGACATCAACCTGGACATGAGTGTGGGAGAGCCCTGAGCC 1286
Db 843 ATCTTGCTGCTGAGAAACATACATTAACCTAGATATCACGGTACCGCCAGCCGCTTCAGC 902
QY 1287 AGAGCACTATGCTGTGGAGGAGTCTCTTTTCCTGCCAGCCCCAGAGAGCTTGGGGGAAG 1346
Db 903 ACCGTTACAGTATTTTGAAGTGTGTGAAGTGCATTAAGCTGGAATATCTGGAGACCA 962
QY 1347 TGATCGACAGGATTTGCTGGGAGCAGGTACACAGCTGGTCTAGTGGAGAGACCCAGC 1406
Db 963 TCGTGGACAGAAATAGTAAGAGCTGAGGTCCATCGGCTGGTGGTAAATGAAGCAGATA 1022
QY 1407 ATCTCTTGGCGTGGTCTCCCTCTCCGACATCTTTCAGGCACTGGTCTCAGCCCTGCTG 1466
Db 1023 GTATGTGGGTATTTTCCCTCTCGGACATTTCTGCAAGCCCTGATCCTCACACCGACAG 1082
QY 1467 G 1467
Db 1083 G 1083

RESULT 3

US-09-272-796-14
; Sequence 14, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASHS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyle Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
US-09-272-796-14

Query Match 22.3%; Score 366.6; DB 4; Length 1435;
Best Local Similarity 62.9%; Pred. No. 3.3e-87;
Matches 567; Conservative 0; Mismatches 334; Indels 0; Gaps 0;

QY 567 TCTACATGGCTTCATGTCAGGAGCACACCTGCTACCATGCGCATGGCACTAGCTTCCAAGC 626
Db 183 TTTACATGGATTCATGAGGTTCACACAGTGTATGACATCGTCCACACAGTTCAAAGC 242
QY 627 TAGTCATCTTCGACACCACTGCTGGAGATCAAGAAGCCCTTCTTTGCTGCTGTGGTGGCAAG 686
Db 243 TTGTTGCTTTGATACTACATTTACAAGTTAAAAGGSCCTTCTTTGCTTGTGTAGCCCAAG 302
QY 687 GTGTGGGGGAGCCCTCTATTTGGACAGCAAGAGCAGAGCTTTGTGGGAGTGTGACCA 746
Db 303 GTGTCCGAGCAGCGCCACTGTGGGAGAGTAAAAAAGAGTTTGTAGAAATGCTAACAA 362
QY 747 TCATGACTTTCATCTGCTGCTGCTACTCGCTACTACAGGTCCCGCTGCTCCAGATCTATG 806
Db 363 TTACAGATTTCAATAATATATCTACATAGATCTATTAATCACCATATGTACAGATTTATG 422
QY 807 AGATTTGAACAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGC 866
Db 423 AATTAGAGGAACATAAAATTGAAACATGGAGGAGCTTTATTTACAAGAAACATTTAAGC 482
QY 867 CTCTGCTCTCCATCTCTCTTAATGATAGCTGTTTGAAGCTGCTTACACCTCATCAAGA 926
Db 483 CTTTGTAGTAATATATCTCCAGATGCAAGCCCTCTTCGATGCTGTATATCTCTTGTATCAAAA 542
QY 927 ACCGGATTCATGCTGCTGCTGCTTTCAGCCCGGTGTTCAGGCAACCTACTCCACATCTCTCA 986
Db 543 ATAAATCCACAGATGCCCCGTTATGACCCCTATCAGTGGGAATGCACCTTTATATACTTA 602
QY 987 CACACAAAGCCCTGCTCAAGTTTCCTTGCACATCTTTGTTCCCTGCTGCCCGGCCCTCT 1046
Db 603 CCCACAAAGAAATCCTCAAGTTTCCTCCAGCTTTTATGTCTGATATGCCAAAGCCCTGCCT 662
QY 1047 TCCTCTACCGCACTATCCCAAGATTTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGC 1106
Db 663 TCATGAAGCAGAAACCTGGATGAGCTTGGAAATAGGAACGTACCAACAAATTCCTTCATAC 722
QY 1107 TGGAGACAGCACCCACTCCTGCTGACTGGACATCTTTGTGGACCGCGGTGTGCTGCAC 1166
Db 723 ATCCAGACACTCCCATCATCAAGCCTTGACATATTTGTGGAAGACGAATATCAGCTC 782
QY 1167 TGCCCTGTGGTCAAGCAATGTGGTCAAGTTCGTTGGGCTCTTATTCGCCGTTTGTGATGTATTC 1226
Db 783 TGCCCTGTGTGGATGAGTCAGGAAAGTTGTAGATATTTATTTCCAAAATTTGATGTAATTA 842
QY 1227 ACCTGGCTGCCAGCAACCTACAAACCTGACATGAGTGTGGGAGAGCCCTGAGGC 1286
Db 843 ATCTTGCTGCTGAGAAACATACAAATACCTAGATATCACGGTGTACCCAGCCGCTTCAGC 902
QY 1287 AGAGCACTATGCTGTGGAGGAGTCTCTTTCCTGCCAGCCCCAGAGAGCTTGGGGGAAG 1346
Db 903 ACCGTTACAGTATTTTGAAGTGTGTGAAGTGTGTGAAGTGAATTAAGCTGGAATATCTGAGACCA 962
QY 1347 TGATCGACAGGATTTGCTCGGAGAGAGGTACACAGGCTGGTGTCTAGTGGACGAGACCCAGC 1406

APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5612201man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5355
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
NAME/KEY: MAGE-41 gene
US-08-299-849B-14

Query Match 2.4%; Score 39.6; DB 1; Length 2531;
Best Local Similarity 44.4%; Pred. No. 0.54;
Matches 159; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 373 CTCCTGACTGTACAGCTCAGCTCCAGCAGATGTGTGGAGCTGGCGACGGA 432
DB 858 CACTGTGTGAGGCAACCAATGAGCGTTCCAGCAGCAAGAGAGAGGGGCCAACAC 917
QY 433 GTTCCAGCCACAGAGCGCTGGAGTGTGAGCTAGAGGCGCTGCTGGAAGAGAGCGCTGC 492
DB 918 CTCGCTGTGAGCGAGAGTCTTGTCCGAGAGAGCACTCAGTAACAAGGTGGATGGTGC 977
QY 493 CCTGTGCTGTCCCCCGAGGCCCATTTCCCAAGCTGGGCTGGGATGAGCACTGGCGAA 552
DB 978 TCATTTTCTGCTCCGCAAGTATCGAGCCAGGAGCTGGTCACAAAGGCGAAGTCTGGA 1037
QY 553 ACCCGCGGCCAGATCTACATCGCTTCATGCGAGGACACACTGCTCAGATGCCATGGC 612
DB 1038 GAGAGTCATCAAAATTACAGCGCTGTTTCTCTGTGATCTTCGGAAGGCTCGAGTC 1097
QY 613 AACTAGTCCAAAGCTAGTCACTTCGACACATGCTGGAGATCAAGAGGCGCTTCTTTGC 672
DB 1098 CTTGAAGATGATCTTTGGCATTGAGCTGAAGGAAGTGGACCCACCAACACACTACAC 1157
QY 673 TCTGGTGGCAACGGTGTCCGGGAGCCCTCTATGGGACAGCAGCAAGCAGCTTTT 730
DB 1158 CTTGTGTCACCTGTGGGCGCTTCTCTATGATGGCGCTCTGGGTAATATCAGATCTTT 1215

RESULT 9
US-08-142-368A-14
; Sequence 14, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:

APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
NAME/KEY: MAGE-41 gene
US-08-142-368A-14

Query Match 2.4%; Score 39.6; DB 2; Length 2531;
Best Local Similarity 44.4%; Pred. No. 0.54;
Matches 159; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 373 CTCCTGACTGTACAGCTCAGCTCCAGCAGATGTGTGGAGCTGGCGACGGA 432
DB 858 CACTGTGTGAGGCAACCAATGAGCGTTCCAGCAGCAAGAGAGAGGGGCCAACAC 917
QY 433 GTTCCAGCCACAGAGCGCTGGAGTGTGAGCTAGAGGCGCTGCTGGAAGAGAGCGCTGC 492
DB 918 CTCGCTGTGAGCGAGTCTTGTTCGAGAGAGCACTCAGTAACAAGGTGGATGGTGGC 977
QY 493 CTTGTGCTGTCCCCCGAGGCCCATTTCCCAAGCTGGGATGAGCACTGGCGAA 552
DB 978 TCATTTTCTGCTCCGCAAGTATCGAGCCAGGAGCTGGTCACAAAGGCGAAGTCTGGA 1037
QY 553 ACCCGCGGCCAGATCTACATCGCTTCATGCGAGGACACACTGCTCAGATGCCATGGC 612
DB 1038 GAGAGTCATCAAAATTACAGCGCTGTTTCTCTGTGATCTTCGGAAGGCTCGAGTC 1097

QY 613 AACTAGCTCCAGAGTGTGAGTCTTCGACACCATGCTGGAGATCAAGAGGCTTCCTTTCG 672
Db 1098 CTTGAGATGATCTTTTGGCATTCACGTGAAGAGTGGACCCACACGACACCTACAC 1157
QY 673 TCTGTGGCCACAGGTGTGGCGGCGCCCTCTATGGGACACGAAGAGCAGAGCTTT 730
Db 1158 CTTGTGCACCTGCGGCGCTTTCTATGATGGCGCTGCTGGTAAATACAGATCTTT 1215

RESULT 10
US-08-967-727-14
; Sequence 14, Application US/08967727
; Patent No. 6025474
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,727
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION NUMBER:
; FILING DATE: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-41 gene
US-08-967-727-14

Query Match 2.4%; Score 39.6; DB 3; Length 2531;
Best Local Similarity 44.4%; Pred. No. 0.54;
Matches 159; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 373 CTCTGAGTGTACAGCCTCAGCTGCAGGCTCCAGCAGACAGATGATGTGGAGCTGGCCACGGA 432
Db 858 CACTTGTGTGAGGCAACCCATAGAGGTTCCAGCACCCCAAGAGAGGAGGCGCCACAGCAC 917
QY 433 GTTCCAGGCCACAGAGGCTGGGAGTGTGAGCTAGAGCCCTGTCTGGGAAGAGGCGCTTC 492
Db 918 CTCGCTGACGCGAGAGTCTTTGTTCCGAGAAGCAGCTCAGTAACAAGGTGGATGAGTTGGC 977
QY 493 CTGTGCTGTCTCCCGCAGAGCCCATTTCCCAAGCTGGGCTGGGATGACGAACTGGCGGAA 552
Db 978 TCATTTTCTGCTCCGCAAGTATCGAGCCAAAGAGAGCTGGTCACAAAAGCAGAAATGCTGGA 1037
QY 553 ACCGGGCGCCAGATCTACATGCGCTTCATGCGAGGAGCACACCTGCTACGATGCCATGGC 612
Db 1038 GAGAGTCATCAAAAATTACAAGCGCTGTTCTCTGTGATCTTCGGCAAGCGCTCCGAGTC 1097
QY 613 AACTAGTCTCCAGCTAGTACTTTCGACACCATCTGCTGGAGATCAAGAGGCGCTTCCTTTCG 672
Db 1098 CTTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCACCACGACACCTACAC 1157
QY 673 TCTGTGGCCACAGGTGTGGCGGCGAGCCCTCTATGGGACACGAAGAGCAGAGCTTT 730
Db 1158 CTTGTGCACCTGCGGCGCTTTCTATGATGGCGCTGCTGGTAAATACAGATCTTT 1215

RESULT 11

US-08-037-230D-14
; Sequence 14, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230D
; FILING DATE: 26-MARCH-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6235525man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884

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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2531 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: genomic DNA
;   FEATURE:
;     NAME/KEY: MAGE-41 gene
;   US-08-037-230D-14
```

```
Query Match          2.4%; Score 39.6; DB 4; Length 2531;
Best Local Similarity 44.4%; Pred. No. 0.54;
Matches 159; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 373 CTCGACGTGTACAGCCTCAGCTGACAGGCTCCAGGCACAGATGATGGAGCTGGCCACGGGA 432
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 858 CACTTGTGTGGAGGCAACCCAAATGAGGGTTCAGCAGCCAAAGAGAGAGGGGCCCAAGCAC 917
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 433 GTTCCAGCCACAGAGCCTGGGAGTGTGAGCTAGAGGCTCTGCGAAGAGAGSCCTGCG 492
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 918 CTCGCGCTGAGCAGAGCTCTTGTTCGAGAAAGCACTCAGTAACAAGGTGGATGGATTGGC 977
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 493 COTGTGCTGTCCCGCAGCGCCCAATTTCCCAAGCTGGGCTGGGATGACGAACCTCGGAA 552
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 978 TCATTTTCTGCTCGCAAGTATCGAGCCAGGAGCTGTCACAAAGGCGAGAAATGCTGGA 1037
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 553 ACCCGGGCCCGAATCATATCGGCTTCATCGCAGACACACCTGCTAGATGCCATGGC 612
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1038 GAGAGTCATCAAAATTAAGCGCTGCTTTCCTGTGATCTTCGGCAAGCCTCCGAGTC 1097
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 613 AACTAGCTCCAAGCTAGTATCTTCGACACCATCTCGACATCAAGAAGGCTTCTTTGC 672
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1098 CCGAAGATGATCTTTGGATTCAGCTGAAGAAAGTGGACCCACCAGCAACACCTACAC 1157
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 673 TCTGTGCGCCAAACGGTGTGCGGCGAGCCCTCTATGGGACAGCAAGAAGCAGAGCTTT 730
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1158 CTTGTACCTGCTGGGCTTTCTCTATGATGGCTGCTGGGTAATAATCAGATCTTT 1215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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```
RESULT 12
US-09-056-105-10
; Sequence 10, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 4895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-10
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Query Match          2.4%; Score 39.6; DB 4; Length 4895;
Best Local Similarity 44.4%; Pred. No. 0.69;
Matches 159; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 373 CTCGACGTGTACAGCCTCAGCTGACAGGCTCCAGGCACAGATGATGGAGCTGGCCACGGGA 432
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3222 CACTTGTGTGGAGGCAACCCAAATGAGGGTTCAGCAGCCAAAGAGAGAGGGGCCCAAGCAC 3281
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 433 GTTCCAGCCACAGAGCCTGGGAGTGTGAGCTAGAAGGCTCTGCGAAGAGAGSCCTGCG 492
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3282 CTCGCGCTGACGACAGTCCTTGTTCGAGAAAGCACTCAGTAACAAGGTGGATGGATTGGC 3341
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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```
QY 493 CCTGTGCTGTCCCGCAGAGCCTCCATTTCCCAAGCTGGGCTGGGATGACGAACCTCGGAA 552
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3342 TCATTTTCTGCTCGCAAGTATCGAGCCAAAGAGGCTGGTCAAAAGGCGAAGATGCTGGA 3401
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 553 ACCCGGGCCCGCAGATCTACATGGCTTCATGCAGGAGCACACCTGCTAGCATGCCATGGC 612
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3402 GAGAGTCATCAAAATTAAGGCGCTGCTTCCCTGTGATCTTCGGCAAGCCTCCGAGTC 3461
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 613 AACTAGCTCCAAGCTAGTATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGC 672
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3462 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCACCAGCAACACCTACAC 3521
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 673 TCTGTGCGCCAAACGGTGTGCGGCGAGCCCTCTATGGGACAGCAAGAAGCAGAGCTTT 730
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3522 CTTGTGTCACCTGGCGCTTTCCTATGATGGCTGCTGGGTAATAATCAGATCTTT 3579
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 13
US-09-007-005-17/C
; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

Query Match          2.4%; Score 38.8; DB 4; Length 289;
Best Local Similarity 5.3%; Pred. No. 0.39;
Matches 10; Conservative 87; Mismatches 93; Indels 0; Gaps 0;

QY 894 GCCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGGATCCATCGCTGCTGTTCTTG 953
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 246 GYAGVTYTYAVCYGYCYGYCTYGYSYNYNYNYNYNYNYNYNYNYNYNYNYNYNY 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 954 ACCCGGTGTGAGGCAAGCTACTCCACATCTCTACACAAACCGCTGCTAAAGTTCTTGC 1013
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 186 NYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNY 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1014 ACATCTTTGTTCTCTGCTGCTGCCCGGCTCTTCTTCTACCGCACTATCCAAAGTTTGG 1073
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 126 NYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNY 67
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QY 1074 GCATCGGCAC 1083
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 NYNYNYNYNY 57
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RESULT 14
US-09-244-796-17/C
; Sequence 17, Application US/09244796
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; Patent No. 5281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Ribe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 007867350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match 2.4%; Score 38.8; DB 4; Length 289;
Best local Similarity 5.3%; Pred. No. 0.39;
Matches 10; Conservative 87; Mismatches 93; Indels 0; Gaps 0;

QY 894 GCGTGTTTGAAGCTGTCTACACCTCATCAAGAACGGGATCCATCGCTGCTGTTCTTG 953
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Db 246 GYAGTYTTCYTCYCAVGYCYTTCYGYNNYNNYNNYNNYNNYNNYNNYNNYNNY 187

QY 954 ACCGGTGTCAGGCAACGATCTCCACATCCTCACACACAAACGCTGCTCAAGTTCCTGC 1013
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 186 NNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNY 127

QY 1014 ACATCTTTGGTTCCTCTGCTGCCCGGCGCTCTCTCTCTACCGCACTATCCAAGATTGG 1073
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 126 NNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNYNNY 67

QY 1074 GCATCGGCAC 1083
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Db 66 NNYNNYNNY 57

RESULT 15
US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: McGivern, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-404-650-1

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 04:39:50 ; Search time 520.839 Seconds
(without alignments)
4579.068 Million cell updates/sec

Title: US-09-826-581-5
Perfect score: 1647
Sequence: 1 ttggctcgggctggccaca.....acaccagctcttagcttc 1647

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0
Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, NA:
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12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1647	100.0	1647	10	US-09-826-581-5
2	407.2	24.7	989	10	US-09-826-581-2
3	393.4	23.9	1691	10	US-09-925-297-2
4	278.8	16.9	1014	10	US-09-826-581-4
5	168.2	10.2	1722	10	US-09-826-581-3
6	127.2	7.7	11527	9	US-10-108-605-70
7	123.6	7.5	1446	9	US-09-822-846-559
8	85	5.2	378	10	US-09-864-761-3373
9	63.2	3.8	427	10	US-09-783-590-11098
c 10	54	3.3	92	10	US-09-864-761-20146
c 11	53.4	3.2	457	9	US-10-198-846-2282
c 12	52.2	3.2	897	9	US-10-198-846-2472
13	52	3.2	821	10	US-09-826-581-1
14	46	2.8	396	9	US-09-918-995-16257
15	43.4	2.6	458	10	US-09-864-761-693
c 16	40.2	2.4	520	9	US-10-184-644-332
c 17	40.2	2.4	520	9	US-10-184-634-332
18	39.6	2.4	321	10	US-09-983-965-2114
19	39.6	2.4	594	9	US-10-123-155-10
					Sequence 5, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 4, Appli
					Sequence 3, Appli
					Sequence 70, Appl
					Sequence 559, App
					Sequence 3373, Ap
					Sequence 11098, A
					Sequence 20146, A
					Sequence 2282, Ap
					Sequence 2472, Ap
					Sequence 1, Appli
					Sequence 16257, A
					Sequence 693, App
					Sequence 332, App
					Sequence 332, App
					Sequence 2114, Ap
					Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-826-581-5
Sequence 5, Application US/09826581
Patent No. US20020142310A1

GENERAL INFORMATION:

APPLICANT: Andersson, Leif
APPLICANT: Luthman, L. Holger
APPLICANT: Marklund, Stefan
TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUI
FILE REFERENCE: 11145-007001
CURRENT APPLICATION NUMBER: US/09/826.581
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/195,665
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1647
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (20)...(1486)
US-09-826-581-5

Query Match 100.0%; Score 1647; DB 10; Length 1647;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTGGCTCGGGCTGGCCACATGAGCCCGGGCTGGAGCAGCAGCTTCTAGAGAGATGAGCTTCTAGAGCAAGAAACAG	60
Db	1	TTGGTCTGGGGCTGGCCACATGAGCCCGGGCTGGAGCAGCAGCTTCTAGAGCAAGAAACAG	60
Qy	61	CTGAGCAGCAGCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCTAGAGCAAGAAACAG	120
Db	61	CTGAGCAGCAGCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCTAGAGCAAGAAACAG	120
Qy	121	CAGCTCATGCCATCACCAGCTGTGTACACAGCTCAGAAAGAAATCCGTGGGAAACGGAG	180
Db	121	CAGCTCATGCCATCACCAGCTGTGTACACAGCTCAGAAAGAAATCCGTGGGAAACGGAG	180
Qy	181	GGCCAAAGCCCTTGAGATGGACAGCAGAGTGGTGGAGAGGGGAGCCACCAGGTCA	240


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Db 181 GGCRAAGCTTGAGATGACAGGCGAAGTCGGTGAGGAAGGAGCCACCAAGTCA 240
QY 241 GGGGAAGTCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGGCTGGAGCCACATTC 300
Db 241 GGGGAAGTCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGGCTGGAGCCACATTC 300
QY 301 CAAGACCACACCTTGCTGCTCAAGCTGATCTGCCGGGGTGGGCACTCCACCAAGGGTG 360
Db 301 CAAGACCACACCTTGCTGCTCAAGCTGATCTGCCGGGGTGGGCACTCCACCAAGGGTG 360
QY 361 GGACTGCCCTCCCTCTGACTGTCACAGCCTCAGCTCAGGCTCCAGCAGACAGATGATGGA 420
Db 361 GGACTGCCCTCCCTCTGACTGTCACAGCCTCAGCTCAGGCTCCAGCAGACAGATGATGGA 420
QY 421 GCTGGCCACGAGTTCCAGCCACAGAGGCTGGGAGTGTGAGTTAAGAGCCCTGCTGGA 480
Db 421 GCTGGCCACGAGTTCCAGCCACAGAGGCTGGGAGTGTGAGTTAAGAGCCCTGCTGGA 480
QY 481 AGAGAGGCTGCCCTGCTGCTGCTGCCCGGAGGCCCATTTCCCAAGCTGGCTGGGATGA 540
Db 481 AGAGAGGCTGCCCTGCTGCTGCTGCCCGGAGGCCCATTTCCCAAGCTGGGCTGGGATGA 540
QY 541 CGAAGTGGGAAACCCGGCGCCAGATCTACATGGCTTCATGAGGAGCAGACCTGCTA 600
Db 541 CGAAGTGGGAAACCCGGCGCCAGATCTACATGGCTTCATGAGGAGCAGACCTGCTA 600
QY 601 CGATGCCATGGCACTAGCTCCAAAGCTAGTATCTTCGACACCATGCTGGAGATCAAGAA 660
Db 601 CGATGCCATGGCACTAGCTCCAAAGCTAGTATCTTCGACACCATGCTGGAGATCAAGAA 660
QY 661 GGCTCTTTGCTGCTGGTGGCCAAACGGTGGGGGAGCCCTCTATGGGACAGCAAGAA 720
Db 661 GGCTCTTTGCTGCTGGTGGCCAAACGGTGGGGGAGCCCTCTATGGGACAGCAAGAA 720
QY 721 GCAGAGCTTTGGGGATGCTGACCAATCACTGACTTCATCTCTGCTGCTGCTGCTGCTA 780
Db 721 GCAGAGCTTTGGGGATGCTGACCAATCACTGACTTCATCTCTGCTGCTGCTGCTGCTA 780
QY 781 CAGGTCCTCCCTGGTCCAGATCTATGAGATTGAACAATAGATTGAGACCTGGAGGGA 840
Db 781 CAGGTCCTCCCTGGTCCAGATCTATGAGATTGAACAATAGATTGAGACCTGGAGGGA 840
QY 841 GATCTACCTGCAAGCTGCTTCAAGCCTGCTGCTCCATCTCTCTTAATGATAGCTGTT 900
Db 841 GATCTACCTGCAAGCTGCTTCAAGCCTGCTGCTCCATCTCTCTTAATGATAGCTGTT 900
QY 901 TGAAGTGTCTACACCTCATCAAGAACCGGATCCATCGCTGCTGCTTCTTGACCCGCT 960
Db 901 TGAAGTGTCTACACCTCATCAAGAACCGGATCCATCGCTGCTGCTTCTTGACCCGCT 960
QY 961 GTCAGGCAAGCTACTCCATCTCTCACACACAAAGCCCTGCTCAAGTTCCTGCAATCTT 1020
Db 961 GTCAGGCAAGCTACTCCATCTCTCACACACAAAGCCCTGCTCAAGTTCCTGCAATCTT 1020
QY 1021 TGGTTCCTGCTGCCCGGCCCTCTCTCTCTACGCACTATCAAGATTGGGCAATCGG 1080
Db 1021 TGGTTCCTGCTGCCCGGCCCTCTCTCTCTACGCACTATCAAGATTGGGCAATCGG 1080
QY 1081 CACATTCGAGACTTGGCTGTGGTGGTGGAGACAGACCCATCTCTGCTGCTGCTGCTGAT 1140
Db 1081 CACATTCGAGACTTGGCTGTGGTGGTGGAGACAGACCCATCTCTGCTGCTGCTGCTGAT 1140
QY 1141 CTTTGTGGACCGGCTGTGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 CTTTGTGGACCGGCTGTGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 CCTCTATTCCGCTTTGATGATTACCTGGCTGCCGCAACCACTTACACACCTTGA 1260
Db 1201 CCTCTATTCCGCTTTGATGATTACCTGGCTGCCGCAACCACTTACACACCTTGA 1260
QY 1261 CATGAGTGTGGGAGAGCCCTGAGGACAGGACACTATGCTTGGAGGAGTCTTTCTTCTG 1320
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Db 1261 CATGAGTGTGGGAGAGCCCTGAGGACAGGACACTATGCTGAGGAGTCTCTTTCTTCTG 1320
QY 1321 CCAGCCCCACGAGAGCTTGGGGAAAGTGATCGACAGGATTCGTCGGGAGCAGGTACACAG 1380
Db 1321 CCAGCCCCACGAGAGCTTGGGGAAAGTGATCGACAGGATTCGTCGGGAGCAGGTACACAG 1380
QY 1381 GCTGGTGTAGTGGAGAGACCCAGCATCTCTTGGGCGTGGTCTCCCTCTCCGACATCTT 1440
Db 1381 GCTGGTGTAGTGGAGAGACCCAGCATCTCTTGGGCGTGGTCTCCCTCTCCGACATCTT 1440
QY 1441 TCAGGCACTGGTGTCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCTGAGAAGATCTGAG 1500
Db 1441 TCAGGCACTGGTGTCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCTGAGAAGATCTGAG 1500
QY 1501 TCTCTAATCCAAAGCCACTGTCACACCTGGAAGCCAAATGAAGGAACTGGAGAACTCAGC 1560
Db 1501 TCTCTAATCCAAAGCCACTGTCACACCTGGAAGCCAAATGAAGGAACTGGAGAACTCAGC 1560
QY 1561 CTTTCATCTTCCCCCACCCTCCATTTGCTGGTTCAGCTATGATTCAGGTAGGCTGCGCTG 1620
Db 1561 CTTTCATCTTCCCCCACCCTCCATTTGCTGGTTCAGCTATGATTCAGGTAGGCTGCGCTG 1620
QY 1621 GGCCATGACACCAAGCCTCTTAGTCTTC 1647
Db 1621 GGCCATGACACCAAGCCTCTTAGTCTTC 1647
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RESULT 2

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US-09-826-581-2
; Sequence 2, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUE
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: DNA
; LENGTH: 989
; ORGANISM: Homo sapiens
; US-09-826-581-2
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Query Match 24.7%; Score 407.2; DB 10; Length 989;
Best Local Similarity 99.3%; Pred. No. 8e-111;
Matches 409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 247 AGGTCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGCTGGAGGCCACATTCGCCAAGAC 306
Db 540 AGGTCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGCTGGAGGCCACATTCGCCAAGAC 599
QY 307 CACACCCTTGGCTCAAGCTGATTCCTGCGGGGTGGGCACTCCACCAACAGGGTGGGACTG 366
Db 600 CACACCCTTGGCTCAAGCTGATTCCTGCGGGGTGGGCACTCCACCAACAGGGTGGGACTG 659
QY 367 CCTCCCTCTGACTGTACAGGCTCAGCTGCAAGGCTCCAGCAGATGATCTGGAGCTGGC 426
Db 660 CCTCCCTCTGACTGTACAGGCTCAGCTGCAAGGCTCCAGCAGATGATCTGGAGCTGGC 719
QY 427 CACGGAGTTCACAGCCACAGAGGCTGGGAGTGTGAGCTAGAGGCTGCTGGAAGAGAG 486
Db 720 CACGGAGTTCACAGCCACAGAGGCTGGGAGTGTGAGCTAGAGGCTGCTGGAAGAGAG 779
QY 487 GCCTGCCCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 546
Db 780 GCCTGCCCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 839
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Db 54 AGATCAAGAGGCTTCTTTGTTGCTCTGTGGCCACGCTGTGGCGGAGCCCCCTC 1
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RESULT 11
US-10-198-846-2282/c
; Sequence 2282, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2282
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2, 3, 4, 5
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-2282

Query Match 3.2%; Score 53.4; DB 9; Length 457;
Best Local Similarity 53.6%; Pred. No. 7.8e-06;
Matches 111; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Qy 978 ACATCCTCACACAAACCCCTCCCAACTTCCTGCGACATCTTTGTTCCCTGCTGCCCC 1037
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Db 234 ACATCCTCACACAAAGCGGCTCTGAAGTTCCTCAAAATGTTTATCATGAGTTCCCA 175
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Qy 1038 GCGCTCCTCTCTACCGCATATCAAGATTTGGCATCGGCACATTCGGAGACTTGG 1097
|||||
Db 174 AGCCAGACTTCATCTCAACTCTCTGGAGACCTACAGATTCGCACCTATGCCAATATG 115
|||||
Qy 1098 CFTGTGGTGTGGAGACAGCACCATCTGACTGCTGACATGAGACTCTTTTGGACCGCGTG 1157
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Db 114 CTATGTTTGGCACTTACACCCCGCTATGTGGCTCTGGGATTTTGTACCTGCCCGGG 55
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Qy 1158 TGTCTGCACTGCTGTGTTCAAGGAT 1184
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Db 54 CGGCGCGCCACCGGGGAGCTCCAAAT 28
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RESULT 12
US-10-198-846-2472/c
; Sequence 2472, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2472
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2, 16, 22, 23, 27, 28, 30, 36, 39, 73, 462, 481, 540, 559,
; LOCATION: 590, 604, 634, 636, 676, 680, 772, 774, 809, 849, 870, 873,
; LOCATION: 876, 886, 893, 895, 896, 897
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-2472

Query Match 3.2%; Score 52.2; DB 9; Length 897;
Best Local Similarity 56.8%; Pred. No. 2.2e-05;
Matches 96; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 978 ACATCCTCACACAAACGCTCTCTCAAGTTCCTGCGACATCTTTGTTCCCTGCTGCCCC 1037
|||||
Db 252 ACATCCTCACCCACACAGCGCATCTTGAAGTTCCTCAAAATTTTATCATGAGTTCCCA 193
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Qy 1038 GCGCTCCTCTCTCTACCGCATATCAAGATTTGGCATCGGCACATTCGGAGACTTGG 1097
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Db 192 AGCCAGAGTTTCATGTCCTCAAGTCTCTGGAAGAGCTACAGATTCGCACCTATGCCAATATG 133
|||||
Qy 1098 CTGTGCTGTGGAGACAGCACCATCTCTGACTGCTGCACTGGCATCTTTGT 1146
|||||
Db 132 CTATGTTTGGCACTTACCACCCCGCTCTATGTGGCTCTGGGATTTTGT 84
|||||

RESULT 13
US-09-826-581-1
; Sequence 1, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SU
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-1

Query Match 3.2%; Score 52; DB 10; Length 821;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCTCTGGGCTGGCCACATGGAGCCGCGCTGGAGCAGCAGCTGGCGAGG 52
|||||
Db 313 TTGCTCTGGGCTGGCCACATGGAGCCGCGCTGGAGCAGCAGCTGGCGAGG 364
|||||

RESULT 14
US-09-918-995-16257
; Sequence 16257, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
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; SEQ ID NO 2472
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2, 16, 22, 23, 27, 28, 30, 36, 39, 73, 462, 481, 540, 559,
; LOCATION: 590, 604, 634, 636, 676, 680, 772, 774, 809, 849, 870, 873,
; LOCATION: 876, 886, 893, 895, 896, 897
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-2472

Query Match 3.2%; Score 52.2; DB 9; Length 897;
Best Local Similarity 56.8%; Pred. No. 2.2e-05;
Matches 96; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 978 ACATCCTCACACAAACGCTCTCTCAAGTTCCTGCGACATCTTTGTTCCCTGCTGCCCC 1037
|||||
Db 252 ACATCCTCACCCACACAGCGCATCTTGAAGTTCCTCAAAATTTTATCATGAGTTCCCA 193
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Qy 1038 GCGCTCCTCTCTCTACCGCATATCAAGATTTGGCATCGGCACATTCGGAGACTTGG 1097
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Db 192 AGCCAGAGTTTCATGTCCTCAAGTCTCTGGAAGAGCTACAGATTCGCACCTATGCCAATATG 133
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Qy 1098 CTGTGCTGTGGAGACAGCACCATCTCTGACTGCTGCACTGGCATCTTTGT 1146
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Db 132 CTATGTTTGGCACTTACCACCCCGCTCTATGTGGCTCTGGGATTTTGT 84
|||||

RESULT 13
US-09-826-581-1
; Sequence 1, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SU
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-1

Query Match 3.2%; Score 52; DB 10; Length 821;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCTCTGGGCTGGCCACATGGAGCCGCGCTGGAGCAGCAGCTGGCGAGG 52
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Db 313 TTGCTCTGGGCTGGCCACATGGAGCCGCGCTGGAGCAGCAGCTGGCGAGG 364
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RESULT 14
US-09-918-995-16257
; Sequence 16257, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
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Best Local Similarity 47.8%; Pred. No. 0.0012;
Matches 133; Conservative 0; Mismatches 145; Indels

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? SOFTWARE: Annamx sequence Listing Engine Vers. 1.1
? SEQ ID NO 693
? LENGTH: 458
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AC006966.3
? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.8
? OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7
? OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.2
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.6
? OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6.5
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.5
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.8
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.7
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
? OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.9
? US-09-864-761-693

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Query Match 2.6%; Score 43.4; DB 10; Length 458;
Best Local Similarity 64.4%; Pred. No. 0.0073;
Matches 65; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

US-09-864-767-693

QY 1369 GCAGGTACACGGTGGTGCTATGTGGACGAGACCACCATCTCTTTGGGGCGTGGTCCTCCT 1428
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Dd 202 GCAGTCCATCGCGTGGTGGTGAATGACAGATAGTAGTATTGGGGGTAATTATTCCT 261

[illegible]

Search completed: June 13, 2003, 09:00:38
Job time : 521.839 secs

Search completed: June 13, 2003, 09:00:38
Job time : 521.839 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: June 13, 2003, 01:49:14 ; Search time 192.613 Seconds
(without alignments)
9216.782 Million cell updates/sec
Title: US-09-826-581-5_COPY_200_260
Perfect score: 61
Sequence: 1 acagcagcaagtcggtgga.....gggggaaggtcccggtcca 61
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
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- 32: em.htg_other.*
- 33: em.htg_mus.*
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- 35: em.htg_rod.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	61	100.0	1647	6	AX281582	AX281582 Sequence
2	61	100.0	2109	6	AX099776	AX099776 Sequence
3	61	100.0	2115	6	AX099802	AX099802 Sequence
4	61	100.0	2115	9	AF214519	AF214519 Homo sapi
5	61	100.0	2290	9	HS249577	AT249777 Homo sapi
6	51	83.6	989	6	AX281579	AX281579 Sequence
c 7	51	83.6	152129	2	AC027416	AC027416 Homo sapi
c 8	51	83.6	206854	9	AC009974	AC009974 Homo sapi
9	41.8	68.5	1867	6	AX099774	AX099774 Sequence
10	41.8	68.5	1873	4	AF214520	AF214520 Sus scrofa
11	41.8	68.5	1873	6	AX099800	AX099800 Sequence
12	41.8	68.5	1873	6	AX398331	AX398331 Sequence
13	41.8	68.5	1873	6	AX398333	AX398333 Sequence
14	41.8	68.5	1873	6	AX398339	AX398339 Sequence
15	41.8	68.5	1873	6	AX099804	AX099804 Sequence
16	41.8	68.5	2022	6	AX398335	AX398335 Sequence
17	40.2	65.9	1873	6	AF214521	AF214521 Sus scrofa
18	33.4	54.8	5888	4	AC128070	AC128070 Rattus no
19	33.4	54.8	14577	2	AC129703	AC129703 Rattus no
20	33.4	54.8	190183	2	AC127107	AC127107 Rattus no
21	33.4	54.8	192968	2	AF336381	AF336381 Mus muscu
22	32.6	53.4	1095	6	AX398341	AX398341 Sequence
c 23	31.8	52.1	227724	2	AF336381	AF336381 Mus muscu
24	31.4	51.5	808	6	AX398342	AX398342 Sequence
25	29.6	48.5	31549	9	AC096857	AC096857 Homo sapi
26	29.6	48.5	78805	2	AC006408	AC006408 Homo sapi
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c 32	28.2	46.2	155012	8	AF003257	AF003257 Oryza sat
c 33	28.2	46.2	170931	2	AL329656	AL329656 Rattus no
34	28	45.9	170586	2	AL356126	AL356126 Homo sapi
c 35	28	45.9	171999	2	AC121225	AC121225 Rattus no
36	28	45.9	172510	9	AL512424	AL512424 Human DNA
c 37	28	45.9	184056	2	AC024551	AC024551 Homo sapi
c 38	27.8	45.6	3630	10	RN05STR1	AF102885 Rattus no
c 39	27.8	45.6	78782	2	AC095594	AC095594 Rattus no
c 40	27.8	45.6	206531	2	AC055858	AC055858 Homo sapi
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c 42	27.6	45.2	168839	9	AC022826	AC022826 Homo sapi
c 43	27.6	45.2	180464	2	AC116351	AC116351 Homo sapi
c 44	27.4	44.9	49721	2	AC104991	AC104991 Homo sapi
c 45	27.4	44.9	58640	2	AC111698	AC111698 Rattus no

ALIGNMENTS

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LOCUS AX281582 1647 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 5 from Patent WO0177305.
ACCESSION AX281582
VERSION AX281582.1 GI:16608833
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Andersson,L., Luthman,H. and Marklund,S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 5 18-OCT-2001;

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
Source
gene
CDS
BASE COUNT
ORIGIN
Query Match
Best Local Similarity
Matches
QY
Db
QY
Db
RESULT 5
HSA249977
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

AF214519.1 GI:8215681
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kaim,E., Roy,P.L., Chardon,P. and Andersson,L.
A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle
Science 288 (5469), 1248-1251 (2000)
2080150
10818001
2 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N., Kaim,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24, Sweden
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TDRIHLRYSPVLQIYEIEQHKIETWREIYLQCFKPLVSPNSDLSFEAVYTLI
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AVYLEAPILTALDIFVDRVVSALPVVNECGQVGLYSRFDVHLAAQIYNHLDMSV
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460 a 622 c 562 y 471 t

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Best Local Similarity 100.0%; Pred. No. 5.4e-08;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 A 61
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Db 166 A 166

RESULT 5
HSA249977
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

HSA249977
Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit (AMPK gamma 3 gene).
AJ249977
AJ249977.1 GI:5688200
AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
Source
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Matches
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RESULT 6
AX281579
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2290)
Cheung,P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D.
Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
Biochem. J. 346 Pt 3, 659-669 (2000)
20164049
10698692
2 (bases 1 to 2290)
Carling,D.
Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 0NN, UNITED KINGDOM
Location/Qualifiers
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GSLPRPSFLYTIQDLIGTFRDLAVYLEAPILTALDIFVDRVVSALPVVNECGQV
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501 a 674 c 617 g 498 t

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Best Local Similarity 100.0%; Pred. No. 5.3e-08;
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QY 61 A 61
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Db 262 A 262

RESULT 6
AX281579
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

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Sequence 2 from Patent WO0177305.
AX281579
AX281579.1 GI:16608830
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Andersson,L., Luthman,H. and Marklund,S.
Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: WO 0177305-A 2 18-OCT-2001;
Arexis AB (SE)

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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
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LOCUS               152129 bp      DNA      linear      HTG 07-JUN-2000
DEFINITION          Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
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ACCESSION            AC027416
VERSION              AC027416.2 GI:8317289
KEYWORDS              HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE               Homo sapiens.
ORGANISM              Homo sapiens
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                    Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE            1 (bases 1 to 152129)
AUTHORS              Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE                Homo sapiens, clone RP11-504G11
JOURNAL              Unpublished
REFERENCE            2 (bases 1 to 152129)
AUTHORS              Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
                    Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
                    Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
                    Campiano,A., Castile,A., Choepel,Y., Colangelo,M., Collins,S.,
                    Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
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                    Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
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                    O'Neill,D., Olivier,T.M., Oliver,J., Peterson,K., Pierre,N.,
                    Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
                    Roy,A., Santos,R., Schaefer,S., Severy,P., Spencer,B.,
                    Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
                    Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,
                    Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                    Young,G., Zainoun,J., Zimmer,A. and Zody,M.
TITLE                Direct Submission
JOURNAL              Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
                    Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT              On Jun 7, 2000 this sequence version replaced gi:7342115.
                    All repeats were identified using RepeatMasker:
                    Smit, A.F.A. & Green, P. (1996-1997)
                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
                    ----- Genome Center
                    Center: Whitehead Institute/ MIT Center for Genome Research
                    Center code: WIBR
                    Web site: http://www-seq.wi.mit.edu
                    Contact: sequence_submissions@genome.wi.mit.edu
                    ----- Project Information
                    Center project name: 17458
                    Center clone name: 504_G_11
                    ----- Summary Statistics
                    Sequencing vector: M13; M7815; 100% of reads
                    Chemistry: Dye-terminator Big Dye; 100% of reads
                    Assembly program: Phrap; version 0.960731

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Consensus quality: 135376 bases at least Q40
Consensus quality: 143264 bases at least Q30
Consensus quality: 146503 bases at least Q20
Insert size: 161000; agarose-fp
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1006 1105: gap of 100 bp
1106 2402: contig of 1297 bp in length
2403 2502: gap of 100 bp
2503 3823: contig of 1321 bp in length
3824 3923: gap of 100 bp
3924 5020: contig of 1097 bp in length
5021 5120: gap of 100 bp
5121 6161: contig of 1041 bp in length
6162 6261: gap of 100 bp
6262 7547: contig of 1286 bp in length
7548 7647: gap of 100 bp
7648 9983: contig of 2336 bp in length
9984 10083: gap of 100 bp
10084 12856: contig of 2473 bp in length
12557 12656: gap of 100 bp
12657 15043: contig of 2387 bp in length
15044 15443: gap of 100 bp
15144 17123: contig of 1980 bp in length
17124 17223: gap of 100 bp
17224 19466: contig of 2243 bp in length
19467 19566: gap of 100 bp
19567 21928: contig of 2362 bp in length
21929 22028: gap of 100 bp
22029 24319: contig of 2291 bp in length
24320 24419: gap of 100 bp
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66596 66695: gap of 100 bp
66696 73218: contig of 6523 bp in length
73219 73318: gap of 100 bp
73319 77115: contig of 3797 bp in length
77116 77215: gap of 100 bp
77216 85022: contig of 7807 bp in length
85023 85122: gap of 100 bp
85123 93314: contig of 8192 bp in length
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93415 101193: contig of 7779 bp in length
101194 101293: gap of 100 bp
101294 113090: contig of 11797 bp in length

* 113091 113190: gap of 100 bp
* 113191 123496: contig of 10306 bp in length
* 123497 123596: gap of 100 bp
* 123597 137837: contig of 14241 bp in length
* 137838 137937: gap of 100 bp
* 137938 152129: contig of 14192 bp in length.
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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2925 ACAAGCGAAGTGGTGGAGGAGGGAGCCACCGAGGTGAGGGGGAAGGT 2875
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RESULT 8
AC009974/c 206854 bp DNA linear PRI 09-JAN-2002
LOCUS Homo sapiens BAC clone RP11-459I19 from 2, complete sequence.
DEFINITION AC009974
ACCESSION AC009974
VERSION AC009974.9 GI:16799058
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 206854)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 206854)
AUTHORS Harris,A. and Cotton,M.
TITLE The sequence of Homo sapiens BAC clone RP11-459I19
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 206854)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 8, 2001 this sequence version replaced gi:13431203.
COMMENT ----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics

Center project name: H_NH0459I19

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanesi, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-4591I19; actual end is at base position 206854 of RP11-4591I19.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

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Db 169877 ACAGGCAGAGTCGCTGGAGGAGGGAGGAGCCACCGAGTCAGGGGAGGT 169877

MEDLINE	20280150
PUBMED	10818001
REFERENCE	2 (bases 1 to 1873)
AUTHORS	Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N., Kalm,E., le Roy,P., Chardon,P. and Andersson,L.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24, Sweden
FEATURES	Location/Qualifiers 1..1873 /organism="Sus scrofa" /db_xref="taxon:9823" /chromosome="15" /map="15q" /tissue_type="skeletal muscle"
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CDS	1..1395 /gene="PRKAG3" /note="AMPKG3" /codon_start=1 /product="AMP-activated protein kinase gamma subunit" /protein_id="AAF73988.1" /db_xref="GI:8215684" /translation="MSFLQGGSRSWPSRAVYTSRSSRHGDGNGKASQSWTRQEDVEEG GPPRGEPQSRPVARSTGOEATFPKATPLAAQAIAEVNDNPTRDILPSCDAASAS DSNTDHLDLGLEFSAASAAGDBLGVEEKPARCPSEVLPLRLGWDELQPKPGAQVTM HPMQHTCYDMATSSKLVIPTMLEIKKAFFALVANGVAAPLMDSKSQSFVGMLTI TDFILVHRYRSPVOIYEIEBKIEITWRREIYLQCCKPLYSISPNDLSLEAVYALI KNRIIRFLTPIDVSGAVLIHLTKRLLAHLIFGLTLPRPSLYRTIQDLGIGTFDRLL AVLEETAPILTDIFVDRRVSALPVWNETGVQVGLYSRFDVTHLAAAOQTYNHLDMMV GEALKQRSLCLEGLVISCOPHETISGVIDRIVREQVHRVLIVDETQHLLGVVLSLDILO ALVLSAPADIALGA"
BASE COUNT	382 a 580 c 535 g 376 t
ORIGIN	
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Best Local Similarity	80.3%; Pred. No. 0.021;
Matches	49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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RESULT 11	
LOCUS	AX099800 1873 bp DNA linear PAT 02-APR-2001
DEFINITION	Sequence 27 from Patent WO0120003.
ACCESSION	AX099800
KEYWORDS	AX099800.1 GI:13538834
SOURCE	sig. scrofa
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactylia; Suina; Suidae; Sus. 1 (bases 1 to 1873) Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.
REFERENCE	Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
AUTHORS	Patent: WO 0120003-A 27 23-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR); Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
FEATURES	Location/Qualifiers 1..1873

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 01:37:39 ; Search time 22.1613 seconds
(without alignments)
6198.732 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	61	100.0	2109	22	AAH43685 PRKAG3 CDNA. Homo
3	61	100.0	2115	22	AAH43685 Human AMPK gamma s
4	51	83.6	989	22	AAH43682 PRKAG3 intron 2 -
5	41.8	68.5	1867	22	AAH43685 Pig AMPK gamma sub
6	41.8	68.5	1873	22	AAH43685 Pig AMPK gamma sub
7	41.8	68.5	1873	24	AAH43685 Pig wild-type PRKA
8	41.8	68.5	1873	24	AAH43685 Pig PRKAG3 polymor
9	41.8	68.5	1873	24	AAH43685 Pig PRKAG3 polymor

10	41.8	68.5	1873	24	AAH43685	Pig PRKAG3 polymor
11	41.8	68.5	2022	22	AAH43685	Sus scrofa PRKAG3
12	40.2	65.9	1873	24	AAH43685	Pig PRKAG3 polymor
13	32.6	53.4	1095	24	AAH43685	Pig PRKAG3 gene 5'
14	31.4	51.5	808	24	AAH43685	Pig PRKAG3 gene 5'
15	26.2	43.0	2541	23	AAH43685	DNA encoding novel
16	25.6	42.0	323	22	AAH43685	Human breast cancer
17	25.6	42.0	711	23	AAH43685	DNA encoding novel
18	25.4	41.6	2238	20	AAH43685	Calcium activated
19	25.4	41.6	2238	24	AAH43685	Human Ika channel
20	25.4	41.6	2261	20	AAH43685	Human calcium acti
21	25.4	41.6	3632	17	AAH43685	T. thermophilus ga
22	25.4	41.6	3632	20	AAH43685	Thermus thermophil
23	25.4	41.6	4999	20	AAH43685	Human LOBO homolog
24	25	41.0	560	24	AAH43685	Human retina speci
25	25	41.0	1188	24	AAH43685	Human retina speci
26	25	41.0	1927	23	AAH43685	Human prostate exp
27	25	41.0	1927	23	AAH43685	Human prostate exp
28	25	41.0	4034	24	AAH43685	Ovary cancer relat
29	25	41.0	4035	11	AAH43685	Sequence encoding
30	25	41.0	4035	11	AAH43685	Human IL-2R beta c
31	25	41.0	8670	20	AAH43685	Human MTH2 relate
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33	24.8	40.7	2006	22	AAH43685	X16619 CDNA clone.
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35	24.6	40.3	1068	23	AAH43685	Drosophila melanog
36	24.6	40.3	2445	21	AAH43685	Murine bone morpho
37	24.6	40.3	2447	17	AAH43685	Murine BMP-9 CDNA.
38	24.6	40.3	2448	14	AAH43685	Encodes murine bon
39	24.6	40.3	2463	22	AAH43685	Human CDNA sequenc
40	24.6	40.3	2996	24	AAH43685	CDNA sequence #179
41	24.6	40.3	3140	23	AAH43685	Drosophila melanog
42	24.6	40.3	3580	24	AAH43685	CDNA encoding huma
43	24.6	40.3	5312	22	AAH43685	DNA encoding human
44	24.6	40.3	5312	22	AAH43685	Human reproductive
45	24.6	40.3	5381	22	AAH43685	Apolipoprotein A-I

ALIGNMENTS

RESULT 1
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ID AAH43685 standard; cDNA; 1647 BP.
AC AAH43685;
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XX 21-JAN-2002 (first entry)
DT PRKAG3 CDNA.
DE
DE PRKAG3 CDNA.
KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
KW metabolic disease; diabetes; obesity; substitution; ss.
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XX Homo sapiens.
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FT /label= "C230G"
FT /note= "Causes P71A"
FT variation 559
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FT /label= "T559C"
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FT variation 1037
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FT /label= "C1037T"
FT /note= "Causes R340W"
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PN WD200177305-A2.
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XX PD
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XX PF
XX 06-APR-2001; 2001WO-SE00765.
XX PR
XX 07-APR-2000; 2000US-195665P.
XX PA
XX (AREX-) AREXIS AB.
XX
XX PI Andersson L, Luthman H, Marklund S;
XX
XX DR WPI; 2001-657170/75.
XX DR P-PSDB; QQB47679.
XX
XX PT New variants of human AMP-activated protein kinase gamma3 subunit
XX associated with a metabolic disease e.g. diabetes or obesity and method
XX for determining a risk estimate of diseases in subject by detecting the
XX variant -
XX
XX PS Disclosure; Fig 5; 25pp; English.
XX
XX CC This sequence represents the full length cDNA encoding the human
XX AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
XX the presence of the PRKAG3 DNA, or a variant, is useful in determining
XX a risk estimate of a metabolic disease, such as diabetes or obesity,
XX in a subject. The variation may occur in exons 3, 4 or 10. In exon
XX 3 variation may be a substitution of a G for a C at nucleotide 320,
XX resulting in the amino acid substitution P71A; in exon 4 variation may
XX be a substitution of a T for a C at nucleotide 550; and in exon 10
XX variation may be a substitution of a T for a C at nucleotide 1037,
XX resulting in the amino acid substitution R340W. There may also be
XX nucleotide variation in intron 6. The numbering of these
XX variations is based on the full length cDNA as given, rather than on
XX position 1 of the open reading frame.
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XX SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;

Query Match 100.0%; Score 61; DB 22; Length 1647;
Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGTGGAGGAGGGAGCCACCGTCCAGGGGAGAGTCCCGGTCC 60
Db |
QY 61 A 61
Db 260 A 260

RESULT 2
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XX DT 13-JUN-2001 (first entry)
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XX DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
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XX KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
XX PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
XX genetic testing; carbohydrate metabolism disorder; skeletal muscle;
XX cystathione beta synthase; CBS; cardiant; gene therapy; ss.
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XX OS Homo sapiens.
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XX FH Key
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XX CDS 472..1389 /*tag= b
XX FT
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FT 3'UTR /product= "Human Prkag3 protein"
FT FT 1390..2109
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XX PN WO200120003-A2.
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XX PD 22-MAR-2001.
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XX PF 11-SEP-2000; 2000WO-EP09896.
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XX PR 10-SEP-1999; 99EP-0402236.
XX PR 18-MAY-2000; 2000EP-0401388.
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XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX PA (ANDE/) ANDERSSON L.
XX PA (LOOF/) LOOFT C.
XX PA (KALM/) KALM E.
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XX PI Andersson L, Loof C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
XX DR WPI; 2001-244810/25.
XX DR P-PSDB; AAE00221.
XX
XX PT New variants of the gamma subunit of vertebrate adenosine
XX monophosphate-activated kinase for diagnosis or treatment of disorders
XX associated with energy metabolism such as diabetes, obesity, and
XX myopathy -
XX
XX PS Claim 12; Fig 2; 71pp; English.
XX
XX CC The present sequence is a cDNA encoding human adenosine monophosphate
XX (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
XX PRKAG3. Mutation in Prkag3 results in an altered regulation of
XX carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
XX useful as therapeutic for treating carbohydrate metabolism disorders such
XX as diabetes, obesity, and disorders associated with muscle metabolism
XX such as myopathy and cardiovascular diseases, to modulate AMPK
XX activity, and for restoring a normal AMPK function. PRKAG3 sequence
XX and its functionally altered mutants are useful for the diagnostic
XX evaluation, genetic testing and prognosis of a metabolic disorder,
XX preferably a carbohydrate metabolism disorder. Primers that can detect
XX a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
XX useful for detecting a dysfunction of carbohydrate metabolism resulting
XX from the expression of a functionally altered allele of PRKAG3.
XX Transgenic animal and host cell transformed with PRKAG3 or a
XX heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
XX screening compounds able to modulate AMPK activity. Nucleic acid
XX encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
XX in a sequence encoding the first cystathione beta synthase (CBS) domain
XX of PRKAG3 and is useful in gene therapy.
XX
XX SQ Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;

Query Match 100.0%; Score 61; DB 22; Length 2109;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGTGGAGGAGGGAGCCACCGTCCAGGGGAGAGTCCCGGTCC 60
Db |
QY 61 A 61
Db 160 A 160

RESULT 3
AAD03320
ID AAD03320 standard; cDNA; 2115 BP.
XX
XX AC AAD03320;
XX

```

DT 13-JUN-2001 (first entry)

DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.

XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;

XX PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;

KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;

KW cystathione beta synthase; CBS; cardiac; gene therapy; ss.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH 1..1395

FT /*tag= a

FT /product= "Human complete Prkag3 protein"

FT

XX WC200120003-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 200WO-EF09896.

XX 10-SEP-1999; 99EP-04022336.

PR 18-MAY-2000; 2000EP-0401388.

XX (INRC) INRA INST NAT RECH AGRONOMIQUE.

PA (ANDE/) ANDERSSON L.

PA (LOOF/) LOOFT C.

PA (KALM/) KALM E.

XX Andersson L., Loof C., Kalm E., Milan D., Robic A., Rogel-Gaillard C;

PI Iannuccelli N., Gellin J., Le Roy P., Chardon P;

PI

XX WPI; 2001-244810/25.

DR P-PSDB; AAE00223.

XX New variants of the gamma subunit of vertebrate adenosine

PT monophosphate-activated kinase for diagnosis or treatment of disorders

PT associated with energy metabolism such as diabetes, obesity, and

PT myopathy -

XX

PS Claim 12; Page 65-68; 71pp; English.

XX

CC The present sequence is a cDNA encoding human adenosine monophosphate

CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,

CC complete PRKAG3. Mutation in Prkag3 results in an altered regulation of

CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is

CC useful as therapeutic for treating carbohydrate metabolism disorders such

CC as diabetes, obesity, and disorders associated with muscle metabolism

CC such as myopathy and cardiovascular diseases, to modulate AMPK

CC activity, and for restoring a normal AMPK function. PRKAG3 sequence

CC and its functionally altered mutants are useful for the diagnostic

CC evaluation, genetic testing and prognosis of a metabolic disorder,

CC preferably a carbohydrate metabolism disorder. Primers that can detect

CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are

CC useful for detecting a dysfunction of carbohydrate metabolism resulting

CC from the expression of a functionally altered allele of PRKAG3.

CC Transgenic animal and host cell transformed with PRKAG3 or a

CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for

CC screening compounds able to modulate AMPK activity. Nucleic acid

CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or

CC in a sequence encoding the first cystathione beta synthase (CBS) domain

CC of PRKAG3 and is useful in gene therapy.

XX

SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;

Query Match 100.0%; Score 61; DB 22; Length 2115;

Best Local Similarity 100.0%; Pred. No. 6.1e-10;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGCAGAGTGGTGGAGGAGGAGCCAGGTGAGGGGAGGTCCCGGTCC 60

|||||

DB 106 ACAAGCAGAGTGGTGGAGGAGGAGCCAGGTGAGGGGAGGTCCCGGTCC 165

Qy 61 A 61

Db 166 A 166

RESULT 4

AAH43682

ID AAH43682 standard; DNA; 989 BP.

XX

XX AAH43682;

XX 21-JAN-2002 (first entry)

XX PRKAG3 intron 2 - intron 4.

XX Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;

XX metabolic disease; diabetes; obesity; substitution; ds.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FH 1..21

FT /*tag= a "Intron 2"

FT /number= "3", portion of intron 2"

FT /note= "3", portion of intron 2"

FT exon 22..177

FT /*tag= b

FT /number= "Exon 3"

FT intron 178..541

FT /*tag= c

FT /number= "Intron 3"

FT exon 542..945

FT /*tag= d

FT /number= "Exon 4"

FT intron 946..989

FT /*tag= e

FT /number= "Intron 4"

FT /note= "5", portion of intron 4"

XX WC200177305-A2.

XX

PD 18-OCT-2001.

XX

XX 06-APR-2001; 2001WO-SE00765.

XX

PR 07-APR-2000; 2000US-195665P.

XX

PA (AREX-) AREXIS AB.

XX

PI Andersson L., Luthman H., Marklund S;

XX

XX WPI; 2001-657170/75.

XX

XX New variants of human AMP-activated protein kinase gamma3 subunit

XX associated with a metabolic disease e.g. diabetes or obesity and method

XX for determining a risk estimate of diseases in subject by detecting the

XX variant -

XX Example 1; Fig 2; 25pp; English.

XX

CC The sequences given in AAH43681-84 represents genomic fragments

CC encoding the human AMP-activated protein kinase gamma 3 subunit

CC (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,

CC is useful in determining a risk estimate of a metabolic disease,

CC such as diabetes or obesity, in a subject. The variation may occur

CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of

CC a G for a C at nucleotide 320, resulting in the amino acid

CC substitution P71A; in exon 4 variation may be a substitution of a

CC T for a C at nucleotide 550; and in exon 10 variation may be a

CC substitution of a T for a C at nucleotide 1037, resulting in the

CC amino acid substitution R340W. There may also be nucleotide variation

CC in intron 6.

XX Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
 Query Match 83.6%; Score 51; DB 22; Length 989;
 Best Local Similarity 100.0%; Pred. No. 7.5e-07;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGCGAGAGTCGGTGGAGGAGGGAGGCCACACAGGTCAGGGGGAAGGT 51
 |||||
 Db 129 ACAAGCGAGAGTCGGTGGAGGAGGGAGGCCACACAGGTCAGGGGGAAGGT 179
 |||||

RESULT 5
 AAD03295
 ID AAD03295 standard; cDNA; 1867 BP.
 XX
 AC AAD03295;
 XX
 DT 13-JUN-2001 (first entry)
 XX
 DE Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
 XX
 KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
 KW chromosome 15; ss.
 XX
 OS Sus scrofa.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..471
 FT CDS /*tag= a
 FT 472..1389 /*tag= b
 FT /*product= "Sus scrofa PRKAG3 protein"
 FT 1390..1867
 FT /*tag= C
 XX
 PN WO200120003-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 11-SEP-2000; 2000WO-EP09896.
 XX
 PR 10-SEP-1999; 99EP-0402236.
 XX
 PR 18-MAY-2000; 2000EP-0401388.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (ANDE/) ANDERSSON L.
 PA (LOOF/) LOOFT C.
 PA (KALM/) KALM E.
 XX
 PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
 PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
 XX
 DR WPI: 2001-244810/25.
 DR P-PSDB; AAE00220.
 XX
 PT New variants of the gamma subunit of vertebrate adenosine
 PT monophosphate-activated kinase for diagnosis or treatment of disorders
 PT associated with energy metabolism such as diabetes, obesity, and
 PT myopathy -
 XX
 PS Claim 12; Fig 2; 71pp; English.
 XX
 CC The present sequence is a cDNA encoding pig adenosine monophosphate
 CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
 CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.
 CC Mutation in Prkag3 results in an altered regulation of carbohydrate
 CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
 CC therapeutic for treating carbohydrate metabolism disorders such as
 CC diabetes, obesity, and disorders associated with muscle metabolism

CC such as myopathy and cardiovascular diseases, to modulate AMPK
 CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
 CC and its functionally altered mutants are useful for the diagnostic
 CC evaluation, genetic testing and prognosis of a metabolic disorder,
 CC preferably a carbohydrate metabolism disorder. Primers that can detect
 CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
 CC useful for detecting a dysfunction of carbohydrate metabolism resulting
 CC from the expression of a functionally altered allele of PRKAG3.
 CC Transgenic animal and host cell transformed with PRKAG3 or a
 CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
 CC screening compounds able to modulate AMPK activity. Nucleic acid
 CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
 CC in a sequence encoding the first cystathione beta synthase (CBS) domain
 CC of PRKAG3 and is useful in gene therapy.
 XX
 SQ Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;
 Query Match 68.5%; Score 41.8; DB 22; Length 1867;
 Best Local Similarity 80.3%; Pred. No. 0.00058;
 Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ACAAGCGAGAGTCGGTGGAGGAGGGAGGCCACACAGGTCAGGGGGAAGGTCCCGGTCC 60
 |||||
 Db 100 ACAAGCGAGAGTCGGTGGAGGAGGGAGGCCCTCCGGGCCGAGGAGGTCCCGGTCC 159
 |||||

QY 61 A 61
 Db 160 A 160

RESULT 6
 AAD03319
 ID AAD03319 standard; cDNA; 1873 BP.
 XX
 AC AAD03319;
 XX
 DT 13-JUN-2001 (first entry)
 XX
 DE Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
 XX
 KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
 KW chromosome 15; ss.
 XX
 OS Sus scrofa.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1395
 FT /*tag= a
 FT /*product= "Sus scrofa complete Prkag3 protein"
 XX
 PN WO200120003-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 11-SEP-2000; 2000WO-EP09896.
 XX
 PR 10-SEP-1999; 99EP-0402236.
 XX
 PR 18-MAY-2000; 2000EP-0401388.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (ANDE/) ANDERSSON L.
 PA (LOOF/) LOOFT C.
 PA (KALM/) KALM E.
 XX
 PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
 PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
 XX
 DR WPI: 2001-244810/25.
 DR P-PSDB; AAE00222.
 XX


```

FT variation          replace (89, C)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX PN WO200220850-A2.
XX PD 14-MAR-2002.
XX
XX PF 10-SEP-2001; 2001WO-US28283.
XX
XX PR 08-SEP-2000; 2000US-231045P.
XX PR 08-JAN-2001; 2001US-260239P.
XX PR 18-JUN-2001; 2001US-299111P.
XX
XX PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
XX DR WPI: 2002-393850/42.
XX DR P-PSDB; AAE22985.
XX
XX PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene -
XX
XX PS Disclosure; Page 89-91; 109pp; English.
XX
XX CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX
XX SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match          68.5%; Score 41.8; DB 24; Length 1873;
Best Local Similarity 80.3%; Pred. No. 0.00058;
Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGTCGAGCAGAGGGGAGCCACCGAGTCAGGGGGAGAGTCCCGGTCC 60
    ||||| || || ||||| || || || || || || || || || || || || || || || ||
Db 106 ACAAGGCAGAGGATGTAGAGGAAGGGGGCCCTCCGGCCCGAGGAGGTCCCGGTCC 165

QY 61 A 61
    |
Db 166 A 166

RESULT 9
AAD36459
ID AAD36459 standard; DNA; 1873 BP.
XX
XX AC AAD36459;
XX
XX DT 09-AUG-2002 (first entry)
XX
XX DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
XX
XX KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
XX KW gene; variant; ds.
XX
XX OS Sus scrofa.
XX
XX FH Key Location/Qualifiers
XX CDS 1..1395
XX FT /*tag= a
XX FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-199)"
XX

```

```

FT variation          replace (595, A)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX PN WO200220850-A2.
XX PD 14-MAR-2002.
XX
XX PF 10-SEP-2001; 2001WO-US28283.
XX
XX PR 08-SEP-2000; 2000US-231045P.
XX PR 08-JAN-2001; 2001US-260239P.
XX PR 18-JUN-2001; 2001US-299111P.
XX
XX PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
XX DR WPI: 2002-393850/42.
XX DR P-PSDB; AAE22987.
XX
XX PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene -
XX
XX PS Disclosure; Page 98-100; 109pp; English.
XX
XX CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
XX
XX SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match          68.5%; Score 41.8; DB 24; Length 1873;
Best Local Similarity 80.3%; Pred. No. 0.00058;
Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGTCGAGCAGAGGGGAGCCACCGAGTCAGGGGGAGAGTCCCGGTCC 60
    ||||| || || ||||| || || || || || || || || || || || || || || || ||
Db 106 ACAAGGCAGAGGATGTAGAGGAAGGGGGCCCTCCGGCCCGAGGAGGTCCCGGTCC 165

QY 61 A 61
    |
Db 166 A 166

RESULT 10
AAD36460
ID AAD36460 standard; DNA; 1873 BP.
XX
XX AC AAD36460;
XX
XX DT 09-AUG-2002 (first entry)
XX
XX DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
XX
XX KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
XX KW gene; variant; ds.
XX
XX OS Sus scrofa.
XX
XX FH Key Location/Qualifiers
XX CDS 1..1395
XX FT /*tag= a
XX FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
XX

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FT variation replace (599, A)
FT /*tag= b
PT /standard_name= "Single nucleotide polymorphism (SNP),"
XX PN
XX PD WO200220850-A2.
XX PD 14-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US28283.
XX PR 08-SEP-2000; 2000US-231045P.
XX PR 08-JAN-2001; 2001US-260239P.
XX PR 18-JUN-2001; 2001US-299111P.
XX PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX DR WPI; 2002-393850/42.
XX DR P-PSDB; AAE22988.
XX PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene .
XX PS Disclosure: Page 102-104; 109pp; English.
XX CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
XX CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
XX SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match 68.5%; Score 41.8; DB 24; Length 1873;
Best Local Similarity 80.3%; Pred. No. 0.00059;
Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGTGGAGGAGGGAGGAGCCACAGTCAGGGGAGGTCCCGGTCC 60
DB 106 ACAAGGCAGGAGTGTAGAGGAAGGGGGCCCTCCGGGCCGAGGAGGTCCCGAGTCC 165
QY 61 A 61
DB 165 A 166

RESULT 11
AAD03321
ID AAD03321 standard; DNA; 2022 BP.
XX AD
AC AAD03321;
XX DT 13-JUN-2001 (first entry)
XX DE Sus scrofa PRKAG3 splice variant DNA.
XX KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
XX PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
XX genetic testing; carbohydrate metabolism disorder; skeletal muscle;
XX cystathione beta synthase; CBS; cardiant; gene therapy; ds.
XX OS Sus scrofa.
XX FH Key Location/Qualifiers
XX FT 1..1545
XX CDS /*tag= a
FT
```

```
FT /product= "Sus scrofa Prkag3 splice variant"
XX PN WO200120003-A2.
XX PD 22-MAR-2001.
XX PF 11-SEP-2000; 2000WO-EP09896.
XX PR 10-SEP-1999; 99EP-0402336.
XX PR 18-MAY-2000; 2000EP-0401388.
XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX PA (ANDE/) ANDERSSON L.
XX PA (LOOF/) LOOFT C.
XX PA (KALM/) KALM E.
XX PI Andersson L, Loof C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX DR WPI; 2001-244810/25.
XX DR P-PSDB; AAE00224.
XX PT New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment of disorders
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy .
XX PS Claim 12; Page 69; 71pp; English.
XX CC The present sequence is pig adenosine monophosphate (AMP)-activated
CC kinase (AMPK) gamma subunit muscle-specific isoform. PRKAG3 splice
CC variant DNA. Prkag3 gene is located in the RN locus of chromosome 15.
CC Mutation in Prkag3 results in an altered regulation of carbohydrate
CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
CC therapeutic for treating carbohydrate metabolism disorders such as
CC diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX SQ Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;

Query Match 68.5%; Score 41.8; DB 22; Length 2022;
Best Local Similarity 80.3%; Pred. No. 0.00059;
Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGTGGAGGAGGGAGCCACAGTCAGGGGAGGTCCCGGTCC 60
DB 256 ACAAGGCAGGAGTGTAGAGGAAGGGGGCCCTCCGGGCCGAGGAGGTCCCGAGTCC 315
QY 61 A 61
DB 316 A 316

RESULT 12
AAD36458
ID AAD36458 standard; DNA; 1873 BP.
XX AC
AC AAD36458;
XX DT 09-AUG-2002 (first entry)
```

XX Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).

XX AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;

KW screening; meat quality; single nucleotide polymorphism; SNP; pig;

KW gene; variant; ds.

XX Sus scrofa.

XX Key Location/Qualifiers

FT CDS 1..1395

FT /tag= a

FT /product= "pig PRKAG3 polymorphic variant (PRKAG3-52)"

FT variation replace (154, A)

FT /tag= b

FT /standard_name= "single nucleotide polymorphism (SNP)"

XX WO200220850-A2.

PN 14-MAR-2002.

PD 10-SEP-2001; 2001WO-US28283.

XX 08-SEP-2000; 2000US-231045P.

PR 08-JAN-2001; 2001US-260239P.

PR 18-JUN-2001; 2001US-299111P.

XX (IOWA) UNIV IOWA STATE RES FOUND INC.

PA Rothschild MF, Ciobanu DC, Malek M, Plastow G;

XX WPI: 2002-393850/42.

DR P-PSDB; AAE22986.

XX Screening animals to determine those likely to produce larger litters

PT and improved meat quality traits involves assaying for the presence of

PT polymorphisms in the AMP activated protein kinase regulatory gamma

PT subunit gene -

XX Claim 34; Page 93-95; 109pp; English.

XX The invention relates to a method for screening animals to determine

CC those more likely to produce large litters and improved meat quality

CC traits. The method involves assaying for the presence of a genotype

CC in the sample of genetic material obtained from animal. The genotype

CC is characterised by polymorphism(s) in the AMP activated protein

CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used

CC for screening animals e.g., pigs to determine those most likely to

CC exhibit improved meat quality traits and to produce larger litters.

CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-52).

XX Query Match 65.9%; Score 40.2; DB 24; Length 1873;

XX Best Local Similarity 78.7%; Pred. No. 0.0018;

XX Matches 48; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 ACAAGGAGGAGTGGTGGAGGAGGAGGCCACCGTCCAGGGGAGGTCCCGGTCC 60

DB 106 ACAAGGAGGAGGTGTAGAGGAGGGGGGCTCCGGGCCGAGGAGGAGTCCCAAGTCC 165

OY 61 A 61

DB 166 A 166

RESULT 13

AAD36461

XX AAD36461 standard; DNA; 1095 BP.

XX AAD36461;

XX 09-AUG-2002 (first entry)

XX Pig PRKAG3 gene 5' flanking region with SINE.

XX AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;

KW screening; meat quality; polymorphism; short interspersed element;

KW pig; SINE; ds.

XX Sus scrofa.

XX Key Location/Qualifiers

FT exon 19..59

FT /tag= a

FT /number= 1

FT intron 60..825

FT /tag= b

FT /number= 1

FT repeat_region 445..749

FT /tag= c

FT /rpt_type= "DIRECT"

FT /note= "Direct repeat between short

FT interspersed element (SINE)"

FT repeat_unit 445..462

FT /tag= d

FT repeat_unit 732..749

FT /tag= e

FT exon 826..979

FT /tag= f

FT /number= 2

XX WO200220850-A2.

PN 14-MAR-2002.

PD 10-SEP-2001; 2001WO-US28283.

XX 08-SEP-2000; 2000US-231045P.

PR 08-JAN-2001; 2001US-260239P.

PR 18-JUN-2001; 2001US-299111P.

XX (IOWA) UNIV IOWA STATE RES FOUND INC.

PA Rothschild MF, Ciobanu DC, Malek M, Plastow G;

XX WPI: 2002-393850/42.

XX Screening animals to determine those likely to produce larger litters

PT and improved meat quality traits involves assaying for the presence of

PT polymorphisms in the AMP activated protein kinase regulatory gamma

PT subunit gene -

XX Disclosure; Fig 2A; 109pp; English.

XX The invention relates to a method for screening animals to determine

CC those more likely to produce large litters and improved meat quality

CC traits. The method involves assaying for the presence of a genotype

CC in the sample of genetic material obtained from animal. The genotype

CC is characterised by polymorphism(s) in the AMP activated protein

CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used

CC for screening animals e.g., pigs to determine those most likely to

CC exhibit improved meat quality traits and to produce larger litters.

CC The present sequence is pig PRKAG3 gene 5' flanking region including

CC exon, intron and short interspersed element (SINE).

XX Sequence 1095 BP; 233 A; 315 C; 267 G; 278 T; 2 other;

SQ Query Match 53.4%; Score 32.6; DB 24; Length 1095;

XX Best Local Similarity 74.5%; Pred. No. 0.41; Indels 0; Gaps 0;

XX Matches 38; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

OY 1 ACAAGGAGGAGTGGTGGAGGAGGAGGCCACCGTCCAGGGGAGGTCCCGGTCC 51

DB 931 ACAAGGAGGAGGTGTAGAGGAGGGGGGCTCCGGGCCGAGGAGGAGGT 981


```
RESULT 14
AAD36462
ID AAD36462 standard; DNA; 808 BP.
XX
AC AAD36462;
XX
DT 09-AUG-2002 (first entry)
XX
DE Pig PRKAG3 gene 5' flanking region including exon and intron.
XX
DE AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; polymorphism; pig; ds.
KW
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT exon 19..59
FT /*tag= a
FT /number= 1
FT intron 60..538
FT /*tag= b
FT /number= 1
FT exon 539..692
FT /*tag= c
FT /number= 2
XX
XX WO200220850-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
XX
XX 08-JAN-2001; 2001US-260239P.
XX
XX 18-JUN-2001; 2001US-299111P.
XX
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
XX WPI; 2002-393850/42.
XX
XX Screening animals to determine those likely to produce larger litters
XX and improved meat quality traits involves assaying for the presence of
XX polymorphisms in the AMP activated protein kinase regulatory gamma
XX subunit gene
XX
XX Disclosure; Fig 2B; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
XX those more likely to produce large litters and improved meat quality
XX traits. The method involves assaying for the presence of a genotype
XX in the sample of genetic material obtained from animal. The genotype
XX is characterised by polymorphism(s) in the AMP activated protein
XX kinase regulatory gamma subunit (PRKAG3) gene. The method is used
XX for screening animals e.g., pigs to determine those most likely to
XX exhibit improved meat quality traits and to produce larger litters.
XX The present sequence is pig PRKAG3 gene 5' flanking region including
XX exon and intron.
XX
XX Sequence 808 BP; 170 A; 230 C; 199 G; 208 T; 1 other;
XX
XX Query Match 51.5%; Score 31.4; DB 24; Length 808;
XX Best Local Similarity 74.5%; Pred. No. 0.94;
XX Matches 38; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
XX
XX 1 ACAAGGCAGGAAGTCGGTGGAGGAGGGAGGCCACCGAGTCCAGGGGGAAGGT 51
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 644 ACAAGGCAGGAGGATATAGAGGAGGGGGGGCTCCGGGCCCGAGGGAAGGT 694
```

RESULT 15

```
AAS84523
ID AAS84523 standard; cDNA; 2541 BP.
XX
AC AAS84523;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #20327.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
KW
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PSDB; ABG20336.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity
XX
XX Claim 1; SEQ ID No 20327; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 2541 BP; 476 A; 780 C; 787 G; 498 T; 0 other;
XX
XX Query Match 43.0%; Score 26.2; DB 23; Length 2541;
XX Best Local Similarity 67.3%; Pred. No. 43;
XX Matches 37; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
XX
XX 5 GGCAGAACTCGGTGGAGGAGGGAGGCCACCGAGTCCAGGGGGAAGTCCCGGTC 59
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 1114 GGCAGGGCCGGTGGGGAACACTGTGGCCCGGAGGTCCAGGGGTCTCTCCACAGTC 1168
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Search completed: June 13, 2003, 02:59:54

Job time : 23.1613 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:37:44 ; Search time 151.839 seconds
(without alignments)
8506.409 Million cell updates/sec

Title: US-09-826-581-5_COPY_200_260

Perfect score: 61

Sequence: 1 acaaggcagaagtcgggga.....gggggaaggtcccggtcca 61

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	38.6	63.3	621	10	BB628877
2	38.6	63.3	655	10	BB629521
3	38.6	63.3	685	10	BB630381
4	37	60.7	399	10	AW356079
5	37	60.7	422	10	AW427435
6	34.2	56.1	444	12	BF890374

7	33.8	55.4	548	13	BI775360
8	32	52.5	516	9	AI664508
9	29	47.5	365	9	AA787203
10	28	45.9	618	10	AW693375
11	28	45.9	669	13	BJ080431
12	27.8	45.6	808	10	BE306360
13	27.4	44.9	590	13	BM489457
14	27.2	44.3	1029	13	BM466469
15	27	44.3	151	12	BG244994
16	26.6	43.6	611	17	CNS01YJK
17	26.6	43.6	1691	12	BG845439
18	26.4	43.3	870	17	AZ166563
19	26.4	43.3	935	14	BQ876192
20	26.2	43.0	255	10	AK353555
21	26.2	43.0	349	12	BE835678
22	26.2	43.0	375	10	AW298840
23	26.2	43.0	475	12	BF773644
24	26.2	43.0	540	13	BI539806
25	26.2	43.0	600	17	BH236198
26	26.2	43.0	704	17	BH235990
27	26.2	43.0	729	17	BH235871
28	26	42.6	276	9	AU257757
29	26	42.6	312	12	BF904178
30	26	42.6	679	10	BB653848
31	26	42.6	709	13	BG963198
32	26	42.6	991	12	BG324609
33	25.8	42.3	459	14	BQ783197
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35	25.8	42.3	547	10	BE121408
36	25.8	42.3	700	9	AL508704
37	25.8	42.3	908	14	BQ230020
38	25.8	42.3	1157	12	BF674061
39	25.6	42.0	467	14	H92825
40	25.6	42.0	483	17	AQ169119
41	25.6	42.0	501	10	BH823175
42	25.6	42.0	590	13	BI507914
43	25.6	42.0	629	14	BM702805
44	25.6	42.0	716	13	BI085954
45	25.6	42.0	1023	14	BQ642252

ALIGNMENTS

RESULT 1

BB628877

LOCUS BB628877 621 bp mRNA linear EST 31-AUG-2001

DEFINITION BB628877 RIKEN full-length enriched, 16 days neonate cerebellum Mus musculus cDNA clone 9630039L22 5', mRNA sequence.

ACCESSION BB628877

VERSION BB628877.1 GI:15399483

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 621)

AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

```

FEATURES
    location/Qualifiers
        1. .655
            /organism="Mus musculus"
            /db_xref="taxon:10090"
            /clone_lib="RIKEN full-length enriched, adult male bone"
            /sex="male"
            /tissue_type="bone"
            /dev_stage="adult"
            /lab_host="DH10B"
            /note="Site 1: SalI; Site 2: BamHI; cDNA library was
            prepared and sequenced in Mouse Genome Encyclopedia
            Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in
            RIKEN. Division of Experimental Animal Research in Riken
            contributed to prepare mouse tissues. 1st strand cDNA was
            primed with a primer [5'
            GAGAGAGAGAGGTCACAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse
            transcriptase and subsequently enriched for full-length
            transcripts."

```


Qy	61 A 61
Dh	97 A 97

longissimus muscle.	
91 a	67 t
147 c	139 g

Query Match 56.1%; Score 34.2; DB 12; Length 444;
Best Local Similarity 76.4%; Pred. No. 3;
Matches 42: Conservative 0; Mismatches 13; Indels 0; Gaps 0;

GAAGTCGGTGGAGGAAGGGGAGCCACCAGGTCAGGGGAAGTCCCCGGTCCA 61

GGAGGATGTAGAGGAAGGGAGCTGCCAGGCCTGGAGGGAGGTCCCCAGTCCA 55

RESULT 7
BI775360
LOCUS BI775360 548 bp mRNA linear EST 25-SEP-2001
DEFINITION 467815 MARC Bos taurus cDNA 5', mRNA sequence.

5360.1 GI:15776346

ORGANISM

BOS LAURUS

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

1 /bases 1 to 5481

REFERENCE

REFERENCE

1 (bases 1 to 548)
bivalves; bivalves; bivalves.

AUTHORS

Smith, T. L., Grosse, W. M., Preking, B. A., Roberts, A. J., Stone, R. T.,
Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett,
G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G.,
Pertepe, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and
Keele, J. W.

me Res. 11 (4), 626-630 (2001)

act: Smith TPL

Dr. J. H. W. Arnott, US Naval Research Center
Box 166, Clay Center, NE 68933-0166, USA

402 762 4390
402 762 4390

IT: sth@email.marc.usda.gov

80904.e. Vector identified by cross_match with the -minscore 18

Primers

WARD: GTTTCCCGTCACGACG

primer: ATTAGTGACACTATAG.

1. .548

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/note="vector: pcm7 sporeg: site 1. Note: site 2. salt:

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Library made from pooled tissue from testis, thymus,

adrenal, and endometrium."

55.48: Score 33.8: DB 13: Length 548:

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		Canc	0.

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1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Figure 1**
 10. **Figure 2**
 11. **Figure 3**
 12. **Figure 4**
 13. **Figure 5**
 14. **Figure 6**
 15. **Figure 7**
 16. **Figure 8**
 17. **Figure 9**
 18. **Figure 10**
 19. **Figure 11**
 20. **Figure 12**
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 23. **Figure 15**
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 178. **Figure 170**
 179. **Figure 171**
 180. **Figure 172**
 181. **Figure 173**
 182. **Figure 174**
 183. **Figure 175**
 184. **Figure 176**
 185. **Figure 177**
 186. **Figure 178**
 187. **Figure 179**
 188. **Figure 180**
 189. **Figure 181**
 190. **Figure 182**
 191. **Figure 183**
 192. **Figure 184**
 193. **Figure 185**
 194. **Figure 186**
 195. **Figure 187**
 196. **Figure 188**
 197. **Figure 189**
 198. **Figure 190**
 199. **Figure 191**
 200. **Figure 192**
 201. **Figure 193**
 202. **Figure 194**
 203. **Figure 195**
 204. **Figure 196**
 205. **Figure 197**
 206. **Figure 198**
 207. **Figure 199**
 208. **Figure 200**
 209. **Figure 201**
 210. **Figure 202**
 211. **Figure 203**
 212. **Figure 204**
 213. **Figure 205**
 214. **Figure 206**
 215. **Figure 207**
 216. **Figure 208**
 217. **Figure 209**

R.A.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula stem library
 Unpublished (2000)
 On Apr 14, 2000 this sequence version replaced gi:7568111.
 Contact: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380
 Email: radixon@noble.org
 Insert Length: 660 Std Error: 0.00
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 Seq primer: TCACACAGGAACAGCTACAC.
 Location/Qualifiers
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 /clone="NF063H10ST"
 /clone_lib="Developing stem"
 /tissue_type="stem"
 /dev_stage="Pooled developmental"
 /note="Vector: lambda Zap; Contains a mixture of
 internodal stem segments"
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 Best Local Similarity 77.3%; Pred.No. 2e+02; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 10;
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 Db 76 ACAGGCAGAGTTCGGTGGAGGAGGTGTCAGTCTATGG 119
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 DEFINITION
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 ACCESSION
 BJ080431
 VERSION
 BJ080431.1 GI:17574127
 KEYWORDS
 EST.
 SOURCE
 African clawed frog.
 ORGANISM
 Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 669)
 Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
 ,Y.
 Expressed genes in X. laevis embryo
 Unpublished (2001)
 Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
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 /clone="XL075j16"
 /clone_lib="NTBB Mochii normalized Xenopus tailbud
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 /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
 were oligo-dT primed and directionally cloned. Staging
 Y."

ACCESSION

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

JOURNAL
COMMENT

FEATURES

sons

BASE COIN[®]

ORIGIN

Query Match
Best Local
Matches

Qy

Db

RESULT 14

BM466469
LOCUS

DEFINITION
ACCESSION
VERSION

SOURCE ORGANISM

REFERENCE

AUTHORS	TITLE	JOURNAL	COMMENT

Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM12336 row: c column: 01
High quality sequence stop: 681.
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/lab_host="DH10B (phage-resistant)"
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Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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DEFINITION 602358260F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4486719 5', mRNA sequence.
ACCESSION BG244994
VERSION BG244994.1 GI:12754809
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM10330 row: h column: 16
High quality sequence stop: 151.
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/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
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Best Local Similarity 66.1%; Pred. No. 3.2e+02;
Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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Db 73 ACTCGCAGAGCCCGGTGGAGGGTGAGGATCACCCGGGAAGGGGGGACGCTGGGTC 131
Search completed: June 13, 2003, 05:58:24
Job time : 155.839 secs

Db 667 ACACAGCAGAGCCGCTCCACAACTGGGAACAGCATCCCTCGGGAAATGCC 721

RESULT 5

US-08-815-652B-1
; Sequence 1, Application US/08815652B
; Patent No. 6034062
; GENERAL INFORMATION:
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony
; APPLICANT: Song, Jeffrey
; APPLICANT: Thies, R. Scott
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,652B
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5186D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: C57B46xCBA
; TISSUE TYPE: liver
; IMMEDIATE SOURCE:
; LIBRARY: Mouse liver cDNA
; CLONE: ML14A
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1564..1893
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 610..1896
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 1..2447
US-08-815-652B-1

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Best Local Similarity 65.5%; Pred. No. 20;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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RESULT 6

US-08-254-353A-1
; Sequence 1, Application US/08254353A
; Patent No. 6287816
; GENERAL INFORMATION:
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Song, Jeffrey
; APPLICANT: Thies, Scott
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5186B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: C57B46xCBA
; TISSUE TYPE: liver
; IMMEDIATE SOURCE:
; LIBRARY: Mouse liver cDNA
; CLONE: ML14A
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1564..1893
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 610..1896
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 1..2447
US-08-254-353A-1

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Best Local Similarity 65.5%; Pred. No. 20;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Db 667 ACACAGCAGAGCCGCTCCACAACTGGGAACAGCATCCCTCGGGAAATGCC 721

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; GENERAL INFORMATION:
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19920625
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5186A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: C57B4xKBA
; TISSUE TYPE: liver
; IMMEDIATE SOURCE:
; LIBRARY: Mouse liver cdna
; CLONE: ML14A
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1564..1893
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PCT-US92-05374A-1

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Best Local Similarity 65.5%; Pred. No. 20;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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RESULT 8
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; Sequence 1, Application PC/TUS9507084
; GENERAL INFORMATION:
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony J.
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5186C-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1210
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: C57B4xKBA
; TISSUE TYPE: liver
; IMMEDIATE SOURCE:
; LIBRARY: Mouse liver cdna
; CLONE: ML14A
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1564..1893
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 610..1896
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 1..2447
PCT-US95-07084-1

Query Match      40.3%; Score 24.6; DB 5; Length 2447;
Best Local Similarity 65.5%; Pred. No. 20;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY   1 ACAAGGCAGAATCGGTGGAGGAGGCCACCACCAAGTCAGGGGAAGTCCCC 55
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Db    667 ACACAGCAGAACCCGCTGCAGAACTGGGAACAAGCATCCCTCGGGAAAAATGCC 721


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US-09-750-580-4
; Sequence 4, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 04:39:50 ; Search time 19,2903 seconds
(without alignments)
4579.068 Million cell updates/sec

Title: US-09-826-581-5_COPY_200_260

Perfect score: 61

Sequence: 1 acaagcagaagtcggtgga.....gggggaagtcgcccggtcca 61

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	27.4	44.9	382	9	US-09-960-352-1640
c 4	27	44.3	74868	9	US-10-175-523-67
5	25	41.0	560	9	US-09-995-793A-32
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8	25	41.0	8670	9	US-09-373-658-69
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14	24.6	40.3	5381	10	US-09-751-877-4
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17	24.6	40.3	81001	10	US-09-751-877-1
18	24.4	40.0	14040	9	US-09-764-891-5478
19	24.4	40.0	14040	9	US-09-764-891-10205

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c 20 24.4 40.0 302250 10 US-09-962-832-154 Sequence 154, Appl
21 24.2 39.7 139 10 US-09-864-761-19511 Sequence 19511, A
22 24.2 39.7 263 10 US-09-294-093B-950 Sequence 950, Appl
23 24.2 39.7 451 10 US-09-864-761-5 Sequence 5, Appli
c 24 24.2 39.7 1448 9 US-09-764-891-8575 Sequence 8575, Ap
c 25 24.2 39.7 34094 9 US-10-199-550-1 Sequence 1, Appli
26 24 39.3 131 10 US-09-864-761-19652 Sequence 19652, A
27 24 39.3 506 9 US-10-198-846-9038 Sequence 9038, Ap
c 28 24 39.3 687 9 US-10-198-846-12192 Sequence 12192, A
c 29 24 39.3 755 9 US-10-198-846-4363 Sequence 4363, Ap
c 30 24 39.3 2235 9 US-09-895-298-34 Sequence 34, Appli
31 24 39.3 2608 9 US-10-054-988-16 Sequence 16, Appl
32 24 39.3 2608 10 US-09-739-254-16 Sequence 16, Appl
33 24 39.3 2608 10 US-09-904-615-16 Sequence 16, Appl
34 23.8 39.0 1942 9 US-09-800-274-1 Sequence 1, Appli
c 35 23.8 39.0 6456 12 US-10-044-090-71 Sequence 71, Appli
c 36 23.8 39.0 14738 9 US-09-764-891-5637 Sequence 5637, Ap
c 37 23.8 39.0 14738 9 US-09-764-891-5639 Sequence 5639, Ap
c 38 23.6 38.7 308 10 US-09-960-352-9061 Sequence 9061, Ap
39 23.6 38.7 2193 10 US-09-822-849A-49 Sequence 49, Appl
40 23.6 38.7 2421 10 US-09-815-242-7677 Sequence 7677, Ap
c 41 23.6 38.7 2692 9 US-09-992-598-298 Sequence 298, App
c 42 23.6 38.7 2692 9 US-09-989-293A-298 Sequence 298, App
c 43 23.6 38.7 2692 9 US-09-989-735-298 Sequence 298, App
c 44 23.6 38.7 2692 9 US-09-990-444-298 Sequence 298, App
c 45 23.6 38.7 2692 9 US-09-989-730-298 Sequence 298, App
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ALIGNMENTS

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RESULT 1
US-09-826-581-5
; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Lutimann, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SU
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5
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Query Match 100.0%; Score 61; DB 10; Length 1647;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAAGCAGAAGTCGTTGGAGGAGGAGCCACGAGTCAGGGGAAGTCCCGGTC 60
Db 200 ACAAGCAGAAGTCGTTGGAGGAGGAGCCACGAGTCAGGGGAAGTCCCGGTC 259
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QY 61 A 61
Db 260 A 260
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RESULT 2
US-09-826-581-2
; Sequence 2, Application US/09826581
; Patent No. US20020142310A1
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; GENERAL INFORMATION:
; APPLICANT: Rajan, Priithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/13795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 74868
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-175-523-67

Query Match 44.3%; Score 27; DB 9; Length 74868;
Best Local Similarity 85.7%; Pred. No. 2.2;
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 AAGGCAGAACTCGGTGGAGGAGGGGAGGCACACAG 37
|||||
Db 73759 AAGGCAGAACTTCAGGAGGAGGGGTTCCACAG 73725

RESULT 5
US-09-995-793A-32
; Sequence 32, Application US/09995793A
; Publication No. US20030054446A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Bernard H.F.
; APPLICANT: Stoehr, Heidi
; TITLE OF INVENTION: No. US20030054446A1 retinal-specific human proteins C7orf9,
; FILE REFERENCE: 033488-001
; CURRENT APPLICATION NUMBER: US/09/995,793A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/253,751
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: genomic DNA, Exon from 101 to 460
US-09-995-793A-32

Query Match 41.0%; Score 25; DB 9; Length 560;
Best Local Similarity 64.9%; Pred. No. 17;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 CAAGCGAGAGTCGGTGGAGGAGGGGAGGCACACAGTCAGGGGAGAGTCCCGGT 58
|||||
Db 249 CAAGCGTCAGAGGGGGGAGGAGGAGTGGGGTGACAGGAGAGCTGTAAAGTCTCCAGT 305

RESULT 6
US-09-995-793A-30
; Sequence 30, Application US/09995793A
; Publication No. US20030054446A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Bernard H.F.

```

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; APPLICANT: Stoehr, Heidi
; TITLE OF INVENTION: No. US2003005446alel retina-specific human proteins C7orf9, C12orf9
; FILE REFERENCE: 033488-001
; CURRENT APPLICATION NUMBER: US/09/995,793A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/253,751
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: artificial sequence, Translation start at 347, stop at 604
US-09-995-793A-30

Query Match          41.0%; Score 25; DB 9; Length 1188;
Best Local Similarity 64.9%; Pred. No. 13;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY      2 CAAGCGAGAGTCGGTGGAGGAGGGGAGGCCACCAGGTCAGGGGGAAGGTCCCGCGT 58
        ||||| || || || || || || || || || || || || || || || || || ||
Db      151 CAAGGCTGACAGAGGGGCGCAGGAAATGCGGGTGACAGAGACGCTGTAAGGCTCCACT 207

RESULT 7
US-09-967-768A-301/c
; Sequence 301, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 301
; LENGTH: 4034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-301

Query Match          41.0%; Score 25; DB 10; Length 4034;
Best Local Similarity 64.9%; Pred. No. 13;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY      5 GGCAGAGTCGGTGGAGGAGGGGAGGCCACCAGGTCAGGGGGAAGGTCCCGGTCCA 61
        ||||| || || ||||| || || || || || || || || || || || || || || ||
Db      184 GGCAGGAGGAGGATGAGGAGGGGCGAGACGCCAGGAGAGGGGCGGCCATTACA 128

RESULT 8
US-09-373-658-69/c
; Sequence 69, Application US/09373658
; Publication No. US20030092900A1
; GENERAL INFORMATION:
; APPLICANT: Iruela-Arispe, Luisa
; APPLICANT: Hastings, Gregg A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Trulli, Stephen H.
; APPLICANT: Fronwald, James A.
; APPLICANT: Terrett, Jonathan A.
```

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; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides
; FILE REFERENCE: 1488.1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 8670
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Unknown
US-09-373-658-69

Query Match          41.0%; Score 25; DB 9; Length 8670;
Best Local Similarity 64.9%; Pred. No. 12;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY      5 GGCAGAGTCGGTGGAGGAGGGGAGGCCACCAGGTCAGGGGGAAGGTCCCGGTCCA 61
        ||||| || ||||| || || || || || || || || || || || || || || || ||
Db      6571 GGCAGGAGCGGTGGAGGAGGTGGAGGCGCGGTATCATGAACAGAGCCCGCCCA 6515

RESULT 9
US-09-880-107-2184
; Sequence 2184, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Vockley, Darci T.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2184
; LENGTH: 33795
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L25880
US-09-880-107-2184

Query Match          40.7%; Score 24.8; DB 10; Length 33795;
Best Local Similarity 67.3%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY      7 CAGAGTCGGTGGAGGAGGGGAGGCCACCAGGTCAGGGGGAAGGTCCCGGT 58
        ||||| || || || || || || || || || || || || || || || || || || ||
Db      999 CAGCAGTGGGCCCAACAATGTAGCCACCAGGTCGGGGGCACAGCCACCAGGT 1050

RESULT 10
US-09-822-830A-179
; Sequence 179, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
```

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 2996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-179

Query Match 40.3%; Score 24.6; DB 10; Length 2996;
Best Local Similarity 65.5%; Pred. No. 19;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 5 GCACAAAGTCGTCGAGAGAGGGAGCCACCAAGTCAAGGGGAGGTCCCGGTC 59
Db 1568 GCCAGGAGGCTCTTTGGAGAGGAGTGTCCCGGTCAGGTGGTCCGCTCCCGGTC 1622

RESULT 11

US-10-091-572-817
; Sequence 817, Application US/10091572
; Publication No. US20030054373A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4118C1
; CURRENT APPLICATION NUMBER: US/10/091,572
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,850
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,239
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210

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; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08

Query Match          40.3%; Score 24.6; DB 9; Length 5312;
Best Local Similarity 65.5%; Pred. No. 18; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 19;

QY      5   GCACGAAGTCGGTGGAGGAGGCACCACGAGTCAGGGGGAAGGTCCCGGGTC 59
Db       | ||| || | ||||| || | ||||| || | ||||| || | ||||| ||
        1867 GCCAGGAGGCTCTTTGGGAAGGAGTGTCGCCGGTCAGGTGGTGGCTCCCGGGTC 1921

RESULT 12
US-09-764-891-9241
; Sequence 9241, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9241
; LENGTH: 5312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9241

Query Match          40.3%; Score 24.6; DB 9; Length 5312;
Best Local Similarity 65.5%; Pred. No. 18; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 19;

QY      5   GCACGAAGTCGGTGGAGGAGGCACCACGAGTCAGGGGGAAGGTCCCGGGTC 59
Db       | ||| || | ||||| || | ||||| || | ||||| || | ||||| ||
        1867 GCCAGGAGGCTCTTTGGGAAGGAGTGTCGCCGGTCAGGTGGTGGCTCCCGGGTC 1921

RESULT 13
US-09-842-364-4
; Sequence 4, Application US/09842364
; Publication No. US20030032783A1
; GENERAL INFORMATION:
; APPLICANT: Yen-Potin, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihaid, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueleret, Lydie
; TITLE OF INVENTION: APOLOPROTEIN &-IV-RELATED PROTEIN: POLYPEPTIDE, POLYNUCLEOTIDE, AND METHODS FOR THE DETECTION AND QUANTIFICATION THEREOF
; FILE REFERENCE: GENSET.50CPZC
; CURRENT APPLICATION NUMBER: US/09/842,364
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 09/469/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pn
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; OTHER INFORMATION: 17-42-319.probe
; NAME/KEY: misc_binding
; LOCATION: 3201..3225
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 17-41-250.probe
US-09-842-364-4

Query Match
Best Local Similarity 40.3%; Score 24.6; DB 9; Length 5381;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 13 TCGGTGGAGGAGGAGGCCACCAAGTTCAGGGGGAAGTCCCGGTC 59
Db 613 TCCTCTTTGGTGCCAGCCAGCAGTCAAGTGGGAGGTTAAGGC 659

RESULT 14
US-09-751-877-4
; Sequence 4, Application US/09751877
; Patent No. US20020142949A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89-US3.REG
; CURRENT APPLICATION NUMBER: US/09/751,877
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 4
; LENGTH: 5381
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..918
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 919..930
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 1442..1498
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 1613..1724
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 2243..3940
; OTHER INFORMATION: exon 4
; NAME/KEY: misc_feature
; LOCATION: 3941..5381
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 319
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 3213
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: conflict
; LOCATION: 1241
; OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
; NAME/KEY: conflict
; LOCATION: 1447
; OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
; NAME/KEY: primer_bind
; LOCATION: 1..11022
; OTHER INFORMATION: 17-42-319.mis
; NAME/KEY: primer_bind
; LOCATION: 300..318
; OTHER INFORMATION: 17-42-319.mis complement
; NAME/KEY: primer_bind
; LOCATION: 320..338
; OTHER INFORMATION: 17-42-319.mis complement
; NAME/KEY: primer_bind
; LOCATION: 3194..3212
; OTHER INFORMATION: 17-41-250.mis
; NAME/KEY: primer_bind
; LOCATION: 3214..3232
; OTHER INFORMATION: 17-41-250.mis complement
; NAME/KEY: misc_binding
; LOCATION: 307..331

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Run on: June 13, 2003, 01:49:14 ; Search time 192.613 Seconds
(without alignments)
9216.782 Million cell updates/sec
Title: US-09-826-581-5_COPY_529_589
Perfect score: 61
Sequence: 1 99gctggatgacgaactgc.....acatgcgtctatgcagag 61
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1	61	100.0	989	6	AX281579 Sequence
2	61	100.0	1647	6	AX281582 Sequence
3	61	100.0	2109	6	AX099776 Sequence
4	61	100.0	2115	6	AX099802 Sequence
5	61	100.0	2115	9	AF214519 Homo sapi
c 6	61	100.0	152129	2	AC027416 Homo sapi
c 7	61	100.0	206854	9	AC009974 Homo sapi
8	57.8	94.8	2290	9	HS249977 Homo sapi
9	48.2	79.0	1867	6	AX099774 Sequence
10	48.2	79.0	1873	4	AF214520 Sus scrofa
11	48.2	79.0	1873	6	AX099800 Sequence
12	48.2	79.0	1873	6	AX398331 Sequence
13	48.2	79.0	1873	6	AX398333 Sequence
14	48.2	79.0	1873	6	AX398335 Sequence
15	48.2	79.0	1873	6	AX398337 Sequence
16	48.2	79.0	1873	6	AX398339 Sequence
17	48.2	79.0	2022	6	AX099804 Sequence
18	48.2	79.0	5888	4	AF214521 Sus scrofa
c 19	47.2	77.4	227724	2	AF336381 Mus muscu
20	41.8	68.5	146577	2	AC128070 Rattus no
21	41.8	68.5	190183	2	AC129703 Rattus no
22	41.8	68.5	192968	2	AC127107 Rattus no
23	27.4	44.9	29641	3	AC005802 Leishmani
c 24	27.4	44.9	35018	3	AC005893 Leishmani
c 25	27.4	44.9	110000	3	AC125735_0 Leishmani
26	26.8	43.9	10346	1	AE009112 Agrobacte
27	26.8	43.9	14856	1	AE008077 Agrobacte
28	26.2	43.0	14101	1	AE009874 Pyrobacul
c 29	26.2	43.0	79397	2	AC115385 Rattus no
30	25.8	42.3	1917	10	AF002245 Cricetulu
31	25.8	42.3	4279	10	AF039574 Mus muscu
32	25.8	42.3	5253	10	AF112855 Mus muscu
c 33	25.8	42.3	17570	1	AE007063 Mycobacte
c 34	25.8	42.3	39430	1	MTCY49 Mycobacteri
35	25.8	42.3	183496	2	AC125075 Mus muscu
36	25.6	42.0	217	11	HSJ11082 STS from
c 37	25.6	42.0	38819	3	AC091120 Leishmani
38	25.6	42.0	92750	2	AC121230 Leishmani
39	25.6	42.0	110000	2	AC124396_2 Continuation (3 of
c 40	25.4	41.6	15586	1	AE000078 Rhizobium
c 41	25.4	41.6	63464	2	AC099721 Homo sapi
c 42	25.4	41.6	140053	2	AC007873 Homo sapi
43	25.4	41.6	158075	2	AC131311 Homo sapi
44	25.4	41.6	158808	2	AC106429 Rattus no
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ALIGNMENTS

RESULT 1
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LOCUS AX281579 989 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 2 from Patent WO0177305.
ACCESSION AX281579
VERSION AX281579.1 GI:16608830
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Andersson, L., Luthman, H. and Marklund, S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 2 18-Oct-2001;

Pred. No. is the number of results predicted by chance to have a

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LOCUS                 1647 bp      DNA      linear      PAT 02-NOV-2001
DEFINITION            Sequence 5 from Patent WO0177305.
ACCESSION              AX281582
VERSION                AX281582.1 GI:16608833
KEYWORDS
SOURCE                 human.
ORGANISM               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE              1
AUTHORS                Andersson, L., Luthman, H. and Marklund, S.
TITLE                  Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL                Patent: WO 0177305-A 5 18-OCT-2001;
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Db 589 G 589
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DEFINITION            Sequence 3 from Patent WO0120003.
ACCESSION              AX099776
VERSION                AX099776.1 GI:13538810
KEYWORDS
SOURCE                 human.
ORGANISM               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE              1
AUTHORS                Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
                        Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
                        Chardon, P.
TITLE                  Variants of the gamma chain of ampk, dna sequences encoding the
                        same, and uses thereof
JOURNAL                Patent: WO 0120003-A 3 22-MAR-2001;
                        INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
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QY 61 G 61
Db 489 G 489
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LOCUS                 2115 bp      DNA      linear      PAT 02-APR-2001
DEFINITION            Sequence 29 from Patent WO0120003.
ACCESSION              AX099802
VERSION                AX099802.1 GI:13538836
KEYWORDS
SOURCE                 human.
ORGANISM               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE              1
AUTHORS                Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
                        Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
                        Chardon, P.
TITLE                  Variants of the gamma chain of ampk, dna sequences encoding the
                        same, and uses thereof
JOURNAL                Patent: WO 0120003-A 29 22-MAR-2001;
                        INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
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Qy 61 G 61
Db 495 G 495

RESULT 5
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LOCUS Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
DEFINITION mRNA, complete cds.
ACCESSION AF214519
VERSION AF214519.1 GI:8215681
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2115)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gallard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
and Andersson,L.
A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle
Science 288 (5469), 1248-1251 (2000)
20280150
10818001
2 (bases 1 to 2115)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gallard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden
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Db 495 G 495

RESULT 6
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LOCUS Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
DEFINITION unordered pieces.
ACCESSION AC027416
VERSION AC027416.2 GI:8317289
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 152129)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-504G11
JOURNAL Unpublished
2 (bases 1 to 152129)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,I., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galegan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lechoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,P., Minova,T., Miranda,C., Mienga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigglio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

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----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7458
Center clone name: 504_G_11
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135376 bases at least Q40
Consensus quality: 143264 bases at least Q30
Consensus quality: 146503 bases at least Q20
Insert size: 161000; agarose-1p
Quality coverage: 3.1 in Q20 bases; agarose-1p
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1106 2402: contig of 1297 bp in length
* 2403 2502: gap of 100 bp
* 2503 3823: contig of 1321 bp in length
* 3824 3923: gap of 100 bp
* 3924 5020: contig of 1097 bp in length
* 5021 5120: gap of 100 bp
* 5121 6161: contig of 1041 bp in length
* 6162 6261: gap of 100 bp
* 6262 7547: contig of 1286 bp in length
* 7548 7647: gap of 100 bp
* 7648 9983: contig of 2336 bp in length
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* 17124 17223: gap of 100 bp
* 17224 19466: contig of 2243 bp in length
* 19467 19566: gap of 100 bp
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* 21929 22028: gap of 100 bp
* 22029 24319: contig of 2291 bp in length
* 24320 24419: gap of 100 bp
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* 77116 77215: gap of 100 bp
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* 85023 85122: gap of 100 bp
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* 137838 137937: gap of 100 bp
* 137938 152129: contig of 14192 bp in length.
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Best Local Similarity 100.0%; Pred. No. 4.1e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 G 61
Db 38046 G 38046

RESULT 7
AC009974/c
LOCUS AC009974 206854 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
ACCESSION AC009974
VERSION AC009974.9 GI:16799058
KEYWORDS HPG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 206854)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 206854)
AUTHORS Harris,A. and Cotton,M.
TITLE The sequence of Homo sapiens BAC clone RP11-459119
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 206854)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 8, 2001 this sequence version replaced gi:13431203.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC

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Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0459119

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., pired quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tatenio,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

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misc_feature	1..37 /note="match to EST AW680850 (NID:g8042860)"
misc_feature	1..37 /note="match to EST BE047599 (NID:g8364652) tz39c01.y1"
misc_feature	1..37 /note="match to EST BE314060 (NID:g9134719)"
misc_feature	1..37 /note="match to EST BF183086 (NID:g11061273)"
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misc_feature	1..37 /note="similar to Homo sapiens EST B1114348 (NID:g14565249)"

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misc_feature 4. .37 /note="match to EST A1670836 (NID:g4850567) wa04g10.xl"
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misc_feature 220. .221 /note="match to EST BG470047 (NID:g13402322)"
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Db 168125 G 168125
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LOCUS Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
DEFINITION (AMPK gamma 3 gene).
ACCESSION AJ249977.1 GI:6688200
VERSION AMP-activated protein kinase; AMPK gamma 3 subunit.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2290)
AUTHORS Cheung,P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D.
TITLE Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
JOURNAL Biochem. J. 346 Pt 3, 659-669 (2000)
MEDLINE 20164049
PubMed 10696692
REFERENCE 2 (bases 1 to 2290)
AUTHORS Carling,D.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 0NN, UNITED KINGDOM
FEATURES
source 1. .2290 /organism="Homo sapiens"
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CDS 22. .1500 /gene="AMPK gamma 3"
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ORIGIN

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Best Local Similarity 96.7%; Pred. No. 4.1e-09;
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QY 61 G 61
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Db 591 G 591

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DEFINITION Sequence 1 from Patent WO0120003.
ACCESSION  AX099774
VERSION     AX099774.1 GI:13538808
KEYWORDS   .
SOURCE     pig.
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 1867)
AUTHORS   Anderson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
            Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., Le Roy, P. and
            Chardon, P.
TITLE     Variants of the gamma chain of ampk, dna sequences encoding the
            same, and uses thereof
JOURNAL   Patent: WO 0120003-A 1 22-MAR-2001;
            INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
            Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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Db 429 GGGCTGGGATGACGAACACTCGCGAAACCGCGGCCGAGTCTACATGCATTCATGCAGGA 488

QY 61 G 61
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Db 489 G 489

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DEFINITION Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
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ACCESSION  AF214520
VERSION     AF214520.1 GI:8215683
KEYWORDS   .
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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SOURCE           Sus scrofa.
ORGANISM         Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 1873)
AUTHORS   Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M.,
            Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H.,
            Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
            and Andersson, L.
TITLE     A mutation in PRKAG3 associated with excess glycogen content in pig
            skeletal muscle
JOURNAL     Science 288 (5469), 1248-1251 (2000)
MEDLINE     20280150
PUBMED     10818001
REFERENCE  2 (bases 1 to 1873)
AUTHORS   Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
            Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
            Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
TITLE     Direct Submission
JOURNAL     Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
            University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
            Sweden
FEATURES   Location/Qualifiers
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                        TDFILVHRYRSPVLQIYEIEHKIETWREIVLQCFKPLVSISPNDSLFAFVALI
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QY 61 G 61
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Db 495 G 495

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LOCUS      1873 bp      DNA      linear      PAT 02-APR-2001
DEFINITION Sequence 27 from Patent WO0120003.
ACCESSION  AX099800
VERSION     AX099800.1 GI:13538834
KEYWORDS   .
SOURCE     pig.
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 01:37:39 ; Search time 22.1613 Seconds
(without alignments)
6198.732 Million cell updates/sec

Title: US-09-826-581-5_COPY_529_589

Perfect score: 61

Sequence: 1 gggctgggagacgaactgc.....acatgcgcttcacgagag 61

Scoring table:

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 24: /SID32/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	61	100.0	989	22	AAH43682
2	61	100.0	1647	22	AAH43685
3	61	100.0	2109	22	AAD03296
4	61	100.0	2115	22	AAD03320
5	48.2	79.0	1867	22	AAD03295
6	48.2	79.0	1873	22	AAD03319
7	48.2	79.0	1873	24	AAD36456
8	48.2	79.0	1873	24	AAD36457
9	48.2	79.0	1873	24	AAD36458

10	48.2	79.0	1873	24	AAD36459	Pig PRKAG3 polymor
11	48.2	79.0	1873	24	AAD36460	Pig PRKAG3 polymor
12	48.2	79.0	2022	22	AAD03321	Sus scrofa PRKAG3
13	25.8	42.3	5259	21	AAA64328	cDNA sequence enco
c 14	25.8	42.3	4403765	22	AAI99683	Mycobacterium tube
c 15	25.8	42.3	4411529	22	AAI99682	Mycobacterium tube
c 16	25.4	41.6	669	21	AAF12737	Aspergillus oryzae
c 17	25.4	41.6	534720	19	AAV30458	Rhizobium species
c 18	25.4	41.6	536165	19	AAV30459	Rhizobium species
c 19	25	41.0	1473	23	AA54367	Pseudomonas aerugi
20	24.8	40.7	7816	22	AAK52934	Human polynucleoti
21	24.8	40.7	7818	22	AAK51950	Human polynucleoti
22	24.8	40.7	14533	23	AA65883	DNA encoding novel
23	24.8	40.7	14917	24	AAD32338	Human lung specif
24	24.4	40.0	1406	23	ABL19505	Drosophila melanog
25	24.4	40.0	2327	17	AAO30376	Phytase gene. Asp
26	24.4	40.0	2327	20	AAZ27414	A. terreus phytase
27	24.4	40.0	3406	23	ABL19504	Drosophila melanog
28	24.4	40.0	3593	23	ABL19502	Drosophila melanog
c 29	24.2	39.7	433	23	AA574013	DNA encoding novel
c 30	24.2	39.7	664	22	AAH99539	Human protein enco
c 31	24.2	39.7	747	23	AA574015	DNA encoding novel
c 32	24.2	39.7	999	23	AA574014	DNA encoding novel
c 33	24.2	39.7	2147	21	AA258309	Human peptidase NA
c 34	24.2	39.7	2197	21	AA258305	Human peptidase NA
c 35	24.2	39.7	2215	21	AA258306	Human peptidase NA
c 36	24.2	39.7	2229	21	AA258308	Human peptidase NA
c 37	24.2	39.7	2320	21	AA258304	Human peptidase NA
c 38	24.2	39.7	2395	21	AA258311	Human peptidase NA
c 39	24.2	39.7	2402	21	AA258310	Human peptidase NA
c 40	24.2	39.7	2689	23	AA574016	DNA encoding novel
c 41	24.2	39.7	2702	21	AA258307	Human peptidase NA
c 42	24.2	39.7	7521	22	AAK81190	Human immune/haema
c 43	24	39.3	1086	24	ABL40464	Human C-C chemokin
c 44	24	39.3	1089	21	AAA47543	Primate GPR2 seque
c 45	24	39.3	1244	24	ABL40463	Human C-C chemokin

ALIGNMENTS

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XX					
DT	21-JAN-2002	(first entry)			
XX					
DE	PRKAG3	intron 2 - intron 4.			
XX					
KW	Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;				
KW	metabolic disease; diabetes; obesity; substitution; ds.				
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OS	Homo sapiens.				
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FH	Key	Location/Qualifiers			
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FT	exon	22..177			
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FT XX /note= "5' portion of intron 4"
PN XX WO200177305-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-SB00765.
XX XX 07-APR-2000; 2000US-195665P.
XX PA (AREX-) AREXIS AB.
XX XX Andersson L, Luthman H, Marklund S;
XX PI WPI; 2001-657170/75.
XX DR
XX XX New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX XX
XX PS Example 1; Fig 2; 25pp; English.
XX CC The sequences given in AAH43681-84 represents genomic fragments
XX encoding the human AMP-activated protein kinase gamma 3 subunit
XX (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
XX is useful in determining a risk estimate of a metabolic disease,
XX such as diabetes or obesity, in a subject. The variation may occur
XX in exons 3, 4 or 10. In exon 3 variation may be a substitution of
XX a G for a C at nucleotide 320, resulting in the amino acid
XX substitution P71A; in exon 4 variation may be a substitution of a
XX T for a C at nucleotide 550; and in exon 10 variation may be a
XX substitution of a T for a C at nucleotide 1037, resulting in the
XX amino acid substitution R340W. There may also be nucleotide variation
XX in intron 6.
XX SQ Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
XX
XX Query Match 100.0%; Score 61; DB 22; Length 989;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-12;
XX Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Qy 61 G 61
XX |
XX Db 882 G 882
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XX RESULT 2
XX AAH43685
XX ID AAH43685 standard; cDNA; 1647 BP.
XX XX
XX AC AAH43685;
XX
XX DT 21-JAN-2002 (first entry)
XX XX
XX DE PRKAG3 cDNA.
XX XX
XX KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
XX metabolic disease; diabetes; obesity; substitution; ss.
XX OS Homo sapiens.
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XX FH Key Location/Qualifiers
XX CDS 20..1489
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FT variation /note= "Causes P71A"
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FT /note= "Silent variation"
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FT /note= "Causes R340W"
XX XX
XX PN WO200177305-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-SB00765.
XX XX
XX PR 07-APR-2000; 2000US-195665P.
XX XX (AREX-) AREXIS AB.
XX PA
XX XX Andersson L, Luthman H, Marklund S;
XX PI WPI; 2001-657170/75.
XX DR P-PSDB; QQB47679.
XX XX
XX PT New variants of human AMP-activated protein kinase gamma3 subunit
XX associated with a metabolic disease e.g. diabetes or obesity and method
XX for determining a risk estimate of diseases in subject by detecting the
XX variant -
XX XX
XX PS Disclosure; Fig 5; 25pp; English.
XX XX
XX CC This sequence represents the full length cDNA encoding the human
XX AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
XX the presence of the PRKAG3 DNA, or a variant, is useful in determining
XX a risk estimate of a metabolic disease, such as diabetes or obesity,
XX in a subject. The variation may occur in exons 3, 4 or 10. In exon
XX 3 variation may be a substitution of a G for a C at nucleotide 320,
XX resulting in the amino acid substitution P71A; in exon 4 variation may
XX be a substitution of a T for a C at nucleotide 550; and in exon 10
XX variation may be a substitution of a T for a C at nucleotide 1037,
XX resulting in the amino acid substitution R340W. There may also be
XX nucleotide variation in intron 6. The numbering of these
XX variations is based on the full length cDNA as given, rather than on
XX position 1 of the open reading frame.
XX SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
XX
XX Query Match 100.0%; Score 61; DB 22; Length 1647;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-12;
XX Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GGGCTGGGATGACGAACCTCGGAAACCGCGGCCAGATCTACATCGCTTCATGCAGGA 60
XX |||||
XX Db 529 GGGCTGGGATGACGAACCTCGGAAACCGCGGCCAGATCTACATCGCTTCATGCAGGA 588
XX
XX Qy 61 G 61
XX |
XX Db 589 G 589
XX
XX RESULT 3
XX AAD03296
XX ID AAD03296 standard; DNA; 2109 BP.
XX XX
XX AC AAD03296;
XX XX
XX DT 13-JUN-2001 (first entry)
XX XX
XX DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
XX KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
XX PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
XX

```

KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
XX Homo sapiens.
XX OS
XX PH Key Location/Qualifiers
XX FT 5'UTR 1..471
XX FT /*tag= a
XX CDS 472..1389
XX FT /*tag= b
XX FT /product= "Human Prkg3 protein"
XX FT 3'UTR 1390..2109
XX FT /*tag= c
XX PN WO200120003-A2.
XX XX
XX PD 22-MAR-2001.
XX XX
XX PF 11-SEP-2000; 2000WO-EP09896.
XX PR 10-SEP-1999; 99EP-0402236.
XX PR 18-MAY-2000; 2000EP-0401388.
XX XX
XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX PA (ANDE/) ANDERSSON L.
XX PA (LOOF/) LOOFT C.
XX PA (KALM/) KALM E.
XX XX
XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX XX
XX DR WPI; 2001-244810/25.
XX DR P-PSDB; AAE00221.
XX XX
XX PT New variants of the gamma subunit of vertebrate adenosine
XX PT monophosphate-activated kinase for diagnosis or treatment of disorders
XX PT associated with energy metabolism such as diabetes, obesity, and
XX PT myopathy -
XX XX
XX PS Claim 12; Fig 2; 71pp; English.
XX XX
XX CC The present sequence is a cDNA encoding human adenosine monophosphate
XX CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
XX CC PRKAG3. Mutation in Prkg3 results in an altered regulation of
XX CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
XX CC useful as therapeutic for treating carbohydrate metabolism disorders such
XX CC as diabetes, obesity, and disorders associated with muscle metabolism
XX CC such as myopathy and cardiovascular diseases, to modulate AMPK
XX CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
XX CC and its functionally altered mutants are useful for the diagnostic
XX CC evaluation, genetic testing and prognosis of a metabolic disorder,
XX CC preferably a carbohydrate metabolism disorder. Primers that can detect
XX CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
XX CC useful for detecting a dysfunction of carbohydrate metabolism resulting
XX CC from the expression of a functionally altered allele of PRKAG3.
XX CC Transgenic animal and host cell transformed with PRKAG3 or a
XX CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
XX CC screening compounds able to modulate AMPK activity. Nucleic acid
XX CC encoding PRKAG3 is useful for detecting mutations in a Prkg3 gene, or
XX CC in a sequence encoding the first cystathione beta synthase (CBS) domain
XX CC of PRKAG3 and is useful in gene therapy.
XX XX
SQ Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
Query Match 100.0%; Score 61; DB 22; Length 2109;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGCTGGATGAGAACTCGGAACCGCGGCCAGATCTACATGCGCTTCATGCAGGA 60
|||||
Db 429 GGGCTGGATGAGAACTCGGAACCGCGGCCAGATCTACATGCGCTTCATGCAGGA 488
Qy 61 G 61

Db 489 G 489
RESULT 4
AAD03320
ID AAD03320 standard; cDNA; 2115 BP.
XX XX
XX AC AAD03320;
XX DT 13-JUN-2001 (first entry)
XX XX
XX DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
XX XX
XX KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT CDS 1..1395
XX FT /*tag= a
XX FT /product= "Human complete Prkg3 protein"
XX XX
XX PN WO200120003-A2.
XX XX
XX PD 22-MAR-2001.
XX XX
XX PF 11-SEP-2000; 2000WO-EP09896.
XX XX
XX PR 10-SEP-1999; 99EP-0402236.
XX PR 18-MAY-2000; 2000EP-0401388.
XX XX
XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX PA (ANDE/) ANDERSSON L.
XX PA (LOOF/) LOOFT C.
XX PA (KALM/) KALM E.
XX XX
XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX XX
XX DR WPI; 2001-244810/25.
XX DR P-PSDB; AAE00223.
XX XX
XX PT New variants of the gamma subunit of vertebrate adenosine
XX PT monophosphate-activated kinase for diagnosis or treatment of disorders
XX PT associated with energy metabolism such as diabetes, obesity, and
XX PT myopathy -
XX XX
XX PS Claim 12; Page 65-68; 71pp; English.
XX XX
XX CC The present sequence is a cDNA encoding human adenosine monophosphate
XX CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
XX CC complete PRKAG3. Mutation in Prkg3 results in an altered regulation of
XX CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
XX CC useful as therapeutic for treating carbohydrate metabolism disorders such
XX CC as diabetes, obesity, and disorders associated with muscle metabolism
XX CC such as myopathy and cardiovascular diseases, to modulate AMPK
XX CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
XX CC and its functionally altered mutants are useful for the diagnostic
XX CC evaluation, genetic testing and prognosis of a metabolic disorder,
XX CC preferably a carbohydrate metabolism disorder. Primers that can detect
XX CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
XX CC useful for detecting a dysfunction of carbohydrate metabolism resulting
XX CC from the expression of a functionally altered allele of PRKAG3.
XX CC Transgenic animal and host cell transformed with PRKAG3 or a
XX CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
XX CC screening compounds able to modulate AMPK activity. Nucleic acid
XX CC encoding PRKAG3 is useful for detecting mutations in a Prkg3 gene, or
XX CC in a sequence encoding the first cystathione beta synthase (CBS) domain
XX CC of PRKAG3 and is useful in gene therapy.
XX XX

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XX SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
Query Match 100.0%; Score 61; DB 22; Length 2115;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTGGGATGACGAACTGGGAAACCCGGCCCGAGATCTACATGCGCTTCATGCAGGA 60
    |||||
Db 435 GGCTGGGATGACGAACTGGGAAACCCGGCCCGAGATCTACATGCGCTTCATGCAGGA 494

QY 61 G 61
    |
Db 495 G 495

RESULT 5
AAD03295
ID AAD03295 standard; cDNA; 1867 BP.
XX AC AAD03295;
XX DT 13-JUN-2001 (first entry)
XX DE Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
XX KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
KW chromosome 15; ss.
XX OS Sus scrofa.
XX FH Key Location/Qualifiers
FT 5'UTR 1..471
FT /*tag= a
FT CDS 472..1389
FT /*tag= b
FT /*product= "Sus scrofa PRKAG3 protein"
FT 3'UTR 1390..1867
FT /*tag= c
XX W0200120003-A2.
XX PD 22-MAR-2001.
XX PF 11-SEP-2000; 2000WO-EP09896.
XX PR 10-SEP-1999; 99EP-0402236.
XX PR 18-MAY-2000; 2000EP-0401388.
XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.
PA (LOOF/) LOOFT C.
PA (KALM/) KALM E.
XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX WPI: 2001-244810/25.
XX DR P-PSDB; AAE00220.
XX New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment of disorders
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy -
XX Claim 12; Fig 2; 71pp; English.
XX The present sequence is a cDNA encoding pig adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.

```

```

CC Mutation in Prkag3 results in an altered regulation of carbohydrate
CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
CC therapeutic for treating carbohydrate metabolism disorders such as
CC diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX SQ Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;

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Query Match 79.0%; Score 48.2; DB 22; Length 1867;
Best Local Similarity 86.9%; Pred. No. 7.6e-08;
Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1 GGCTGGGATGACGAACTGGGAAACCCGGCCCGAGATCTACATGCGCTTCATGCAGGA 60
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Db 429 GGCTGGGATGATGAGTGGCAGAAGCCGGGGCCCGAGTCTACATGCGCTTCATGCAGGA 488

QY 61 G 61
    |
Db 489 G 489

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RESULT 6
AAD03319
ID AAD03319 standard; cDNA; 1873 BP.
XX AC AAD03319;
XX DT 13-JUN-2001 (first entry)
XX DE Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
XX KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
KW chromosome 15; ss.
XX OS Sus scrofa.
XX FH Key Location/Qualifiers
FT CDS 1..1395
FT /*tag= a
FT /*product= "Sus scrofa complete Prkag3 protein"
XX W0200120003-A2.
XX PD 22-MAR-2001.
XX PF 11-SEP-2000; 2000WO-EP09896.
XX PR 10-SEP-1999; 99EP-0402236.
XX PR 18-MAY-2000; 2000EP-0401388.
XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.
PA (LOOF/) LOOFT C.
PA (KALM/) KALM E.
XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;

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XX WPI: 2001-244810/25.
DR P-PSDB; AAE00222.
DR
XX
XX New variants of the gamma subunit of vertebrate adenosine
FT monophosphate-activated kinase for diagnosis or treatment of disorders
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy
XX
XX
PS Claim 12; Page 62-64; 71pp; English.
XX
XX The present sequence is a cDNA encoding pig adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome
CC 15. Mutation in Prkag3 results in an altered regulation of carbohydrate
CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
CC therapeutic for treating carbohydrate metabolism disorders such as
CC diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX
SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 79.0%; Score 48.2; DB 22; Length 1873;
Best Local Similarity 86.9%; Pred. No. 7.6e-08;
Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGGCTGGATGACGAACTCGGAAACCGCGCCGACATCTACATCGCTTCATGCAGGA 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 435 GGGCTGGATGATGAGCTGCAGAACCGGGGGCCCGAGTCTACATGCATGCAGGA 494

QY 61 G 61
|
Db 495 G 495

RESULT 7
AAD36456
ID AAD36456 standard; DNA; 1873 BP.
XX
AC AAD36456;
XX
XX 09-AUG-2002 (first entry)
XX
XX Pig wild-type PRKAG3 gene.
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; ds.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT CDS 1..1395
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FT replace (89, C)
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (154, A)
FT /tag= c

FT variation /standard_name= "Single nucleotide polymorphism (SNP)"
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FT /tag= d
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (599, A)
FT /tag= e
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200220850-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28283.
XX
PR 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Globanu DC, Malek M, Plastow G;
PI
XX WPI: 2002-393850/42.
DR P-PSDB; AAE22984.
XX
XX Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
FT subunit gene
XX
PS Claim 17; Fig 1; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig wild-type PRKAG3 gene.
XX
SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 79.0%; Score 48.2; DB 24; Length 1873;
Best Local Similarity 86.9%; Pred. No. 7.6e-08;
Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGGCTGGATGACGAACTCGGAAACCGCGCCGACATCTACATCGCTTCATGCAGGA 60
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Db 435 GGGCTGGATGATGAGCTGCAGAACCGGGGGCCCGAGTCTACATGCATGCAGGA 494

QY 61 G 61
|
Db 495 G 495

RESULT 8
AAD36457
ID AAD36457 standard; DNA; 1873 BP.
XX
AC AAD36457;
XX
XX 09-AUG-2002 (first entry)
XX
XX Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; variant; ds.
XX
OS Sus scrofa.
XX

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FH Key Location/Qualifiers
FT CDS 1..1395
FT /*tag= a
FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
FT variation replace (89, C)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200220850-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
XX WPI; 2002-393850/42.
DR P-PSDB; AAE22985.
XX
XX Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene
XX
XX Disclosure; Page 89-91; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX
SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 79.0%; Score 48.2; DB 24; Length 1873;
Best Local Similarity 86.9%; Pred. No. 7.6e-08;
Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGGCTGGGATGACGACACTCGGAAACCGCGCCGACATCTACATCGCTTCATGCAGGA 60
DB ||||| ||||| || ||||| || || ||||| ||||| ||||| ||||| |||||
435 GGGCTGGGATGATGAGCTGCAGAGCCGGGGGCCAGGTCTACATGCACCTTCATGCAGGA 494

QY 61 G 61
DB 495 G 495

RESULT 9
AAD36458
ID AAD36458 standard; DNA; 1873 BP.
XX
XX AAD36458;
AC
XX
XX 09-AUG-2002 (first entry)
DT
XX
XX Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
DE
XX
XX AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; variant; ds.
XX
XX Sus scrofa.
OS
XX

```

```

FH Key Location/Qualifiers
FT CDS 1..1395
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FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
FT variation replace (154, A)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200220850-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
XX WPI; 2002-393850/42.
DR P-PSDB; AAE22986.
XX
XX Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene
XX
XX Claim 34; Page 93-95; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
XX
SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match 79.0%; Score 48.2; DB 24; Length 1873;
Best Local Similarity 86.9%; Pred. No. 7.6e-08;
Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGGCTGGGATGACGACACTCGGAAACCGCGCCGACATCTACATCGCTTCATGCAGGA 60
DB ||||| ||||| || ||||| || || ||||| ||||| ||||| ||||| |||||
435 GGGCTGGGATGATGAGCTGCAGAGCCGGGGGCCAGGTCTACATGCACCTTCATGCAGGA 494

QY 61 G 61
DB 495 G 495

RESULT 10
AAD36459
ID AAD36459 standard; DNA; 1873 BP.
XX
XX AAD36459;
AC
XX
XX 09-AUG-2002 (first entry)
DT
XX
XX Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
DE
XX
XX AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; variant; ds.
XX
XX Sus scrofa.
OS
XX

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OM nucleic - nucleic search, using sw model

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9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
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21: em_gss_vrt.*
22: em_gss_fun.*
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27: em_gss_rod.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	45.6	74.8	444	12	BF890374 291826 MA
2	45.6	74.8	548	13	BF775360 467815 MA
3	44	72.1	685	10	BB630381 BB630381
4	27.4	44.9	910	17	CNS02SVT AL212510 Tetraodon
5	27.4	44.9	1010	17	CNS038S6 AL233007 Tetraodon
6	27.2	44.6	955	12	BC394974 602457369

7	26.8	43.9	581	13	BJ005207
8	26.4	43.3	442	17	AQ641446
9	26	42.6	248	10	BE711478
10	26	42.6	349	9	AI606158
11	26	42.6	580	17	BH140228
12	26	42.6	593	17	BH140663
13	25.8	42.3	648	10	AW024446
14	25.8	42.3	680	10	BE198231
15	25.8	42.3	738	13	BG918873
16	25.8	42.3	986	12	BF120119
17	25.6	42.0	738	13	BM006421
18	25.6	42.0	812	9	AA519383
19	25.6	42.0	1004	17	CNS03ERS
20	25.4	41.6	1000	13	BM468546
21	25.2	41.3	369	14	W68459
22	25.2	41.3	432	13	BI616099
23	25.2	41.3	482	13	BI537568
24	25	41.0	481	10	AW488804
25	25	41.0	636	13	BJ060200
26	25	41.0	1083	12	BF135856
27	24.8	40.7	339	12	BF773519
28	24.8	40.7	414	10	AW501053
29	24.8	40.7	567	10	AV392022
30	24.8	40.7	591	14	BM707454
31	24.8	40.7	605	9	AA195150
32	24.8	40.7	658	13	BF171961
33	24.8	40.7	707	17	AG130442
34	24.8	40.7	718	10	AV753229
35	24.8	40.7	738	12	BG700791
36	24.8	40.7	742	10	BE394076
37	24.8	40.7	888	13	BM011144
38	24.8	40.7	904	12	BF033403
39	24.6	40.3	284	17	CNS03VW1
40	24.6	40.3	481	14	BQ508350
41	24.6	40.3	509	13	BM088002
42	24.6	40.3	532	12	BG599496
43	24.6	40.3	532	14	BQ508349
44	24.6	40.3	542	12	BE809466
45	24.6	40.3	554	12	BE755789

ALIGNMENTS

RESULT 1
BF890374
LOCUS BF890374 444 bp mRNA linear EST 25-APR-2001
DEFINITION 291826 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF890374
VERSION BF890374.1 GI:12281760
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 444)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W., Rohrer,G.A., Chitko-McKown,C.G.,
Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
COMMENT Contact: Smith,TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred


```

source
1. .585
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A030014A04"
/clone_lib="RIKEN full-length enriched, 6 days neonate
skin"
/tissue_type="skin"
/dev_stage="6 days neonate"
/lab_host="DH10B"
/note="Site 1: Salt; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in RIKEN
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTTTNN 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 185.0. Second
strand cDNA was prepared with the primer adaptor of
sequence [5' GAGAGAGAGATTCGAGTTAAATTAAATTAATCCGCCGCCGCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FHC i. a
BASE COUNT      165 a 199 c 198 g 123 t
ORIGIN
Query Match      72.1%; Score 44; DB 10; Length 685;
Best Local Similarity 83.3%; Pred. No. 0.00012;
Matches 50; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1  GGGCTGGGATGACGAACTCCGGAACCGCGCCCGCAGATCTACATCGCTTCATCGAGGA 60
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      522  GAGTGGGATGACCAACTTCACAAACCGGAGCCCGAGCTCTACATGCATTTATCGAGA 581
      1  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
CNS02SVT      910 bp      DNA      linear      GSS 15-MAY-2000
LOCUS      Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION      163617 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION      AL212510
VERSION      AL212510.1      GI:7871329
KEYWORDS      GSS: genome survey sequence.
SOURCE      Tetraodon nigroviridis.
ORGANISM      Tetraodon nigroviridis.
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
      Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;
      Tetraodontidae; Tetraodon.
REFERENCE      1 (bases 1 to 910)
AUTHORS      Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
      Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
      Saurin,W. and Weissenbach,J.
TITLE      Human gene number estimate provided by genome wide analysis using
      Tetraodon nigroviridis DNA sequence
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 910)
AUTHORS      Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
      Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
      Weissenbach,J.
TITLE      Characterization and repeat analysis of the compact genome of the
      freshwater pufferfish Tetraodon nigroviridis
JOURNAL      Unpublished
REFERENCE      3 (bases 1 to 910)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      Submitted (12-APR-2000)
COMMENT      This sequence is a single read and was generated as part of a large
      scale clone-end sequencing project of the Tetraodon nigroviridis

```

```

genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
    source
        1..910
            /organism="Tetraodon nigroviridis"
            /db_xref="taxon:99883"
            /clone="163g17"
            /clone_lib="G"
            /note="Genoscope sequence ID : COAG163AD09LP1-end : T7"
BASE COUNT    179 a   263 c   305 g   160 t   3 others
ORIGIN

Query Match      44.9%; Score 27.4; DB 17; Length 910;
Best Local Similarity 65.6%; Pred. No. 49;
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      1  GGGCTGGGATGACGAACTGGCGAACCAGCCGGCCGAGATCTACATGCGCTTCATCGAGGA 60
        |||||
Db       273 GGGCATGATAGGCGTACACAGCTGACCCCGACGACCTGGACTTCATCGAGCATCGAGGA 333
        |||||

QY      61  G  61
        |
Db       333  G  333

RESULT 5
CNS038S6
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
005N22 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL233007
VERSION
AL233007.1 GI:7892142
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 1010)
Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Winkler,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 1010)
Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
3 (bases 1 to 1010)
Genoscope.
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
    source
        1..1010
            /organism="Tetraodon nigroviridis"
            /db_xref="taxon:99883"
            /clone="005N22"
            /clone_lib="G"
            /note="Genoscope sequence ID : C08C005DG11XD1-end : T7"
BASE COUNT    174 a   313 c   312 g   210 t   1 others
ORIGIN

Query Match      44.9%; Score 27.4; DB 17; Length 1010;

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```

Best Local Similarity 65.6%; Pred. No. 50;
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 GGCCTGGATGACGAAGTCCGGAAACCCGGCCCGCAGATCAGATCGGTTTCATCCAGGA 60
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 620 GGGCATGAAGGGCTACAGCTACCCCGCAGCGACTGCGATTCATCCGACCATGACGGA 679
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 G 61
Db 680 G 680

RESULT 6
BG394974
LOCUS BG394974
DEFINITION 581 bp mRNA linear EST 05-DEC-2001
ACCESSION BJ005207
VERSION BJ005207
KEYWORDS MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA076804 5',
EST. mRNA sequence.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 955)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM1297 row: j column: 17
High quality sequence stop: 717.
FEATURES
Location/Qualifiers
SOURCE 1..955
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4579696"
/clone_lib="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 268 a 208 c 225 g 254 t
ORIGIN

Query Match 44.6%; Score 27.2; DB 12; Length 955;
Best Local Similarity 67.9%; Pred. No. 58;
Matches 38; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 4 CTGGATGACGAAGTCCGGAAACCCGGCCCGCAGATCAGATCGGTTTCATCCAGG 59
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 836 CTTAGATGACTACTCCGGAATCTGCGCCCGGAAACCCGGTTTCATGAAGG 891
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
BJ005207
LOCUS BJ005207
DEFINITION 581 bp mRNA linear EST 05-DEC-2001
ACCESSION BJ005207
VERSION BJ005207
KEYWORDS MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA076804 5',
EST. mRNA sequence.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 955)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM1297 row: j column: 17
High quality sequence stop: 717.
FEATURES
Location/Qualifiers
SOURCE 1..955
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4579696"
/clone_lib="NIH_MGC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 268 a 208 c 225 g 254 t
ORIGIN

Query Match 44.6%; Score 27.2; DB 12; Length 955;
Best Local Similarity 67.9%; Pred. No. 58;
Matches 38; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 4 CTGGATGACGAAGTCCGGAAACCCGGCCCGCAGATCAGATCGGTTTCATCCAGG 59
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 836 CTTAGATGACTACTCCGGAATCTGCGCCCGGAAACCCGGTTTCATGAAGG 891
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
AJ064144/c
LOCUS AJ064144/c
DEFINITION RPC193-ECORI-4I13.TJ RPC193-ECORI Trypanosoma brucei genomic clone
ACCESSION AJ064144/c
VERSION AJ064144.1 GI:5118156
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 442)
AUTHORS El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams M.
TITLE Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPOI-93
JOURNAL Library for gene discovery and sequence-ready map construction
COMMENT Unpublished (1999)
Other_GSSs: RPC193-ECORI-4I13.TV
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org
Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.bufile.edu). BAC end sequences search
page: http://www.tigr.org/tdb/mbd/tbdb/.
Seq primer: SP6
Class: BAC ends.
FEATURES
Location/Qualifiers

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KEYWORDS Japanese medaka.
SOURCE Oryzias latipes
ORGANISM Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE 1 (bases 1 to 581)
AUTHORS Kohara,Y., Shin-I,T., Kimura,T., Marita,T., Jindo,T. and Takeda,H.
TITLE Medaka EST Project in Takeda's lab
JOURNAL Medaka EST Project in Takeda's lab
COMMENT Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
Location/Qualifiers
SOURCE 1..581
/organism="Oryzias latipes"
/strain="Hd-r"
/db_xref="taxon:8090"
/clone="MF01SSA076804"
/clone_lib="MF01SSA CDNA"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"
BASE COUNT 134 a 235 c 119 g 91 t
ORIGIN

Query Match 43.9%; Score 26.8; DB 13; Length 581;
Best Local Similarity 73.9%; Pred. No. 71;
Matches 34; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 16 ACTGCGGAACCCGGCCGAGATCTACATGCGCTTCATGCAGGAG 61
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 442 ACGGCTAAACCCGGACACCCGCTCTACACAGCTACATGCAGGAG 487
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
AJ064144/c
LOCUS AJ064144/c
DEFINITION RPC193-ECORI-4I13.TJ RPC193-ECORI Trypanosoma brucei genomic clone
ACCESSION AJ064144/c
VERSION AJ064144.1 GI:5118156
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 442)
AUTHORS El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams M.
TITLE Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPOI-93
JOURNAL Library for gene discovery and sequence-ready map construction
COMMENT Unpublished (1999)
Other_GSSs: RPC193-ECORI-4I13.TV
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org
Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.bufile.edu). BAC end sequences search
page: http://www.tigr.org/tdb/mbd/tbdb/.
Seq primer: SP6
Class: BAC ends.
FEATURES
Location/Qualifiers

```

```

source
1. 442
/organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="RPC193-EcoRI-4113"
/clone_lib="RPC193-EcoRI"
/notes="Vector: pBACE3.6; Site_1: Eco RI; Site_2: Eco RI;
Constructed for The Institute for Genomic Research by
Bobui Zhao in Pieter de Jong's laboratory (Roswell Park
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
brucei TREU927/4 GUTat 10.1 agarose embedded DNA was
partially digested with a combination of Eco RI and Eco RI
methylase (RPC193-EcoRI segment) or Dpn II (RPC193-DpnII
segment). High molecular weight fragments were ligated in
pBACE3.6 vector digested with Eco RI or Bam HI.
respectively. The average insert size is 141 Kb. Total
coverage (both segments): > 90 x the haploid
non-minichromosomal genome."
BASE COUNT 104 a 118 c 118 g 102 t
ORIGIN
Query Match 43.38; Score 26.4; DB 17; Length 442;
Best Local Similarity 65.04; Pred. No. 90;
Matches 39; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 GGCTGGATGACGAACTCGGAAACCCGGCCCGACAGATCTACATGGCTTCATGCAGA 60
|||||
Db 287 GGCTGGATGACGAACTCGGAAACCCGGCCCGACAGATCTACATGGCTTCATGCAGA 228
|||||

RESULT 9
BB711478 248 bp mRNA linear EST 11-OCT-2001
BB711478 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA
clone R020024106 3', mRNA sequence.
BB711478
BB711478.1 GI:16064647
EST.
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Akimura,T., Arahawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotoi,K., Ishii
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
Matahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)
TITLE
Unpublished (2001)
JOURNAL
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp
URL:http://genome.gsc.riken.go.jp/
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format

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```

sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
Location/Qualifiers
1. 248
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="R020024106"
/clone_lib="RIKEN full-length enriched, 2 cells egg"
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/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATCTCGAGTTAATTAATTCCTCCCTCCCTCCCTCC 3']. cDNA
was cleaved with XhoI and BamHI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC 1."
BASE COUNT 92 a 47 c 33 g 76 t
ORIGIN
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Best Local Similarity 65.58; Pred. No. 11e+02;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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RESULT 10
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AI606158 vol5c02.x1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:1049954 3', mRNA sequence.
AI606158
AI606158.1 GI:4615325
EST.
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M./WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the

```

FEATURES

	Qy	1	GGCTGGGATGACGA	CTGGGA	ACCCGG	CGCCAG	ATCTAC	ATGGCTTC	ATGCAG	58
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/lab_host="DH108"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      257 a      150 c      216 g      115 t
ORIGIN

Query Match      42.3%; Score 25.8; DB 13; Length 738;
Best Local Similarity 67.9%; Pred. No. 1.6e+02;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Db      146 ATGGAAACTGCGAGCAGCGGAGGAGCATCTTCAGGCGCTTTGAGCAGAG 198
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Search completed: June 13, 2003, 05:58:28
Job time : 155.839 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:39:09 ; Search time 4.64516 Seconds

(without alignments)
4027.262 Million cell updates/sec

Title: US-09-826-581-5 COPY 529 589

Perfect score: 61

Sequence: 1 gggctgggatgacgaactgc.....acatgcgcttcatgcaggag 61

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 441362 seqs. 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

100% Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/1na/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/1na/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/1na/PCUTS_COMB.seq: *
6: /cgn2_6/ptodata/1/1na/backfiles.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match					
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C 2	25.8	42.3	4411529	4	US-09-103-840A-1		Sequence 1, Appli
C 3	24.4	40.0	2327	4	US-08-868-435-1		Sequence 1, Appli
C 4	24.4	40.0	2327	4	US-08-744-231-1		Sequence 1, Appli
C 5	23.4	38.4	1508	4	US-09-518-914-1		Sequence 3, Appli
C 6	23.4	38.4	1541	4	US-09-518-914-3		Sequence 3, Appli
C 7	23.2	38.0	44377	2	US-08-804-2270-7		Sequence 7, Appli
C 8	23.2	38.0	44377	2	US-08-804-198-1		Sequence 1, Appli
C 9	22.8	37.4	1320	3	US-09-221-654-1		Sequence 1, Appli
C 10	22.8	37.4	1320	3	US-08-989-358A-1		Sequence 1, Appli
C 11	22.8	37.4	1593	3	US-08-993-359-23		Sequence 23, Appli
C 12	22.6	37.0	1233	1	US-08-362-670B-27		Sequence 27, Appli
C 13	22.6	37.0	1233	3	US-08-333-576C-27		Sequence 27, Appli
C 14	22.6	37.0	1233	4	US-08-808-324-27		Sequence 27, Appli
C 15	22.6	37.0	1233	5	PCR-US94-14030A-27		Sequence 27, Appli
C 16	22.6	37.0	1260	1	US-07-841-646-4		Sequence 4, Appli
C 17	22.6	37.0	1260	1	US-07-901-703-14		Sequence 14, Appli
C 18	22.6	37.0	1260	1	US-08-147-023-3		Sequence 4, Appli
C 19	22.6	37.0	1260	1	US-08-447-570-4		Sequence 4, Appli
C 20	22.6	37.0	1260	2	US-08-448-700-4		Sequence 4, Appli
C 21	22.6	37.0	1260	2	US-08-449-659A-4		Sequence 4, Appli
C 22	22.6	37.0	1260	5	PCR-US93-05446-14		Sequence 14, Appli
C 23	22.6	37.0	1314	4	US-08-713-556B-39		Sequence 39, Appli
C 24	22.6	37.0	1547	1	US-08-377-292-2		Sequence 2, Appli
C 25	22.6	37.0	1607	1	US-07-679-451-1		Sequence 1, Appli
C 26	22.6	37.0	1607	2	US-07-989-847-1		Sequence 1, Appli
C 27	22.6	37.0	1607	3	US-07-721-847A-3		Sequence 3, Appli

C 28	22.6	37.0	1607	4	US-08-469-411-1	Sequence 1, Appli
C 29	22.6	37.0	1607	4	US-08-925-779-3	Sequence 3, Appli
C 30	22.6	37.0	1607	6	5166058-3	Patent No. 5166058
C 31	22.4	36.7	2900	2	US-09-027-337-9	Sequence 9, Appli
C 32	22.4	36.7	2900	4	US-09-644-600-9	Sequence 9, Appli
C 33	22	36.1	787	4	US-08-943-731-200	Sequence 200, App
C 34	22	36.1	1133	4	US-09-395-674B-5	Sequence 5, Appli
C 35	22	36.1	20084	4	US-08-943-731-5	Sequence 5, Appli
C 36	21.8	35.7	261	2	US-08-774-025A-3	Sequence 3, Appli
C 37	21.8	35.7	261	2	US-08-774-025A-4	Sequence 3, Appli
C 38	21.8	35.7	261	4	US-09-244-093-3	Sequence 3, Appli
C 39	21.8	35.7	261	4	US-09-244-093-4	Sequence 3, Appli
C 40	21.8	35.7	1567	4	US-08-568-435-34	Sequence 4, Appli
C 41	21.8	35.7	1567	4	US-08-744-231-34	Sequence 34, Appli
C 42	21.8	35.7	1567	4	US-09-047-118-13	Sequence 13, Appli
C 43	21.8	35.7	1809	1	US-08-459-586-14	Sequence 14, Appli
C 44	21.8	35.7	1809	2	US-08-282-696-14	Sequence 14, Appli
C 45	21.8	35.7	3208	1	US-07-972-721-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2 4403765
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

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Best Local Similarity 63.9%; Pred. No. 7.4;
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Db      2324489 GGGCGGCGRAGACCCCCCAGCGCACCGCGCCAGCGTTACC CGGCTGTCTATCTGGG 23244430

Qy      61 G 61
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RESULT 2
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; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
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Query Match 40.08; Score 24.4; DB 4; Length 2327;

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; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
; FILE REFERENCE: 59138-A/JFW
; CURRENT APPLICATION NUMBER: US/09/518,914
; CURRENT FILING DATE: 2000-03-03
; EARLIER APPLICATION NUMBER: US 09/303,593
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-518-914-1
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Best Local Similarity 67.3%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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RESULT 6

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US-09-518-914-3
; Sequence 3, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhiani, Parul P.
; APPLICANT: Adham, Nika
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; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
; FILE REFERENCE: 59138-A/JFW
; CURRENT APPLICATION NUMBER: US/09/518,914
; CURRENT FILING DATE: 2000-03-03
; EARLIER APPLICATION NUMBER: US 09/303,593
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-518-914-3
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Best Local Similarity 67.3%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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Db 685 GAGGGGTTCGTGACATCTCTGCTCTGCGACTACATGAGCTTCACGCGG 733
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RESULT 7

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US-08-804-227C-7
; Sequence 7, Application US/08804227C
; Patent No. 5875991
; GENERAL INFORMATION:
; APPLICANT: Dehoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rostek, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
```

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; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII(DOS) text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35,784
; REFERENCE/DOCKET NUMBER: X-8231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..14002
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14046..20036
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20110..31284
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31329..36071
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; NAME/KEY: CDS
; LOCATION: 36155..41830
US-08-804-227C-7
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Best Local Similarity 70.5%; Pred. No. 26;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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RESULT 8

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US-08-804-198-1
; Sequence 1, Application US/08804198
; Patent No. 5945320
; GENERAL INFORMATION:
; APPLICANT: Burgett, Stanley G.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rao, Nagaraja R.
; APPLICANT: Richardson, Mark A.
; APPLICANT: Rostek, Paul R., Jr.
; TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAUL R. CANTRELL 1138
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/804,198
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 350..14002
FEATURE:
NAME/KEY: CDS
LOCATION: 14046..20036
FEATURE:
NAME/KEY: CDS
LOCATION: 20110..31284
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LOCATION: 31329..36071
FEATURE:
NAME/KEY: CDS
LOCATION: 36155..41830
US-08-804-198-1

Query Match 38.0%; Score 23.2; DB 2; Length 44377;
Best Local Similarity 70.5%; Pred. No. 26;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 GGCGTGGATGACGAACTGCGGAAACCGCGGCCCGAGATCTACA 44
Db 27492 GGGCAGCGCGTGCAGCACTGCCGGAGTCCGGTGACCGGATGTACA 27535

RESULT 9
US-09-221-654-1
Sequence 1, Application US/09221654
Patent No. 6054306
GENERAL INFORMATION:
APPLICANT: Lassen, Soren
APPLICANT: Bech, Lisbeth
APPLICANT: Fuglsang, Claus
APPLICANT: Ohmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6054306 No. 6054306disk of No. 6054306th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,654
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,358

FILING DATE: 12-DEC-1997
APPLICATION NUMBER: 0529/97
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5101.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-221-654-1

Query Match 37.4%; Score 22.8; DB 3; Length 1320;
Best Local Similarity 66.0%; Pred. No. 18;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 4 CTGGATGACGAACTGCGGAAACCGCGGCCCGAGATCTACAATCGCTTCA 53
Db 360 CGGGCTAACAATCGCACCAACCGCGCCGATATGTATACCGCTACA 409

RESULT 10
US-08-989-358A-1
Sequence 1, Application US/08989358A
Patent No. 6060298
GENERAL INFORMATION:
APPLICANT: Lassen, Soren
APPLICANT: Bech, Lisbeth
APPLICANT: Fuglsang, Claus
APPLICANT: Ohmann, Anders
APPLICANT: Breinholt, Jens
APPLICANT: Ostergaard, Peter
TITLE OF INVENTION: Peniophora Phytase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6060298 No. 6060298disk of No. 6060298th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,358A
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1481/96
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: 0529/97
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/046,081
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 5101.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123

```

; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-989-358A-1

Query Match          37.4%; Score 22.8; DB 3; Length 1320;
Best Local Similarity 66.0%; Pred. No. 18;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 4 CTGGGATGACGAACTCGCGGAACCCGGCGCCAGATCTACATGCGCTTCA 53
   ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||
Db 360 CGGGCTACCAATCGCAACCAACCGCGCCAGATATGTATACGCGCTACA 409

RESULT 11
US-08-993-359-23
; Sequence 23, Application US/08993359A
; Patent No. 6039942
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Breinholt, Jens
; APPLICANT: Ohmann, Anders
; APPLICANT: Fuglsang, Claus C.
; APPLICANT: Ostergaard, Peter R.
; TITLE OF INVENTION: Phylase Polypeptides
; FILE REFERENCE: 5383,500-US
; CURRENT APPLICATION NUMBER: US/08/993,359A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 1480/96
; EARLIER FILING DATE: 1996-12-20
; EARLIER APPLICATION NUMBER: 1481/96
; EARLIER FILING DATE: 1996-12-20
; EARLIER APPLICATION NUMBER: 0301/97
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 0529/97
; EARLIER FILING DATE: 1997-05-07
; EARLIER APPLICATION NUMBER: 1388/97
; EARLIER FILING DATE: 1997-12-01
; EARLIER APPLICATION NUMBER: 60/046,082
; EARLIER FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Peniophora lycii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)...(1439)
; NAME/KEY: sig_peptide
; LOCATION: (123)...(212)
; NAME/KEY: mat_peptide
; LOCATION: (213)...(1439)
; US-08-993-359-23

Query Match          37.4%; Score 22.8; DB 3; Length 1593;
Best Local Similarity 66.0%; Pred. No. 18;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 4 CTGGGATGACGAACTCGCGGAACCCGGCGCCAGATCTACATGCGCTTCA 53
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Db 482 CGGGCTACCAATCGCAACCAACCGCGCCAGATATGTATACGCGCTACA 531

RESULT 12
US-08-362-670B-27/c
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; Sequence 27, Application US/08362670B
; Patent No. 5658882
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,670B
; FILING DATE: December 22, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1233 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
; CLONE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1233
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 847..1233
; US-08-362-670B-27

Query Match          37.0%; Score 22.6; DB 1; Length 1233;
Best Local Similarity 64.2%; Pred. No. 21;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GGGCTGGGATGACGAACTCGCGGAACCCGGCGCCAGATCTACATGCGCTTCA 53
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 135 GGGCTGGGATGAGGGCGGCGCGGAGAGAGCGCGCGGAACTCTCTCGGCGCCA 83

RESULT 13
US-08-333-576C-27/c
; Sequence 27, Application US/08333576C
; Patent No. 6027919
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
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; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,576C
; FILING DATE: No. 6027919ember 2, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1233 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
; CLONE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1233
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 847..1233
; US-08-333-576C-27

Query Match 37.0%; Score 22.6; DB 3; Length 1233;
Best Local Similarity 64.2%; Pred. No. 21;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 GCGCTGGGATGACCACTCGGAAACCCGCGCCCGACATCTACATCGCTTCA 53
|||||
Db 135 GGGCTGGGATGAGGGCGCGCGGAGACGCGCGCGAACTTCTCGGCGCCA 83

RESULT 14
US-08-808-324-27/c
; Sequence 27, Application US/08808324
; Patent No. 6284872
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,324
; FILING DATE: Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1233 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
; CLONE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1233
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 847..1233
; US-08-808-324-27

Query Match 37.0%; Score 22.6; DB 4; Length 1233;
Best Local Similarity 64.2%; Pred. No. 21;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 GGGCTGGGATGACCACTCGGAAACCCGCGCGCCCGACATCTACATCGCTTCA 53
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Db 135 GGGCTGGGATGAGGGCGCGCGGAGACGCGCGCGAACTTCTCGGCGCCA 83

RESULT 15
PCT-US94-14030A-27/c
; Sequence 27, Application PC/TUS9414030A
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14030A
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/164,103
; FILING DATE: 07-DEC-1993
; APPLICATION NUMBER: US 08/217,780
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 08/333,576
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:


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; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202D-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1233 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1233
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 847..1233
; PCT-US94-14030A-27

Query Match      37.0%; Score 22.6; DB 5; Length 1233;
Best Local Similarity 64.2%; Pred. No. 21;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Db      135 GGGCTGGGATGAGGGCGCGCGCGGACGACGCGCGCGGAACTCTCTGCGGCCCA 83

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Job time : 11.6452 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
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Perfect score: 61
Sequence: 1 gggctggatgacgaactgc.....acatgcgttcacgaggag 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, NA:*

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14:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	61	100.0	1647	10	US-09-826-581-5
3	25.4	41.6	536165	9	US-09-939-964-1
4	25	41.0	1473	10	US-09-815-242-8004
5	24.8	40.7	14917	9	US-09-909-567B-11
6	24	39.3	1086	10	US-09-931-381A-19
7	24	39.3	1089	9	US-09-898-751A-1
8	24	39.3	1244	10	US-09-931-381A-17
9	23.8	39.0	600	10	US-09-764-864-166
10	23.6	38.7	573	9	US-10-108-605-84
11	23.6	38.7	2760	10	US-09-934-868-51
12	23.4	38.4	1508	9	US-10-146-835-1
13	23.4	38.4	1541	9	US-10-146-835-3
14	23.2	38.0	1323	10	US-09-917-800A-1694
15	23.2	38.0	3627	9	US-09-927-827-4
16	23.2	38.0	4204	9	US-10-007-270-23
17	23.2	38.0	7356	9	US-09-927-827-1
18	23.2	38.0	27847	9	US-10-265-593-3
19	23	37.7	242	10	US-09-960-352-12740

C	20	23	37.7	416	9	US-09-764-891-6224	Sequence 6224, Ap
C	21	23	37.7	416	9	US-09-764-891-6227	Sequence 6227, Ap
C	22	23	37.7	5535	9	US-09-373-658-67	Sequence 67, Appl
	23	22.8	37.4	232	10	US-09-923-876-2303	Sequence 2303, Ap
	24	22.8	37.4	240	10	US-09-764-864-602	Sequence 602, Ap
C	25	22.8	37.4	8907	9	US-09-738-626-934	Sequence 934, Ap
C	26	22.8	37.4	3309400	9	US-09-738-626-1	Sequence 1, Appl
C	27	22.6	37.0	1233	9	US-09-945-182-27	Sequence 27, Appl
C	28	22.6	37.0	1260	7	US-08-957-425-4	Sequence 4, Appl
C	29	22.6	37.0	1547	9	US-10-044-716-1	Sequence 1, Appl
C	30	22.6	37.0	1607	9	US-09-804-625-3	Sequence 3, Appl
C	31	22.6	37.0	4839	9	US-10-073-961-476	Sequence 476, Ap
C	32	22.6	37.0	4839	10	US-09-764-887-476	Sequence 476, Ap
C	33	22.6	37.0	14759	10	US-09-952-360-1	Sequence 1, Appl
C	34	22.4	36.7	363	10	US-09-878-574-5173	Sequence 5173, Ap
C	35	22.4	36.7	471	9	US-09-918-995-29143	Sequence 29143, A
C	36	22.4	36.7	1089	9	US-09-898-751A-3	Sequence 3, Appl
C	37	22.4	36.7	1451	10	US-09-822-830A-330	Sequence 330, Ap
C	38	22.4	36.7	2175	9	US-09-764-891-7546	Sequence 7546, Ap
C	39	22.4	36.7	3432	9	US-10-300-834-4	Sequence 4, Appl
	40	22.2	36.4	303	10	US-09-923-876-3718	Sequence 3718, Ap
	41	22.2	36.4	984	10	US-09-815-242-7872	Sequence 7872, Ap
	42	22	36.1	238	10	US-09-923-876-2600	Sequence 2600, Ap
	43	22	36.1	306	10	US-09-294-093B-79	Sequence 79, Appl
	44	22	36.1	531	9	US-09-918-995-31548	Sequence 31548, A
C	45	21.8	35.7	261	10	US-09-866-607-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-826-581-2
; Sequence 2, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Lelf
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUI
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-2

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Best Local Similarity	100.0%	Pred. No. 3.4e+14;		
Matches	61;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
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Qy	61	G 61		
Db	882	G 882		

RESULT 2

US-09-826-581-5
; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Lelf
; APPLICANT: Luthman, L. Holger

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; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5

Query Match      100.0%; Score 61; DB 10; Length 1647;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 529 GGCTGGGATGACGAAGTGGGAAACCGCGGCCGACATCTACATGCGCTTCATGCAGGA 588

QY 61 G 61
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Db 589 G 589

RESULT 3
US-09-939-964-1/c
; Sequence 1, Application US/09939964
; Publication No. US2003005422A1
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; APPLICANT: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; FILE REFERENCE: Plasmid
; CURRENT APPLICATION NUMBER: US/09/939,964
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/214,808
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1

Query Match      41.6%; Score 25.4; DB 9; Length 536165;
Best Local Similarity 64.4%; Pred. No. 3.1;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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RESULT 4
US-09-815-242-8004/c
; Sequence 8004, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
```

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; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8004
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1473)
US-09-815-242-8004

Query Match      41.0%; Score 25; DB 10; Length 1473;
Best Local Similarity 64.9%; Pred. No. 2.7;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 GGCTGGGATGACGAAGTGGGAAACCGCGGCCGACATCTACATGCGCTTCATGCAG 58
|||||
Db 792 GTGCGGAAAGATGATCAGCGGGGACTTGGCGGCCAGCTCCATGGTCACTCCCTTCAG 736

RESULT 5
US-09-909-567B-11
; Sequence 11, Application US/09909567B
; Publication No. US2003002257A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto A.
; APPLICANT: Nair, Manoj
; APPLICANT: Chen, Selyu
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: DEX-0214
; CURRENT APPLICATION NUMBER: US/09/909,567B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,834
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 14917
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-909-567B-11

Query Match      40.7%; Score 24.8; DB 9; Length 14917;
Best Local Similarity 67.3%; Pred. No. 4;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 8 GATGACGAAGTGGGAAACCGCGGCCGACATCTACATGCGCTTCATGCAGG 59
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Db 2869 GAAGAGGACCTGCAGAACCTCTGTGACAGAGCCAGACGATGAGTCCACAGG 2920
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Qy 11 GACGAACTGCGAAACCCGGCGCCAGATCTACATGCGTTTCATGCAGGAG 61

GenCore version 5.1.6
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Title: US-09-826-581-5_COPY_1007_1067
Perfect score: 61
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Scoring table: IDENTITY_NUC
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

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4: gb_om.*

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6: gb_pat.*

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10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pi.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	61	100.0	1647	6	AX281582 Sequence
2	61	100.0	2109	6	AX099776 Sequence
3	61	100.0	2115	6	AX099802 Sequence
4	61	100.0	2115	9	AF214519 Homo sapi
5	61	100.0	2290	9	BSA249977 Homo sapi
6	56.2	92.1	1867	6	AX099774 Sequence
7	56.2	92.1	1873	4	AF214520 Sus scrof
8	56.2	92.1	1873	6	AX099800 Sequence
9	56.2	92.1	1873	6	AX398331 Sequence
10	56.2	92.1	1873	6	AX398333 Sequence
11	56.2	92.1	1873	6	AX398335 Sequence
12	56.2	92.1	1873	6	AX398337 Sequence
13	56.2	92.1	1873	6	AX398339 Sequence
14	56.2	92.1	2022	6	AX099804 Sequence
15	46.2	75.7	1722	6	AX281580 Sequence
16	46.2	75.7	152129	2	AC027416 Homo sapi
17	46.2	75.7	206854	9	AC009974 Homo sapi
18	43.4	71.1	5888	4	AF214521 Sus scrof
19	41.2	67.5	146577	2	AC128070 Rattus no
20	41.2	67.5	190183	2	AC129703 Rattus no
21	41.2	67.5	192968	2	AC127107 Rattus no
22	41.2	67.5	227724	2	AF336381 Mus muscu
23	29.8	48.9	196208	2	AC129702 Rattus no
24	29.2	47.9	1681	4	AF334948 Canis fam
25	29.2	47.9	107799	2	AC112601 Rattus no
26	29.2	47.9	166397	2	AC112066 Rattus no
27	29.2	47.9	178452	2	AC096427 Rattus no
28	28.2	46.2	249536	10	AL663072 Mouse DNA
29	28	45.9	143720	10	AC087332 Mus Muscu
30	28	45.9	153605	2	AC019360 Homo sapi
31	28	45.9	154746	2	AC063943 Homo sapi
32	28	45.9	183861	2	HS75N14 Z97199 Homo sapien
33	28	45.9	187546	2	AC129236 Homo sapi
34	28	45.9	195325	2	AC125616 Homo sapi
35	28	45.9	204767	2	AL772255 Mus muscu
36	28	45.9	209336	2	AL845470 Mus muscu
37	27.8	45.6	71165	2	AC101452 Mus muscu
38	27.6	45.2	75131	2	AC023022 Homo sapi
39	27.6	45.2	115004	2	AC108872 Oryza sat
40	27.6	45.2	119563	9	HSJ894D12 Human DNA
41	27.6	45.2	140181	2	AC025266 Homo sapi
42	27.6	45.2	141990	9	AC004691 Homo sapi
43	27.6	45.2	143277	2	AC105743 Oryza sat
44	27.6	45.2	153170	9	HS1103G7 AL034548 Human DNA
45	27.6	45.2	156335	9	AC018818 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS AX281582 1647 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 5 from Patent WO0177305.
ACCESSION AX281582
VERSION AX281582.1 GI:16608833
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUthORS Anderson, L., Luthman, H. and Marklund, S.
TITLe Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAl Patent: WO 0177305-A 5 18-OCT-2001;

FEATURES
source
CDS

Arexis AB (SE)
Location/Qualifiers
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BASE COUNT 346 a 502 c 462 g 337 t
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Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 G 61
Db 1067 G 1067

RESULT 2
AX099776
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Sequence 3 from Patent WO0120003.
AX099776
AX099776.1 GI:13538810
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2109)
Anjersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
Patent: WO 012003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)

FEATURES
source
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YRTIQDLGTFTRDLAVLETPALITDIFVDRVSALPVPVNECGQVYGLYSRFDVI
HLAAQTYNHLDMSVGALRQRTLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDE
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BASE COUNT 458 a 621 c 560 g 470 t
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Best Local Similarity 100.0%; Pred. No. 9.4e-10;
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Qy 61 G 61
Db 967 G 967

RESULT 3
AX099802
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Sequence 29 from Patent WO0120003.
AX099802
AX099802.1 GI:13538836
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2115)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
Patent: WO 012003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)

FEATURES
source
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AVLETPALITDIFVDRVSALPVPVNECGQVYGLYSRFDVTHLAAQTYNHLDMSV
GENLRQRTLCLEGLVSCQPHESLGEVIDRIAREQVHRLVLDVDETHLGLVSLSDIILQ
ALVLPAGIDALGA"

BASE COUNT 460 a 622 c 562 g 471 t
ORIGIN

Query Match 100.0%; Score 61; DB 6; Length 2115;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 G 61
Db 973 G 973

RESULT 4
AF214519
LOCUS
DEFINITION
ORIGIN

2115 bp mRNA linear PRI 03-JUN-2000
Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
mRNA, complete cds.

AF214519
AF214519


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VERSION
KEYWORDS
SOURCE
ORGANISM
AP214519.1 GI:8215681
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
and Andersson,L.
TITLE
A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle
JOURNAL
Science 288 (5469), 1248-1251 (2000)
MEDLINE
20380350
PUBMED
10818001
REFERENCE
AUTHORS
2 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
TITLE
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden
FEATURES
source
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1..2115
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DB 913 TTCCTGCACATCTTTGGTTCCTGCTGCCCGCGCCCTCTCTCTACCGCACTATCAA 972
QY 61 G 61
DB 973 G 973
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HSA249977
LOCUS
HSA249977 2290 bp mRNA linear PRI 07-APR-2000
DEFINITION
Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
(AMPK gamma 3 gene).
ACCESSION
AJ249977
VERSION
AJ249977.1 GI:6688200
KEYWORDS
AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.

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SOURCE
ORGANISM
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 2290)
Cheung,P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D.
Characterization of AMP-activated protein kinase gamma-subunit
isoforms and their role in AMP binding
JOURNAL
Biochem. J. 346 Pt 3, 659-669 (2000)
MEDLINE
20164049
PUBMED
10698692
REFERENCE
AUTHORS
2 (bases 1 to 2290)
Carling,D.
Direct Submission
TITLE
Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC
Clinical Sciences Centre, Hammersmith Hospital, Duane Road,
London, W12 0NN, UNITED KINGDOM
FEATURES
source
Location/Qualifiers
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ANGVRAAPLWDSKQSFVGMFTITDILVHRPLVDPVSGNVLHILTHKRLKFLHIF
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QY 61 G 61
DB 1069 G 1069
RESULT 6
AX099774
LOCUS
AX099774 1867 bp DNA linear PAT 02-APR-2001
DEFINITION
Sequence 1 from Patent WO0120003.
ACCESSION
AX099774
VERSION
AX099774.1 GI:13538808
KEYWORDS
pig.
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS
1 (bases 1 to 1867)
Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
Variants of the gamma chain of ampk, dna sequences encoding the

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same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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BASE COUNT 380 a 583 c 529 g 375 t
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Db 907 TTCTCGACATCTTTGGCACCCCTGCTGCGCGCGCCTCTCTCTACCGCACTCCAA 966
QY 61 G 61
Db 967 G 967

RESULT 7
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LOCUS AF214520 1873 bp mRNA linear MAM 03-JUN-2000
DEFINITION Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
mRNA, complete cds.
ACCESSION AF214520
VERSION AF214520.1 GI:8215683
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1873)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.B., Chardon,P.
and Andersson,L.
TITLE A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle
JOURNAL Science 288 (5469), 1248-1251 (2000)
MEDLINE 20280150
PubMed 10818001
REFERENCE 2 (bases 1 to 1873)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden
FEATURES Location/Qualifiers
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/map="15q"
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1. .1873
gene

CDS
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1. .1395
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BASE COUNT 382 a 580 c 535 g 376 t
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Best Local Similarity 95.1%; Pred. No. 3.5e-08;
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QY 61 G 61
Db 973 G 973

RESULT 8
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LOCUS AX099800 1873 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 27 from Patent WO0120003.
ACCESSION AX099800
VERSION AX099800.1 GI:13538834
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1873)
AUTHORS Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 973 G 973

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DEFINITION Sequence 1 from Patent WO0220850.
ACCESSION AX398331
VERSION AX398331.1 GI:21261106
KEYWORDS
SOURCE
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkg3 alleles and use of the same as genetic markers for reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 1 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)

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source Location/Qualifiers
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BASE COUNT 382 a 580 c 535 g 376 t
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Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DEFINITION Sequence 3 from Patent WO0220850.
ACCESSION AX398333
VERSION AX398333.1 GI:21261108
KEYWORDS
SOURCE pig.

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkg3 alleles and use of the same as genetic markers for reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)

FEATURES
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Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 61 G 61
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Db 973 G 973

RESULT 11
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DEFINITION Sequence 5 from Patent WO0220850.
ACCESSION AX398335
VERSION AX398335.1 GI:21261110
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SOURCE pig.

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkg3 alleles and use of the same as genetic markers for reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 5 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)

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VERSION AX398337.1 GI:21261112
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SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 7 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
LOCATION/Qualifiers
FEATURES
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Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 973 G 973
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ACCESSION AX099804
VERSION AX099804.1 GI:13538838
KEYWORDS .
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 2022)
AUTHORS Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Charbon,P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
LOCATION/Qualifiers
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/organism="Sus scrofa"

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VERSION AX398339.1 GI:21261114
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 9 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
LOCATION/Qualifiers
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BASE COUNT 383 a 580 c 534 g 376 t
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Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 913 TTCTGCACATCTTTGGCACCTCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCAA 972
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DB 973 G 973
RESULT 14
AX099804
LOCUS AX099804 2022 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 31 from Patent WO0120003.
ACCESSION AX099804
VERSION AX099804.1 GI:13538838
KEYWORDS .
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 2022)
AUTHORS Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Charbon,P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
LOCATION/Qualifiers
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VERSION	AX281580.1 GI:16608831			
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1			
AUTHORS	Andersson, L., Luthman, H. and Marklund, S.			
TITLE	Variants of the human amp-activated protein kinase gamma 3 subunit			
JOURNAL	Patent: WO 0177305-A 3 18-OCT-2001;			
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	56.2	92.1	1867	22	Pig AMPK gamma sub
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7	56.2	92.1	1873	24	Pig wild-type PRKA
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9	56.2	92.1	1873	24	Pig PRKAG3 polymor

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c 14	28	45.9	3238	23	AAS77333	DNA encoding novel
c 15	28	45.9	9979	22	AAK81194	Human immune/haema
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c 17	28	45.9	13673	22	AAK81195	Human immune/haema
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c 19	27.4	44.9	2289	23	ABL08199	Drosophila melanog
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c 21	26.8	43.9	4984	21	AAA07842	Nucleotide sequenc
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c 23	26.6	43.6	2416	21	AAC64726	Mouse tumour suppr
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c 30	26	42.6	1231	21	AAF20891	Human bradykinin r
c 31	26	42.6	1231	21	AAA34759	Human adenosine re
c 32	26	42.6	1231	21	AAA34760	Human adenosine re
c 33	26	42.6	1231	21	AAA34768	Human adenosine re
c 34	26	42.6	1231	21	AAA34769	Human adenosine re
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c 36	26	42.6	1682	21	AAC98901	Human pancreatic c
c 37	26	42.6	2239	21	AAF20879	Human bradykinin r
c 38	26	42.6	2239	21	AAF20888	Human bradykinin r
c 39	26	42.6	2239	21	AAA34757	Human adenosine re
c 40	26	42.6	2239	21	AAA34766	Human adenosine re
c 41	26	42.6	2478	21	AAF20880	Human bradykinin r
c 42	26	42.6	2478	21	AAF20889	Human bradykinin r
c 43	26	42.6	2478	21	AAA34758	Human adenosine re
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ALIGNMENTS

RESULT 1

ABR08485

ID ABR08485 standard; CDNA; 547 BP.

XX ABR08485;

AC ABR08485;

XX ABR08485;

DT 11-JAN-2002 (first entry)

XX Human AMP-activated protein kinase subunit homologue CDNA, SEQ ID NO:261.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytotactic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer; ss.

XX Homo sapiens.

OS WO200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US03800.

PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI: 2001-457740/49.
DR P-PSDB; ABB11241.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
XX Claim 1; Page 429; 1963pp; English.
XX
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
SQ Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;

Query Match 100.08; Score 61; DB 22; Length 547;
Best local Similarity 100.08; Pred. No. 1.5e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGACATCTTTGGTTCCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAA 60
Db 270 TTCTGACATCTTTGGTTCCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAA 329

QY 61 G 61
Db 330 G 330

RESULT 2
AAH43685
ID AAH43685 standard; cDNA; 1647 BP.
XX

AC AAH43685;
DT 21-JAN-2002 (first entry)
XX
XX PRKAG3 CDNA.
XX
KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
KW metabolic disease; diabetes; obesity; substitution; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 20..1489
FT /tag= a
FT /product= "PRKAG3"
FT variation 230
FT /tag= b
FT /label= "C230G"
FT /note= "Causes P71A"
FT variation 559
FT /tag= c
FT /label= "T559C"
FT /note= "Silent variation"
FT variation 1037
FT /tag= d
FT /label= "C1037T"
FT /note= "Causes R340W"
XX
XX WO200177305-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-SE00765.
XX
XX 07-APR-2000; 2000US-195665P.
XX
XX (AREX-) AREXIS AB.
XX
XX Andersson L, Luthman H, Marklund S;
XX
XX WPI; 2001-657170/75.
XX P-PSDB; QQB47679.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
XX associated with a metabolic disease e.g. diabetes or obesity and method
XX for determining a risk estimate of diseases in subject by detecting the
XX variant -
XX
XX Disclosure; Fig 5; 25pp; English.
XX
XX This sequence represents the full length cDNA encoding the human
XX AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
XX the presence of the PRKAG3 DNA, or a variant, is useful in determining
XX a risk estimate of a metabolic disease, such as diabetes or obesity,
XX in a subject. The variation may occur in exons 3, 4 or 10. In exon
XX 3 variation may be a substitution of a G for a C at nucleotide 320,
XX resulting in the amino acid substitution P71A; in exon 4 variation may
XX be a substitution of a T for a C at nucleotide 550; and in exon 10
XX variation may be a substitution of a T for a C at nucleotide 1037,
XX resulting in the amino acid substitution R340W. There may also be
XX nucleotide variation in intron 6. The numbering of these
XX variations is based on the full length cDNA as given, rather than on
XX position 1 of the open reading frame.
XX
SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;

Query Match 100.08; Score 61; DB 22; Length 1647;
Best local Similarity 100.08; Pred. No. 1.7e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGACATCTTTGGTTCCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAA 60
Db 1007 TTCTGACATCTTTGGTTCCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAA 1066

CC complete PRKAG3. Mutation in Prkag3 results in an altered regulation of
CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
CC useful as therapeutic for treating carbohydrate metabolism disorders such
CC as diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.

XX
SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;

Query Match 100.0%; Score 61; DB 22; Length 2115;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGCACATCTTTGGTTCCCTGCTGCGCCGCCCTCTCTCTACCGCACTATCCAA 60
|||||
Db 913 TTCTGCACATCTTTGGTTCCCTGCTGCGCCGCCCTCTCTCTACCGCACTATCCAA 972

QY 61 G 61
|
Db 973 G 973

RESULT 5
AAD03295
ID AAD03295 standard; cDNA; 1867 BP.

XX AAD03295;
XX
XX
DT 13-JUN-2001 (first entry)
XX Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.

XX Pig: gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
KW chromosome 15; ss.
XX
OS Sus scrofa.

XX
FH Key Location/Qualifiers
FT 5'UTR 1..471
FT /*tag= a
FT CDS 472..1389
FT /*tag= b
FT /*product= "Sus scrofa PRKAG3 protein"
FT 3'UTR 1390..1867
FT /*tag= c

XX WO200120003-A2.
XX
XX
PD 22-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-EF09896.
XX 10-SEP-1999; 99EP-0402236.
PR 18-MAY-2000; 2000EP-0401388.
XX
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.
PA (LOOF/) LOOFT C.

(KALM/) KALM E.
XX
PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
PI Iannuccelli N, Geillin J, Le Roy P, Chardon P;
XX
DR WPI: 2001-244810/25.
DR P-PSDB; AAE00220.
XX
PT New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment of disorders
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy
XX
PS Claim 12; Fig 2; 71pp; English.

CC The present sequence is a cDNA encoding pig adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.
CC Mutation in Prkag3 results in an altered regulation of carbohydrate
CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
CC therapeutic for treating carbohydrate metabolism disorders such as
CC diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.

XX
SQ Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;

Query Match 92.1%; Score 56.2; DB 22; Length 1867;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTGCACATCTTTGGTTCCCTGCTGCGCCGCCCTCTCTCTACCGCACTATCCAA 60
|||||
Db 907 TTCTGCACATCTTTGGTGGACCTGCTGCGCCGCCCTCTCTCTACCGCACTATCCAA 966
QY 61 G 61
|
Db 967 G 967

RESULT 6
AAD03319
ID RAD03319 standard; cDNA; 1873 BP.

XX AAD03319;
XX
XX
DT 13-JUN-2001 (first entry)

XX Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
XX
XX Pig: gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
KW chromosome 15; ss.
XX
OS Sus scrofa.

XX
FH Key Location/Qualifiers
FT CDS 1..1395
FT /*tag= a

```
FT XX /product= "Sus scrofa complete Prkg3 protein"
PN XX WO200120003-A2.
XX
XX PD 22-MAR-2001.
XX
XX PF 11-SEP-2000; 2000WO-EP09896.
XX
XX PR 10-SEP-1999; 99EP-0402236.
XX
XX PR 18-MAY-2000; 2000EP-0401388.
XX
XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX PA (ANDE/) ANDERSSON L.
XX PA (LOOF/) LOOFT C.
XX PA (KALM/) KALM E.
XX
XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
XX DR WPI: 2001-244810/25.
XX DR P-PSDB; AAE00222.
XX
XX PT New variants of the gamma subunit of vertebrate adenosine
XX PT monophosphate-activated kinase for diagnosis or treatment of disorders
XX PT associated with energy metabolism such as diabetes, obesity, and
XX PT myopathy -
XX
XX PS Claim 12; Page 62-64; 71pp; English.
XX
XX CC The present sequence is a cDNA encoding pig adenosine monophosphate
XX CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
XX CC complete PRKAG3. Prkg3 gene is located in the RN locus of chromosome
XX CC 15. Mutation in Prkg3 results in an altered regulation of carbohydrate
XX CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
XX CC therapeutic for treating carbohydrate metabolism disorders such as
XX CC diabetes, obesity, and disorders associated with muscle metabolism
XX CC such as myopathy and cardiovascular diseases, to modulate AMPK
XX CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
XX CC and its functionally altered mutants are useful for the diagnostic
XX CC evaluation, genetic testing and prognosis of a metabolic disorder,
XX CC preferably a carbohydrate metabolism disorder. Primers that can detect
XX CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
XX CC useful for detecting a dysfunction of carbohydrate metabolism resulting
XX CC from the expression of a functionally altered allele of PRKAG3.
XX CC Transgenic animal and host cell transformed with PRKAG3 or a
XX CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
XX CC screening compounds able to modulate AMPK activity. Nucleic acid
XX CC encoding PRKAG3 is useful for detecting mutations in a Prkg3 gene, or
XX CC in a sequence encoding the first cystathione beta synthase (CBS) domain
XX CC of PRKAG3 and is useful in gene therapy.
XX
XX SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 92.1%; Score 56.2; DB 22; Length 1873;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCCTGCACATCTTTGGTTCCCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAA 60
DB 913 TTCCTGCACATCTTTGGACCCCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAA 972

QY 61 G 61
DB 973 G 973

RESULT 7
ID AAD36456
AD AAD36456 standard; DNA; 1873 BP.
XX
XX AC AAD36456;
XX
XX DT 09-AUG-2002 (first entry)
```

```
XX DE Pig wild-type PRKAG3 gene.
XX
XX KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
XX KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
XX KW gene; ds.
XX
XX OS Sus scrofa.
XX
XX FH Key Location/Qualifiers
XX CDS 1..1395
XX FT /*tag= a
XX FT /product= "Pig PRKAG3 wild-type protein"
XX FT replace (89, C)
XX FT /*tag= b
XX FT variation
XX FT
XX FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX FT replace (154, A)
XX FT /*tag= c
XX FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX FT replace (595, A)
XX FT /*tag= d
XX FT variation
XX FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX FT replace (599, A)
XX FT /*tag= e
XX FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX PN WO200220850-A2.
XX
XX PD 14-MAR-2002.
XX
XX PF 10-SEP-2001; 2001WO-US28283.
XX
XX PR 08-SEP-2000; 2000US-231045P.
XX PR 08-JAN-2001; 2001US-260239P.
XX PR 18-JUN-2001; 2001US-299111P.
XX
XX PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX PI Rothschild MF, Cioabanu DC, Malek M, Piastow G;
XX
XX WPI; 2002-393850/42.
XX P-PSDB; AAE22984.
XX
XX PT Screening animals to determine those likely to produce larger litters
XX PT and improved meat quality traits involves assaying for the presence of
XX PT polymorphisms in the AMP activated protein kinase regulatory gamma
XX PT subunit gene -
XX
XX PS Claim 17; Fig 1; 109pp; English.
XX
XX CC The invention relates to a method for screening animals to determine
XX CC those more likely to produce large litters and improved meat quality
XX CC traits. The method involves assaying for the presence of a genotype
XX CC in the sample of genetic material obtained from animal. The genotype
XX CC is characterised by polymorphism(s) in the AMP activated protein
XX CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
XX CC for screening animals e.g., pigs to determine those most likely to
XX CC exhibit improved meat quality traits and to produce larger litters.
XX CC The present sequence is pig wild-type PRKAG3 gene.
XX
XX SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 92.1%; Score 56.2; DB 24; Length 1873;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCCTGCACATCTTTGGTTCCCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAA 60
DB 913 TTCCTGCACATCTTTGGACCCCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAA 972

QY 61 G 61
DB 973 G 973
```

RESULT 8
AAD36457
ID AAD36457 standard; DNA; 1873 BP.
XX
AC AAD36457;
XX
DT 09-AUG-2002 (first entry)
XX
DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; variant; ds.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT CDS 1..1395
FT /*tag= a
FT /product= *Pig PRKAG3 polymorphic variant (PRKAG3-30)*
FT variation replace (89, C)
FT /*tag= b
FT /standard_name= *Single nucleotide polymorphism (SNP)*
XX
PN WC200220850-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX WPI; 2002-393850/42.
DR P-PSDB; AAE22985.
XX
XX Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene
XX
XX Disclosure; Page 89-91; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX
SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 92.1%; Score 56.2; DB 24; Length 1873;
Best Local Similarity 95.1%; Pred. NO. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTCCTGCACATCTTTGGTTCCTGCTGCTGCCCGGCCCTCTCTCTACCGCATTATCCAA 60
DB 913 TTCTGTGCACATCTTTGGCACCTGTGCTGCCCGGCCCTCTCTCTACCGCATTATCCAA 972
QY 61 G 61
DB 973 G 973

RESULT 9
AAD36458
ID AAD36458 standard; DNA; 1873 BP.
XX
AC AAD36458;
XX
DT 09-AUG-2002 (first entry)
XX
DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; variant; ds.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT CDS 1..1395
FT /*tag= a
FT /product= *Pig PRKAG3 polymorphic variant (PRKAG3-52)*
FT variation replace (154, A)
FT /*tag= b
FT /standard_name= *Single nucleotide polymorphism (SNP)*
XX
PN WC200220850-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX WPI; 2002-393850/42.
DR P-PSDB; AAE22986.
XX
XX Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene
XX
XX Claim 34; Page 93-95; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
XX
SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match 92.1%; Score 56.2; DB 24; Length 1873;
Best Local Similarity 95.1%; Pred. NO. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTCCTGCACATCTTTGGTTCCTGCTGCTGCCCGGCCCTCTCTCTACCGCATTATCCAA 60
DB 913 TTCTGTGCACATCTTTGGCACCTGTGCTGCCCGGCCCTCTCTCTACCGCATTATCCAA 972
QY 61 G 61
DB 973 G 973

RESULT 10

AAD36459
ID AAD36459 standard; DNA; 1873 BP.
XX
AC AAD36459;
XX
DT 09-AUG-2002 (first entry)
XX
DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; variant; ds.
XX
OS Sus scrofa.
XX
PH Key Location/Qualifiers
FT CDS 1..1395
FT /*tag= a
FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-199)"
FT variation replace (595, A)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200220850-A2.
XX
PD 14-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US28283.
XX
PR 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
DR WPI; 2002-393850/42.
DR P-PSDB; AAE22987.
XX
PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene
XX
PS Disclosure; Page 98-100; 109pp; English.
XX
CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
XX
SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match 92.1%; Score 56.2; DB 24; Length 1873;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTGTCACATCTTTGGTTCCGTCGCCGCCCTCTCTCTACCGCACTATCCAA 60
DB 913 TTCTGTCACATCTTTGGCACTTCGTCGCCGCCCTCTCTCTACCGCACTATCCAA 972

QY 61 G 61

DB 973 G 973

RESULT 11

AAD36460
ID AAD36460 standard; DNA; 1873 BP.
XX
AC AAD36460;
XX
DT 09-AUG-2002 (first entry)
XX
DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; variant; ds.
XX
OS Sus scrofa.
XX
PH Key Location/Qualifiers
FT CDS 1..1395
FT /*tag= a
FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
FT variation replace (599, A)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200220850-A2.
XX
PD 14-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US28283.
XX
PR 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
DR WPI; 2002-393850/42.
DR P-PSDB; AAE22988.
XX
PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene
XX
PS Disclosure; Page 102-104; 109pp; English.
XX
CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
XX
SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match 92.1%; Score 56.2; DB 24; Length 1873;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTGTCACATCTTTGGTTCCGTCGCCGCCCTCTCTCTACCGCACTATCCAA 60
DB 913 TTCTGTCACATCTTTGGCACTTCGTCGCCGCCCTCTCTCTACCGCACTATCCAA 972

QY 61 G 61

DB 973 G 973

RESULT 12
AAD03321
ID RAD03321 standard; DNA: 2022 BP.
XX
AC RAD03321;
XX
DT 13-JUN-2001 (first entry)
XX
XX
DE Sus scrofa PRKAG3 splice variant DNA.
XX
KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiac; gene therapy; ds.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT CDS 1..1545
FT FT /*tag= a
FT FT /product= "Sus scrofa Prkag3 splice variant"
XX
PN W0200120003-A2.
XX
PD 22-MAR-2001.
XX
PF 11-SEP-2000; 2000WO-EF09896.
XX
PR 10-SEP-1999; 9SEP-0402236.
PR 18-MAY-2000; 2000EP-0401388.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.
PA (LOOF/) LOOFT C.
PA (KALM/) KALM E.
XX
PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
DR WPI: 2001-244810/25.
DR P-PSDB: AAE00224.
XX
PT New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment of disorders
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy -
XX
PS Claim 12; Page 69; 71pp; English.
XX
CC The present sequence is pig adenosine monophosphate (AMP)-activated
CC kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice
CC variant DNA. Prkag3 gene is located in the RN locus of chromosome 15.
CC Mutation in Prkag3 results in an altered regulation of carbohydrate
CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
CC therapeutic for treating carbohydrate metabolism disorders such as
CC diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.

SQ Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
Query Match 92.1%; Score 56.2; DB 22; Length 2022;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 1063 TTCTTGCACATCTTTGGCACCTGCTGCGCCGCGCCCTCTCTCTACCGCACTCCAA 1122
OY 61 G 61
DB 1123 G 1123
RESULT 13
AAH43683
ID AAH43683 standard; DNA: 1722 BP.
XX
AC AAH43683;
XX
DT 21-JAN-2002 (first entry)
XX
DE PRKAG3 intron 4 - intron 10.
XX
KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
KW metabolic disease; diabetes; obesity; substitution; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT intron 1..13
FT FT /*tag= a
FT FT /number= "Intron 4"
FT FT /note= "3' portion of intron 4"
FT FT 14..95
FT FT /*tag= b
FT FT /number= "Exon 5"
FT FT 96..552
FT FT /*tag= c
FT FT /number= "Intron 5"
FT FT 553..611
FT FT /*tag= d
FT FT /number= "Exon 6"
FT FT 612..736
FT FT /*tag= e
FT FT /number= "Intron 6"
FT FT 737..782
FT FT /*tag= f
FT FT /number= "Exon 7"
FT FT 783..986
FT FT /*tag= g
FT FT /number= "Intron 7"
FT FT 987..1041
FT FT /*tag= h
FT FT /number= "Exon 8"
FT FT 1042..1242
FT FT /*tag= i
FT FT /number= "Intron 8"
FT FT 1243..1369
FT FT /*tag= j
FT FT /number= "Exon 9"
FT FT 1370..1522
FT FT /*tag= k
FT FT /number= "Intron 9"
FT FT 1523..1688
FT FT /*tag= l
FT FT /number= "Exon 10"
FT FT 1689..1722
FT FT /*tag= i
FT FT /number= "Intron 10"
FT FT /note= "5' portion of intron 10"
XX

PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.

PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 36006; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM92170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased

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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:37:44 ; Search time 151.839 Seconds
(without alignments)
6506.409 Million cell updates/sec

Title: US-09-826-581-5_COPY_1007_1067

Perfect score: 61

Sequence: 1 ttctcacatctttgttc.....cctctaccgcactatccaag 61

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estil:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56.2	92.1	572	13	BI344527
c 2	29.4	48.2	1173	13	BM556730
3	28	45.9	389	17	AQ997354
c 4	27.6	45.2	626	12	BF528264
c 5	27.4	44.9	619	12	BF978092
c 6	27.4	44.9	701	10	BE408262

c 7	27.4	44.9	706	12	BG744371
c 8	27.4	44.9	715	12	BF488250
c 9	27.4	44.9	754	9	AI063338
c 10	27.4	44.9	757	12	BG479057
c 11	27.4	44.9	913	12	BG290491
c 12	27.4	44.9	921	10	BE275257
c 13	27.4	44.9	926	12	BG291149
c 14	27.2	44.6	569	14	BQ048516
c 15	27.2	44.6	887	12	BG174779
c 16	26.8	43.9	442	9	AI583845
c 17	26.8	43.9	543	14	W03359
c 18	26.8	43.9	606	13	BI735773
c 19	26.8	43.9	617	13	BI526922
c 20	26.8	43.9	668	10	BE307400
c 21	26.8	43.9	693	13	BG974543
c 22	26.8	43.9	720	13	BI155021
c 23	26.8	43.9	815	13	BI664379
c 24	26.8	43.9	836	12	BF136865
c 25	26.8	43.9	970	12	BG288506
c 26	26.8	43.9	973	14	BQ171536
c 27	26.8	43.9	1060	12	BF581580
c 28	26.8	43.9	1088	12	BF788164
c 29	26.8	43.9	1106	14	BM917705
c 30	26.8	43.9	1647	13	BM564338
c 31	26.8	43.9	1794	11	BQ014747
c 32	26.6	43.6	322	10	AM486152
c 33	26.6	43.6	324	14	W53632
c 34	26.6	43.6	343	10	AM478129
c 35	26.6	43.6	392	9	AA009100
c 36	26.6	43.6	432	9	AA030295
c 37	26.6	43.6	504	12	BF470814
c 38	26.6	43.6	517	9	AI746867
c 39	26.6	43.6	526	9	AI509176
c 40	26.6	43.6	527	10	BE030622
c 41	26.6	43.6	553	12	BE948793
c 42	26.6	43.6	556	9	AL661556
c 43	26.6	43.6	606	13	BI134085
c 44	26.6	43.6	611	10	BE618484
c 45	26.6	43.6	643	9	AI726042

ALIGNMENTS

RESULT 1
BI344527
LOCUS 373008 MARC 2P1G Sus scrofa cDNA 5', mRNA linear EST 30-JUL-2001
DEFINITION BI344527
ACCESSION BI344527
VERSION BI344527.1 GI:15037807
KEYWORDS EST.
SOURCE Pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 572)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithfemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCACGACG
 Plate: 119 row: 1 column: 11
 Seq primer: ATTAGGTGACACTATAG.

FEATURES

source

Location/Qualifiers
 1..572
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_lib="MARC 2P1G"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 Library made from pooled tissue from testis, ovary,
 endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT
 ORIGIN

106 a 190 c 151 g 124 t

Query Match 92.1%; Score 56.2; DB 13; Length 572;
 Best Local Similarity 95.1%; Pred. No. 4.3e-06;
 Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTGCGACATTTGGTTCCTGCTGCCCGCGCTCTCTCTCTACCGCACTATCCAA 60
 |||||
 Db 169 TTCTGCGACATTTGGCACCTGCTGCCCGCGCTCTCTCTCTACCGCACTATCCAA 228
 |||||

QY 61 G 61

Db 229 G 229

RESULT 2

BM556730/c

LOCUS

DEFINITION BM556730 1173 bp mRNA linear EST 20-FEB-2002
 AGENCOURT_6540753 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737918
 5', mRNA sequence.

ACCESSION BM556730

VERSION BM556730.1

GI:18798193

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1173)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cyabps-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM12748 row: m column: 23

High quality sequence stop: 473.

Location/Qualifiers

1..1173

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5737918"

/clone_lib="NIH_MGC_88"

/tissue_type="duodenal adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: small intestine; Vector: pCMV-SPORT6;

Site_1: NotI; Site_2: SalI; Cloned unidirectionally;

oligo-dr primed. Average insert size 1.767 kb. Library

enriched for full-length clones and constructed by Life

Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 218 a 400 c 377 g 175 t

ORIGIN

Query Match

48.2%; Score 29.4; DB 13; Length 1173;

BF528264/c

Best Local Similarity 70.9%; Pred. No. 1.5e+02;
 Matches 39; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 5 TGCACATCTTTGGTTCCTGCTGCCCGCGCTCTCTCTCTACCGCACTATCCA 59
 |||||
 Db 897 TGCACATCTTTGGTTCCTGCTGCCCGCGCTCTCTCTCTACCGCACTATCCA 843
 |||||

RESULT 3

AQ997354

LOCUS

DEFINITION AQ997354 389 bp DNA linear GSS 24-FEB-2000
 RPCI-23-271P21.TV RPCI-23 Mus musculus genomic clone RPCI-23-271P21
 , DNA sequence.

ACCESSION AQ997354.1

VERSION AQ997354

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 389)

AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Aklnret

,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.

and Fraser,C.M

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other_GSSs: RPCI-23-271P21.TJ

COMMENT Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 271 row: P column: 21

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..389

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-271P21"

/clone_lib="RPCI-23"

/sex="Female"

/lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:

EcoRI; Site_2: EcoRI; female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of EcoRI and EcoRI Methylase. Size

selected DNA was cloned into the pBACE3.6 vector at the

EcoRI sites. The ligation products were transformed into

DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 99 a 106 c 96 g 88 t

ORIGIN

Query Match 45.9%; Score 28; DB 17; Length 389;

Best Local Similarity 71.2%; Pred. No. 3.1e+02;

Matches 37; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 TCCGTGACATCTTTGGTTCCTGCTGCCCGCGCTCTCTCTCTACCGCACTATCCA 53
 |||||

Db 54 TCCGTGACATCTTTGGTTCCTGCTGCCCGCGCTCTCTCTCTACCGCACTATCCA 105
 |||||

RESULT 4

BF528264/c

```
Email: oliver@helix.nih.gov,
http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 73 row: g column: 07
Seq primer: M13RPL reverse primer (ABI).
FEATURES             source
    Location/Qualifiers
      1..619
        /organism="Drosophila melanogaster"
        /strain="y[*] w[67cl]/Y*"
        /db_xref="taxon:7227"
        /clone="bs73g07"
        /clone_lib="Drosophila melanogaster adult testis library"
        /sex="male"
        /dev_stage="1-5 day adult"
        /lab_host="SOLR (Stratagene)"
        /note="Organ: testis; Vector: pBluescript SK (Stratagene);
Site 1: EcoRI; Site 2: Xho I; Testes dissected from 1-5
day adult y[*] w[67cl]/Y males raised at 25OC. RNA
isolated using Trizol (Life Technologies) and a single
round of Poly(A)+ selection using Oligotex (Qiagen). cDNA
library constructed using Stratagene ZAP-cDNA synthesis
kit. Oligo dt-primerd, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBluescript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."
BASE COUNT          171 a   144 c   162 g   142 t
ORIGIN

Query Match               44.9%; Score 27.4; DB 12; Length 619;
Best Local Similarity     69.8%; Pred. No. 4.9e+02;
Matches                    37; Conservative         0; Mismatches 16; Indels       0; Gaps       0;

QY           6 GCACATCTTTGGTCGTCCGCGGCCGCCTCCTCTCATCGCACTATCC 58
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Db            176 GCTCATCAAGGTGACTACCTGTCTCGTGCTCTCTCTCATCTATACC 124

RESULT 6
BE408262/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Rutherfordia; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at: image.llnl.gov
Plate: LLCM336 row: g column: 03
High quality sequence start: 7
High quality sequence stop: 645.
Location/Qualifiers
      1..701
        /organism="Homo sapiens"
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melanogaster cDNA clone GH03085 5 similar to CG4714: FBan0004714 located on: 2R 49F15-50A1;; 04/10/2001, mRNA sequence.

AI063338
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster
fruit fly.
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 754)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
On Jul 23, 1998 this sequence version replaced gi:3339282.
Other_ESTs: GH03085.3prime
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
hit genomic AE003819: arm:2R [8082036,8314191]
estimated-cyto:49F2-50A3: 04/10/2001
Plate: GH.30 row: H column: 1
High quality sequence stop: 754
POLYA=No.

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/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site:1: EcoRI; Site:2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
BASE COUNT 241 a 177 c 198 g 138 t
ORIGIN

Query Match 44.9%; Score 27.4; DB 9; Length 754;
Best Local Similarity 69.8%; Pred. No. 5.1e-02;
Matches 37; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 6 GCACATCTTGGTTCCTGCTGCGCCGCCCTTCCTACGCACTATCC 58
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Db 547 GCTCATCAAGGTGACTACTGTCCTGCTCTCTCTACCTCATATCC 495

RESULT 10
LOCUS BC479057/c 757 bp mRNA linear EST 21-MAR-2001
DEFINITION 602526134F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4649792 5', mRNA sequence.
ACCESSION BC479057
VERSION BC479057.1 GI:13411336
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 757)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Arrayed by: Ling Hong/Rubin Laboratory
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
High quality sequence stop: 757.
High quality sequence stop: 757.
High quality sequence stop: 701.

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4517004"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 Kb. Library enriched for full-length clones and constructed by Life Technologies.

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
High quality sequence stop: 757.
High quality sequence stop: 757.
High quality sequence stop: 701.

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BASE COUNT 180 a 203 c 228 g 145 t 1 others
ORIGIN

Query Match 44.9%; Score 27.4; DB 12; Length 757;
Best Local Similarity 75.6%; Pred. No. 5.1e-02;
Matches 34; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TTCTGCACATCTTGGTTCCTGCTGCGCCGCCCTCTCTCTC 45
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Db 693 TTCTGCACCTCCAGGCTGCTGCTGCCAGACCCCTGCTGCTC 649

RESULT 11
LOCUS BG290491/c 913 bp mRNA linear EST 21-FEB-2001
DEFINITION 602388351F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4517004 5', mRNA sequence.
ACCESSION BG290491
VERSION BG290491.1 GI:13047386
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 913)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
High quality sequence stop: 701.
High quality sequence stop: 701.

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:4517004"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 Kb. Library enriched for full-length clones and constructed by Life Technologies.

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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:39:09 ; Search time 4.64516 Seconds
(without alignments)
4027.262 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	26	42.6	387	4	US-08-148-708-7
2	26	42.6	909	4	US-08-148-708-9
3	26	42.6	1179	4	US-08-148-708-3
4	26	42.6	1378	1	US-08-759-848-2
5	26	42.6	1378	4	US-08-148-708-6
6	26	42.6	1378	5	PCT-US95-09383-2
7	24.8	40.7	1260	1	US-07-866-979-3
8	24.8	40.7	1260	2	US-08-466-906B-3
9	24.8	40.7	1260	3	US-08-706-281A-3
10	24.8	40.7	1260	4	US-09-201-746-3
11	24.8	40.7	1260	4	US-09-097-231-3
12	24.2	39.7	261	2	US-08-592-383-7
13	24.2	39.7	2561	4	US-09-347-878-25
14	24.2	39.7	2658	2	US-08-592-383-3
15	24.2	39.7	2928	2	US-08-095-728B-3
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17	24.2	39.7	2940	2	US-08-592-383-1
18	24.2	39.7	2940	6	5171671-1
19	23.8	39.0	1929	4	US-09-040-229B-7
20	23.4	38.4	1101	1	US-08-759-848-7
21	23.4	38.4	1101	5	PCT-US95-09383-7
22	23.4	38.4	2051	4	US-09-399-913-52
23	23.4	38.4	3680	1	US-08-759-848-1
24	23.4	38.4	3680	5	PCT-US95-09383-1
25	23.4	38.4	4406	1	US-08-369-043-1
26	23	37.7	3258	2	US-08-729-955A-2
27	23	37.7	4403765	4	US-09-103-840A-2
					Sequence 2, Appli

c	28	23	37.7	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	29	22.8	37.4	3943	1	US-08-369-796-3	Sequence 3, Appli
	30	22.8	37.4	3943	2	US-08-852-091-3	Sequence 3, Appli
	31	22.8	37.4	3943	2	US-08-820-754-3	Sequence 3, Appli
	32	22.8	37.4	3943	3	US-08-956-652-3	Sequence 3, Appli
	33	22.8	37.4	3943	3	US-08-956-869-3	Sequence 3, Appli
	34	22.8	37.4	3943	3	US-08-948-547-3	Sequence 3, Appli
	35	22.8	37.4	3943	4	US-09-364-970-10	Sequence 10, Appli
	36	22.8	37.4	3943	4	US-08-956-653A-3	Sequence 3, Appli
	37	22.8	37.4	3943	5	PCT-US95-17025-3	Sequence 3, Appli
	38	22.8	37.4	4003	4	US-09-087-465-1	Sequence 1, Appli
	39	22.8	37.4	35060	3	US-08-814-095-7	Sequence 7, Appli
c	40	22.8	37.4	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	41	22.8	37.4	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	42	22.4	36.7	960	4	US-09-576-160B-10	Sequence 10, Appli
	43	22.4	36.7	1053	4	US-09-576-160B-11	Sequence 11, Appli
c	44	22.4	36.7	1161	4	US-09-199-637A-164	Sequence 164, App
c	45	22.4	36.7	4440	1	US-08-200-016-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-148-708-7
; Sequence 7, Application US/08148708
; Patent No. 6407207
; GENERAL INFORMATION:
; APPLICANT: Hess, John W
; Strader, Catherine D
; Borkowski, Joseph B
; Ransom, Richard W
; TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
; BK-2 Receptor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,708
; FILING DATE: 08-No. 6407207-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,709
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruso, Charles M
; REGISTRATION NUMBER: 30161
; REFERENCE/DOCKET NUMBER: 18713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4830
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-148-708-7
Query Match 42.6%; Score 26; DB 4; Length 387;
Best Local Similarity 65.5%; Pred. No. 3.7;


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Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 2 TCCTGCACATCTTTGTCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCA 59
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Db 281 TCCTGAATGCTGGGCTTCTGTCGCCCTGAGTGTATCATCACCCTTCTGCACGATGCA 338

RESULT 2
US-08-148-708-9
; Sequence 9, Application US/08148708
; Patent No. 6407207
; GENERAL INFORMATION:
; APPLICANT: Hess, John W
; Strader, Catherine D
; Borkowski, Joseph B
; Ransom, Richard W
; TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
; BK-2 Receptor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,708
; FILING DATE: 08-No. 6407207-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,709
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruso, Charles M
; REGISTRATION NUMBER: 30161
; REFERENCE/DOCKET NUMBER: 18713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4830
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-148-708-9

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Best Local Similarity 65.5%; Pred. No. 4.2;
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RESULT 3
US-08-148-708-3
; Sequence 3, Application US/08148708
; Patent No. 6407207
; GENERAL INFORMATION:
; APPLICANT: Hess, John W
; Strader, Catherine D
; Borkowski, Joseph B
; Ransom, Richard W
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; TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
; BK-2 Receptor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,708
; FILING DATE: 08-No. 6407207-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,709
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruso, Charles M
; REGISTRATION NUMBER: 30161
; REFERENCE/DOCKET NUMBER: 18713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4830
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1179 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-148-708-3

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Best Local Similarity 65.5%; Pred. No. 4.4;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 2 TCCTGCACATCTTTGTCCTGCTGCCCGGCCCTCTCTACCGCACTATCCA 59
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Db 686 TCCTGAATGCTGGGCTTCTGTCGCCCTGAGTGTATCATCACCCTTCTGCACGATGCA 743

RESULT 4
US-08-759-848-2
; Sequence 2, Application US/08759848
; Patent No. 5750826
; GENERAL INFORMATION:
; APPLICANT: Borkowski, Joseph A.
; APPLICANT: Strader, Catherine D.
; APPLICANT: Hess, John W.
; APPLICANT: Chen, Howard Y.
; APPLICANT: Trumbauer, Myrna E.
; TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Wallen III
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,848
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/281,393
; FILING DATE: 27-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen III, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 19234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4720
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-759-848-2

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Best Local Similarity 65.5%; Pred. No. 4.5;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TCCTGCACATCTTTGGTTCCTGTCGCCCGCCCTCTTCTCTACCGCACTATCCA 59
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Db 821 TCCTGAATGTCGTGGGCTTCCTGTCGCCCTGAGTGTGCATCATCCTTCTGCAGGATGCA 878

RESULT 5
US-08-148-708-6
; Sequence 6, Application US/08148708
; Patent No. 6407207
; GENERAL INFORMATION:
; APPLICANT: Hess, John W
; Strader, Catherine D
; Borkowski, Joseph B
; Ransom, Richard W
; TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
; BK-2 Receptor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,708
; FILING DATE: 08-No. 6407207-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,709
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruso, Charles M
; REGISTRATION NUMBER: 30161
; REFERENCE/DOCKET NUMBER: 18713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4830
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1378 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-148-708-6

Query Match 42.6%; Score 26; DB 4; Length 1378;
Best Local Similarity 65.5%; Pred. No. 4.5;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TCCTGCACATCTTTGGTTCCTGTCGCCCGCCCTCTTCTCTACCGCACTATCCA 59
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Db 821 TCCTGAATGTCGTGGGCTTCCTGTCGCCCTGAGTGTGCATCATCCTTCTGCAGGATGCA 878

RESULT 6
PCT-US95-09383-2
; Sequence 2, Application PC/TUS9509383
; GENERAL INFORMATION:
; APPLICANT: Borkowski, Joseph A.
; APPLICANT: Strader, Catherine D.
; APPLICANT: Hess, John W.
; APPLICANT: Chen, Howard Y.
; APPLICANT: Trumbauer, Myrna E.
; TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
; TITLE OF INVENTION: NON-HUMAN ANIMALS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Wallen III
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09383
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/281,393
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen III, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 19234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-09383-2

Query Match 42.6%; Score 26; DB 5; Length 1378;
Best Local Similarity 65.5%; Pred. No. 4.5;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TCCTGCACATCTTTGGTTCCTGTCGCCCGCCCTCTTCTCTACCGCACTATCCA 59
      ||||| | ||| | ||||| ||||| | || | ||||| |||
Db 821 TCCTGAATGTCGTGGGCTTCCTGTCGCCCTGAGTGTGCATCATCCTTCTGCAGGATGCA 878

RESULT 7
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[illegible]

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA: US/08/706,281A
/ APPLICATION NUMBER: 04-SEP-1996
/ FILING DATE: 04-SEP-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6100048nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 96,886
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1260 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: 1..14
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 15..959
/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: 960..1260
/ US-08-706-281A-3

Query Match 40.7%; Score 24.8; DB 3; Length 1260;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 CCTGCACATCTTTGGTTCCTGCGCCGCCCTCTCTCTACCGCACT 54
DB 371 CGTGCTCATCTGTGGTCCATGTCAGTCTCTGCTTCTCTGGGCATCA 422

RESULT 10
US-09-201-746-3
/ Sequence 3, Application US/09201746
/ Patent No. 6268221
/ GENERAL INFORMATION:
/ APPLICANT: Cone, Roger D
/ TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
/ TITLE OF INVENTION: and Uses
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
/ STREET: 300 South Wacker Drive
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/201,746
/ FILING DATE: 01-DEC-1998
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6268221nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,154-J
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
```

```
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1260 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: 1..14
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 15..959
/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: 960..1260
/ US-09-201-746-3

Query Match 40.7%; Score 24.8; DB 4; Length 1260;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 CCTGCACATCTTTGGTTCCTGCGCCGCCCTCTCTCTACCGCACT 54
DB 371 CGTGCTCATCTGTGGTCCATGTCAGTCTCTGCTTCTCTGGGCATCA 422

RESULT 11
US-09-097-231-3
/ Sequence 3, Application US/09097231
/ Patent No. 6278038
/ GENERAL INFORMATION:
/ APPLICANT: Cone, Roger D
/ TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
/ STREET: 300 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/097,231
/ FILING DATE: 12-Jun-1998
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6278038nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 96,886-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1260 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: 1..14
```

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;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..959
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 960..1260
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-097-231-3

Query Match      40.7%; Score 24.8; DB 4; Length 1260;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY      3  CQTGCACATCTTGTCCTGCTGCCCGCGCCCTCTCTCTACCGCACT 54
Db      371 CGTGCTAATGTCGTCCTGTCGTCAGTCTCTCTCTCCGGGCATCAT 422

RESULT 12
US-08-592-383-7
; Sequence 7, Application US/08592383
; Patent No. 5830760
; GENERAL INFORMATION:
; APPLICANT: Tsai, S. and S.J. Collins
; TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Recept
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows 5.01-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,383
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/099,242
; FILING DATE: July 28, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: FHCR-1-7190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; DESCRIPTION: page 11, RAR-alpha N-terminal region; positions 103 to 363 of SEQ.
; IMMEDIATE SOURCE:
; LIBRARY: cDNA
US-08-592-383-7

Query Match      39.7%; Score 24.2; DB 2; Length 261;
Best Local Similarity 66.0%; Pred. No. 13;
Matches 35; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY      6  GCACATCTTGTCCTGCTGCCCGCGCCCTCTCTCTACCGCACTATCC 58
Db      42  GCACCTCAATGGGTACCGGTGCTCCCTAGCGCTTCTTCTCCCGCCATGC 94

RESULT 13
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US-09-347-878-25/G
; Sequence 25, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 2561
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1131)..(2399)
; OTHER INFORMATION: Escherichia coli nucleic acid encoding
; OTHER INFORMATION: folypolyglutamate synthetase-dihydrofolate
; OTHER INFORMATION: synthetase
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M32445/GenBank
US-09-347-878-25

Query Match      39.7%; Score 24.2; DB 4; Length 2561;
Best Local Similarity 62.3%; Pred. No. 19;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      1  TTCTCGCACATCTTTGTCCTGCTGCCCGCGCCCTCTCTCTACCGCACTATCCAA 60
Db      386 TTTCGGCTCAAGCTCGCTACCCAGCTCCACAGGCTTCCTTCATCTACAGGCTATGCAG 327

QY      61 G 61
Db      326 G 326

RESULT 14
US-08-592-383-3
; Sequence 3, Application US/08592383
; Patent No. 5830760
; GENERAL INFORMATION:
; APPLICANT: Tsai, S. and S.J. Collins
; TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Rec
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows 5.01-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,383
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/099,242
; FILING DATE: July 28, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: FHCR-1-7190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct)
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; GENERAL INFORMATION:
 ; APPLICANT: Andersson, Leif
 ; APPLICANT: Luthman, L. Holger
 ; APPLICANT: Marklund, Stefan
 ; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
 ; FILE REFERENCE: 11145-007001
 ; CURRENT APPLICATION NUMBER: US/09/826,581
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: US 60/195,665
 ; PRIOR FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1722
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-826-581-3

Query Match 75.7%; Score 46.2; DB 10; Length 1722;
 Best Local Similarity 86.4%; Pred. No. 3.le-07;
 Matches 51; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CCTGCACATCTTTGGTTCCTGCTGCCCGCCGCCCTCCTCTCTACCGCACTATCCAAG 61
 || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1510 CCATCCTACCAGGTTCCTGCTGCCCGCCGCCCTCCTCTCTACCGCACTATCCAAG 1568

RESULT 3
 US-10-255-536-159/c
 ; Sequence 159, Application US/10255536
 ; Publication No. US20030087807A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Greenspan, Ralph J.
 ; TITLE OF INVENTION: Methods for Identifying Compounds for
 ; TITLE OF INVENTION: Motion Sickness, Vertigo and Other Disorders Related to
 ; FILE REFERENCE: P-NI 3864
 ; CURRENT APPLICATION NUMBER: US/10/255,536
 ; CURRENT FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: US/09/669,751
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US 60/168,579
 ; PRIOR FILING DATE: 1999-12-02
 ; NUMBER OF SEQ ID NOS: 261
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 159
 ; LENGTH: 566
 ; TYPE: DNA
 ; ORGANISM: Drosophila
 US-10-255-536-159

Query Match 44.9%; Score 27.4; DB 9; Length 566;
 Best Local Similarity 69.8%; Pred. No. 1.2;
 Matches 37; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 6 GCACATCTTTGGTTCCTGCTGCCCGCCGCCCTCCTCTCTACCGCACTATCC 58
 || ||||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 544 GCTCATCAAAGGTGACTACCTGTTCCGCTCTCTCTACCTCATTTATCC 492

RESULT 4
 US-10-045-815-7
 ; Sequence 7, Application US/10045815
 ; Patent No. US20020160498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wadhwa, Renu
 ; APPLICANT: Sugihara, Takashi
 ; APPLICANT: Ohide, Akiko
 ; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
 ; FILE REFERENCE: 06501-091001
 ; CURRENT APPLICATION NUMBER: US/10/045,815
 ; CURRENT FILING DATE: 2001-10-26
 ; PRIOR APPLICATION NUMBER: PCT/JF00/02731


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Qy 1 TTCTGCGACATCTTTGGTTCCTGCTGCGCGGCCCTCTCTCTCTACCGCAC 53
  || || | | || || || || || || || || || || || || || || || ||
Db 9604 TTGATGCCCTCCCGGSGTCCCTGCTGCGCTGGCGACGCCCTCTCTCCCCAC 9552

RESULT 9
US-09-764-891-2280/c
; Sequence 2280, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2280
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-2280

Query Match 41.0%; Score 25; DB 9; Length 635;
Best Local Similarity 64.9%; Pred. No. 8.2;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 TTCCTGCGACATCTTTGGTTCCTGCTGCGCGGCCCTCTCTCTACCGCACTATC 57
  || || | | || || || || || || || || || || || || || || || ||
Db 610 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 554

RESULT 10
US-09-764-891-6987
; Sequence 6987, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6987
; LENGTH: 22585
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9701)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-6987

Query Match 41.0%; Score 25; DB 9; Length 22585;
Best Local Similarity 64.9%; Pred. No. 8.4;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 4 CTGACATCTTTGGTTCCTGCTGCGCGGCCCTCTCTCTACCGCACTATCCAA 60
  || || | | || || || || || || || || || || || || || || || ||
Db 2602 GAGCCCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2658

RESULT 11
US-09-815-944-21
; Sequence 21, Application US/09815944
; Patent No. US20020038467A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Matthews, William
; APPLICANT: Moore, Mark
```

```
; APPLICANT: Phillips, Russell
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING MELANOCYTE
; FILE REFERENCE: R-654
; CURRENT APPLICATION NUMBER: US/09/815,944
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,236
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/215,214
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/218,075
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/219,167
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting vector
US-09-815-944-21

Query Match 40.7%; Score 24.8; DB 10; Length 200;
Best Local Similarity 67.3%; Pred. No. 9.5;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CTGCGACATCTTTGGTTCCTGCTGCGCGGCCCTCTCTCTACCGCACT 54
  || || || || || || || || || || || || || || || || || || || ||
Db 82 CGTGCTCATCTGTGGTCCCATGCTGCCAGTCTCTGCTCTCTGGGCATCAT 133

RESULT 12
US-10-288-160-3
; Sequence 3, Application US/10288160
; Publication No. US20030105024A1
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; Fan, Wei
; Boston, Bruce A
; Kesterton, Robert A
; Lu, Dongsi
; Chen, Wenbiao
; TITLE OF INVENTION: Methods and Reagents for Discovering and
; Using Mammalian Melanocortin Receptor Agonists and Antag
; To Modulate Feeding Behavior in Animals
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/288,160
; FILING DATE: US-No. US20030105024A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,281
; FILING DATE: 04-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. US20030105024Alnan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
```

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;
; TELEFAX: 312-913-0002
; TELEX: <UNKNOWN>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..959
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 960..1260
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-288-160-3

Query Match 40.7%; Score 24.8; DB 9; Length 1260;
Best Local Similarity 67.3%; Pred. No. 9.7;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 CCTGCACATCTTTGGTTCCTGCTGCGCGGCCCTCTCTCTACCGCACT 54
Db 371 CGTGTCACTGTGGCTCCATGGTGTCCAGTCTCTGCTTCTGCGCATATT 422

RESULT 13
US-09-815-944-19
; Sequence 19, Application US/09815944
; Patent No. US20020038467A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; APPLICANT: Matthews, William
; APPLICANT: Moore, Mark
; APPLICANT: Phillips, Russell
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING MELANOCYTE
; FILE REFERENCE: R-654
; CURRENT APPLICATION NUMBER: US/09/815,944
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,236
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/215,214
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/218,075
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/219,167
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-815-944-19

Query Match 40.7%; Score 24.8; DB 10; Length 1260;
Best Local Similarity 67.3%; Pred. No. 9.7;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 CCTGCACATCTTTGGTTCCTGCTGCGCGGCCCTCTCTCTACCGCACT 54
Db 371 CGTGTCACTGTGGCTCCATGGTGTCCAGTCTCTGCTTCTGCGCATATT 422

RESULT 14
US-09-880-107-3428/c
; Sequence 3428, Application US/09880107
; Patent No. US20020142981A1

; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherif, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3428
; LENGTH: 99014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U78027
US-09-880-107-3428

Query Match 40.7%; Score 24.8; DB 10; Length 99014;
Best Local Similarity 67.3%; Pred. No. 10;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 CCTGCACATCTTTGGTTCCTGCTGCGCGGCCCTCTCTCTACCGCACT 54
Db 15006 CCTCGGCTCTTTGGTTCCTGCTTCCCTGCCCTGCCGCTCTCTCCCT 14955

RESULT 15
US-10-044-090-92/c
; Sequence 92, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 92
; LENGTH: 733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 416842.32
; NAME/KEY: unsure
; LOCATION: 665, 690, 698
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-92

Query Match 40.0%; Score 24.4; DB 12; Length 733;
Best Local Similarity 63.8%; Pred. No. 13;
Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 TCCTGCACATCTTTGGTTCCTGCTGCGCGGCCCTCTCTCTACCGCACTATCCA 59
Db 192 TCCAGCAGGTCCACCCCTGGACTGCGAGGCTCTTCTCTTCCATTGCACTGTCCA 135

Search completed: June 13, 2003, 09:00:42
Job time : 20.2903 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: June 14, 2003, 11:14:11 ; Search time 4487 Seconds
(Without alignments)
11168.939 Million cell updates/sec

Title: us-09-826-581-3
Perfect score: 1722
Sequence: 1 cctggccctcagatcaaga.....gatgagaggtcggcgctgga 1722

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1722	100.0	1722	6	AX281580	AX281580 Sequence
c 2	1719.4	99.8	152129	2	AC027416	AC027416 Homo sapi
c 3	1697	98.5	206854	9	AC009974	AC009974 Homo sapi
c 4	612.6	35.6	5888	4	AF214521	AF214521 Sus scrofa
c 5	209.4	12.2	227724	2	AF336381	AF336381 Mus muscu
c 6	196.2	11.4	146577	2	AC128070	AC128070 Rattus no
c 7	196.2	11.4	190183	2	AC129703	AC129703 Rattus no
c 8	168.2	9.8	1647	6	AX281582	AX281582 Sequence
c 9	168.2	9.8	2109	6	AX099776	AX099776 Sequence
c 10	168.2	9.8	2115	6	AX099802	AX099802 Sequence
c 11	168.2	9.8	2115	9	AF214519	AF214519 Homo sapi
c 12	168.2	9.8	2290	9	HSA249977	HSA249977 Homo sapi
c 13	151.2	8.8	192868	2	AC127107	AC127107 Rattus no
c 14	148	8.6	1867	6	AX099774	AX099774 Sequence
c 15	148	8.6	1873	4	AF214520	AF214520 Sus scrofa
c 16	148	8.6	1873	6	AX099800	AX099800 Sequence
c 17	148	8.6	1873	6	AX398331	AX398331 Sequence
c 18	148	8.6	1873	6	AX398333	AX398333 Sequence
c 19	148	8.6	1873	6	AX398335	AX398335 Sequence
c 20	148	8.6	1873	6	AX398337	AX398337 Sequence
c 21	148	8.6	1873	6	AX398339	AX398339 Sequence
c 22	148	8.6	2022	6	AX099804	AX099804 Sequence
c 23	91.4	5.3	106	11	G67375	G67375 A898 Human
c 24	91.2	5.3	192968	2	AC127107	AC127107 Rattus no
c 25	82.2	4.8	142903	2	AL627254	AL627254 Danio rer
c 26	79.4	4.5	14411	4	AF329081	AF329081 Bos tauru
c 27	77	4.5	73638	2	AC015613	AC015613 Homo sapi
c 28	74.2	4.3	81210	2	AC019242	AC019242 Homo sapi
c 29	74.2	4.3	174400	9	AC011603	AC011603 Homo sapi
c 30	74.2	4.3	183565	2	AC073610	AC073610 Homo sapi
c 31	74.2	4.3	189141	2	AC025256	AC025256 Homo sapi
c 32	70.4	4.1	1578	9	HS042412	HS042412 Human 5'-AM
c 33	70.4	4.1	1677	9	BC000358	BC000358 Homo sapi
c 34	70.4	4.1	1683	9	AK097606	AK097606 Homo sapi
c 35	70.4	4.1	1774	6	AX364914	AX364914 Sequence
c 36	69.4	4.0	101215	9	AC006966	AC006966 Homo sapi
c 37	68	3.9	3497	3	AF094763	AF094763 Drosophila
c 38	68	3.9	80069	2	AC019671	AC019671 Drosophila
c 39	68	3.9	173634	3	AC009344	AC009344 Drosophila
c 40	68	3.9	195868	3	AC008308	AC008308 Drosophila
c 41	68	3.9	230266	3	AE003733	AE003733 Drosophila
c 42	67.6	3.9	7218	6	I66494	I66494 Sequence 14
c 43	65.8	3.8	1905	6	AX482695	AX482695 Sequence
c 44	65.8	3.8	2082	3	AF094764	AF094764 Drosophila
c 45	65.8	3.8	3210	3	AY084138	AY084138 Drosophila

ALIGNMENTS

RESULT 1
AX281580
LOCUS AX281580 1722 bp DNA linear PAT 03-NOV-2001
DEFINITION Sequence 3 from Patent WO0177305.
ACCESSION AX281580
VERSION AX281580.1 GI:16608831
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1
TITLE Andersson, L., Luthman, H. and Marklund, S.
VARIANTS Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 3 18-OCT-2001;

FEATURES		Arexilis AB (SE)		Location/Qualifiers	
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		/db_xref="taxon:9606"			
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Best Local Similarity 100.0%; Pred. No. 0;					
Matches 1722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	CTGCGCCCTCAGATCAAGAGGCTTCTTTGCTCTGCTGGCCAAACGGTGTGGGGCAGC	60		
DB	1	CTGCGCCCTCAGATCAAGAGGCTTCTTTGCTCTGCTGGCCAAACGGTGTGGGGCAGC	60		
QY	61	CCCTCATGGGACACGAAGAGAGACTTTGTGGGTGAGGAGAGGCTGGGGAGGTGAAG	120		
DB	61	CCCTCATGGGACACGAAGAGAGAGACTTTGTGGGTGAGGAGAGGCTGGGGAGGTGAAG	120		
QY	121	GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTTGTTCTGGGGCTGATCTCTGATAT	180		
DB	121	GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTTGTTCTGGGGCTGATCTCTGATAT	180		
QY	181	ACCACAAAGCTTGGCTTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGGAAAGTCCATCC	240		
DB	181	ACCACAAAGCTTGGCTTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGGAAAGTCCATCC	240		
QY	241	GGAGTGTGATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGTGAGCGCT	300		
DB	241	GGAGTGTGATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGTGAGCGCT	300		
QY	301	ATGACAGGTGACACCTTTACCTCCGCTACTGCATGCGCTGTGCATAGTGTGCTAGGG	360		
DB	301	ATGACAGGTGACACCTTTACCTCCGCTACTGCATGCGCTGTGCATAGTGTGCTAGGG	360		
QY	361	AGCAATGGGGGAGGAGGAGAGAAAGACCCCACTTCTCAGGCCCTGGGGGCTGCCCC	420		
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QY	421	ACTGTCTGTCTCCACAGTCCCCACTGTGTCTCAGCACAAAGACACTGGCAGGGTGGGA	480		
DB	421	ACTGTCTGTCTCCACAGTCCCCACTGTGTCTCAGCACAAAGACACTGGCAGGGTGGGA	480		
QY	481	GGGATCTGACCTCAACCTGCTTCCACCAAGGCCCGGGCTGACCTCTCTCCCGCC	540		
DB	481	GGGATCTGACCTCAACCTGCTTCCACCAAGGCCCGGGCTGACCTCTCTCCCGCC	540		
QY	541	CCTCCCTCGAGGGATGCTGACCATCACTGACCTTCATCTGCTGCTGCTGCTACTACA	600		
DB	541	CCTCCCTCGAGGGATGCTGACCATCACTGACCTTCATCTGCTGCTGCTGCTACTACA	600		
QY	601	GGTCCCTCGTGGAGAGTGGGCTGGGAATCTTATGGGCACCCAGAGGGGGGGGGCGGG	660		
DB	601	GGTCCCTCGTGGAGAGTGGGCTGGGAATCTTATGGGCACCCAGAGGGGGGGGGCGGG	660		
QY	661	AGGGAGTCTCTCTGAGGCTGTGGCTTAGAAGCCACGCTTCTTCTGACTTCTTGAGTGC	720		
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QY	721	CTGTGATGTCTCTAGGTCCAGATCTATGAGATTGAACAACATAGATTGAGACCTGGAG	780		
DB	721	CTGTGATGTCTCTAGGTCCAGATCTATGAGATTGAACAACATAGATTGAGACCTGGAG	780		
QY	781	GGGTGATGGGGAGAGGAACCCGAAAGGGGCTGTGTGTGTGTGTGGCCAGGGCTTTAAG	840		
DB	781	GGGTGATGGGGAGAGGAACCCGAAAGGGGCTGTGTGTGTGTGTGGCCAGGGCTTTAAG	840		
QY	841	GTGAGGATGGGCATGGGGATGTCTCTGGAGTGCAACAGGGGAGGACAAATAGAGCCTCG	900		
DB	841	GTGAGGATGGGCATGGGGATGTCTCTGGAGTGCAACAGGGGAGGACAAATAGAGCCTCG	900		
QY	901	GGTCCCTGACCGAAGGAGGCTGCTGGGACTGCAAGGTGAGGCAAGGTGACCGGCTCCCC	960		

DB	901	GGTGCTGACGAAGGAAGCTGCTGGGACTGCAAGGTGAGGAGGTGACCGGCTCCCC	960		
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DB	961	TGCGCTGACTTGCGCTCTTTCTGAGAGATCTACCTGCAAGGCTGCTTCAAGGCTCTGGT	1020		
QY	1021	CTCCATCTCTCTATGATAGGTGGGTGCTCTGCTCATTCACCTGAGGCTCTCTCTCC	1080		
DB	1021	CTCCATCTCTCTATGATAGGTGGGTGCTCTGCTCATTCACCTGAGGCTCTCTCTCC	1080		
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QY	1201	CTCCCTGAGGCTGCGCCGAGGCTCACTGCTCCATCTCTGACGCTGCTTCAAGCTGTCTA	1260		
DB	1201	CTCCCTGAGGCTGCGCCGAGGCTCACTGCTCCATCTCTGACGCTGCTTCAAGCTGTCTA	1260		
QY	1261	CACCTCATCAAGAACCGGATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1320		
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DB	1321	ACTCCACATCTCAGACACAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1380		
QY	1381	CCAGGTGGGAGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1440		
DB	1381	CCAGGTGGGAGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1440		
QY	1441	CCCTGAGCTGCTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1500		
DB	1441	CCCTGAGCTGCTGGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1500		
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DB	1501	ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1560		
QY	1561	TATCCAAAGATTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1620		
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DEFINITION Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32					
unordered pieces.					
AC027416					
VERSION AC027416.2 GI:8317289					
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.					
SOURCE Homo sapiens.					
ORGANISM Homo sapiens					
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS 1 (bases 1 to 152129)					
TITLE Birren, B., Linton, L., Nusbaum, C. and Lander, E.					
JOURNAL Homo sapiens, clone RP11-504G11					
REFERENCE 2 (bases 1 to 152129)					

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Glnde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,C., Hagos,B., Hearford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lakoque,K., Lamazares,R., Landers,T., Lehoczkzy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Melchior,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollard,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center Project name: L7458

Center clone name: 504_G11

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 135376 bases at least Q40

Consensus quality: 143264 bases at least Q30

Consensus quality: 146503 bases at least Q20

Insert size: 161000; agarose-fp

Insert size: 149029; sum-of-contigs

Quality coverage: 3.1 in Q20 bases; agarose-fp

Quality coverage: 3.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1005: contig of 1005 bp in length
* 1006 1105: gap of 100 bp
* 1106 2402: contig of 1297 bp in length
* 2403 2502: gap of 100 bp
* 2503 3823: contig of 1321 bp in length
* 3824 3923: gap of 100 bp
* 3924 5020: contig of 1097 bp in length
* 5021 5120: gap of 100 bp
* 5121 6161: contig of 1041 bp in length
* 6162 6261: gap of 100 bp
* 6262 7547: contig of 1286 bp in length
* 7548 7647: gap of 100 bp
* 7648 9983: contig of 2336 bp in length
* 9984 10083: gap of 100 bp
* 10084 12556: contig of 2473 bp in length
* 12557 12656: gap of 100 bp
* 12657 15043: contig of 2387 bp in length

* 15044 15143: gap of 100 bp
* 15144 17123: contig of 1980 bp in length
* 17124 17223: gap of 100 bp
* 17224 19466: contig of 2243 bp in length
* 19467 19566: gap of 100 bp
* 19567 21928: contig of 2362 bp in length
* 21929 22028: gap of 100 bp
* 22029 24313: contig of 2291 bp in length
* 24320 24419: gap of 100 bp
* 24420 27059: contig of 2640 bp in length
* 27060 27159: gap of 100 bp
* 27160 30170: contig of 3011 bp in length
* 30171 30270: gap of 100 bp
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* 33969 34068: gap of 100 bp
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* 38180 38279: gap of 100 bp
* 38280 42366: contig of 4087 bp in length
* 42367 42466: gap of 100 bp
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* 43366 45465: gap of 100 bp
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* 51286 51385: gap of 100 bp
* 51386 55871: contig of 4486 bp in length
* 55872 55971: gap of 100 bp
* 55972 60595: contig of 4624 bp in length
* 60596 60695: gap of 100 bp
* 60696 66595: contig of 5900 bp in length
* 66596 66695: gap of 100 bp
* 66696 73218: contig of 6523 bp in length
* 73219 73318: gap of 100 bp
* 73319 77113: contig of 3797 bp in length
* 77116 77213: gap of 100 bp
* 77216 85022: contig of 7807 bp in length
* 85023 85122: gap of 100 bp
* 85123 93314: contig of 8192 bp in length
* 93315 93414: gap of 100 bp
* 93415 101193: contig of 7779 bp in length
* 101194 101293: gap of 100 bp
* 101294 113090: contig of 11797 bp in length
* 113091 113190: gap of 100 bp
* 113191 123496: contig of 10306 bp in length
* 123497 123596: gap of 100 bp
* 123597 137837: contig of 14241 bp in length
* 137838 137937: gap of 100 bp
* 137938 152129: contig of 14192 bp in length.

FEATURES

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Db 35118 ACCTGGTCCCATCTTAACAGGGTTCCCTGCTGCCCGGCCCTCCTCTCTACCGCAC 35059

QY 1561 TATCAAGATTGGGATCGCACATTCGAGACTTGGCTGTGCTGGACAGCACC 1620

Db 35058 TATCAAGATTGGGATCGCACATTCGAGACTTGGCTGTGCTGGACAGCACC 34999

QY 1621 CATCCTGACTGCACCTGCACATCTTTGTGGACCGCGTGTCTGTGCACCTGCCGTGGTCAA 1680

Db 34998 CATCCTGACTGCACCTGCACATCTTTGTGGACCGCGTGTCTGTGCACCTGCCGTGGTCAA 34939

QY 1681 CGAATGTGGTACCCACCCCGAGGATGAGAGCTCGGGCTGG 1721

Db 34938 CGAATGTGGTACCCACCCCGAGGATGAGAGCTCGGGCTGG 34898

RESULT 3

AC009974/c

LOCUS AC009974 Homo sapiens BAC clone RP11-459119 from 2, complete sequence. PRI 09-JAN-2002

DEFINITION

ACCESSION AC009974

VERSION AC009974.9 GI:16799058

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 206854)

AUTHORS Sulston,J.E. and Waterston,R.

TITLE Toward a complete human genome sequence

JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE 99063792

PUBMED 9847074

REFERENCE 2 (bases 1 to 206854)

AUTHORS Harris,A. and Cotton,M.

TITLE The sequence of Homo sapiens BAC clone RP11-459119

JOURNAL Unpublished (2001)

REFERENCE 3 (bases 1 to 206854)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (08-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 206854)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (08-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 206854)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 6 (bases 1 to 206854)

AUTHORS Waterston,R.

TITLE Direct Submission

JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT On Nov 8, 2001 this sequence version replaced gi:13431203.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@watson.wustl.edu

----- Summary Statistics

Center project name: H_NH0459119

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tatenio,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries: Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

	Location/Qualifiers	Source
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	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/chromosome="2"	
	/map="2"	
	/clone="RP11-459119"	
	/clone_lib="RPC1-11"	
misc_feature	1..37	/note="match to EST AL567345 (NID:g12920610)"
misc_feature	1..37	/note="match to EST AW880850 (NID:g8042860)"
misc_feature	1..37	/note="match to EST BE047599 (NID:g8364652) tz39c01.y1"
misc_feature	1..37	/note="match to EST BE314060 (NID:g9134719)"
misc_feature	1..37	/note="match to EST BF183086 (NID:g11061273)"
misc_feature	1..37	/note="match to EST BF304755 (NID:g11251653)"
misc_feature	1..37	/note="match to EST BG477625 (NID:g13409904)"
misc_feature	1..37	/note="match to EST BI059713 (NID:g14467240)"
misc_feature	1..37	/note="similar to Homo sapiens EST B1114348 (NID:g14565249)"
misc_feature	3..37	/note="match to EST BE908408 (NID:g10402954)"
misc_feature	4..37	/note="match to EST A1670836 (NID:g4850567) wa04g10.x1"
misc_feature	164..662	/note="match to EST C05773 (NID:g1502549)"
misc_feature	220..221	/note="match to EST BG470047 (NID:g13402322)"
misc_feature	281..344	/note="match to EST A1670836 (NID:g4850567) wa04g10.x1"

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

misc_feature 281..344 /note="match to EST AL567345 (NID:g12920610)"
misc_feature 281..344 /note="match to EST AW880850 (NID:g8042860)"
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misc_feature 281..344 /note="match to EST BE908408 (NID:g10402954)"
misc_feature 281..344 /note="match to EST BF183086 (NID:g11061273)"
misc_feature 281..344 /note="match to EST BF304755 (NID:g11251653)"
misc_feature 281..344 /note="match to EST BG477625 (NID:g13409904)"
misc_feature 281..344 /note="match to EST BI059713 (NID:g14467240)"
misc_feature 281..344 /note="similar to Homo sapiens EST BI114348 (NID:g14565249)"
misc_feature 294..344 /note="match to EST BG470047 (NID:g13402322)"
misc_feature complement(557..558)
misc_feature /note="match to EST AA043371 (NID:g1521226) zk53e10.rl"
misc_feature 588..929 /note="match to EST T64073 (NID:g667938) yc05dl12.rl"
misc_feature 594..764 /note="match to EST BI059713 (NID:g14467240)"
misc_feature 594..763 /note="match to EST AA043371 (NID:g1521226) zk53e10.rl"
misc_feature 594..763 /note="match to EST AI670836 (NID:g4850567) wa04g10.xl"
misc_feature 594..763 /note="match to EST AW880850 (NID:g8042860)"
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misc_feature 594..763 /note="match to EST BF183086 (NID:g11061273)"
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misc_feature 594..763 /note="match to EST BG470047 (NID:g13402322)"
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misc_feature 594..763 /note="similar to Homo sapiens EST BI114348 (NID:g14565249)"
misc_feature 594..742 /note="match to EST BE047599 (NID:g8364652) tz39c01.y1"
misc_feature 594..731 /note="match to EST BE314060 (NID:g9134719)"
misc_feature 599..763 /note="match to EST AL567345 (NID:g12920610)"
misc_feature 617..1084 /note="match to EST AA481361 (NID:g2210913) zv44e01.rl"
misc_feature 622..763 /note="match to EST AI860958 (NID:g5514574) w156f05.xl"
misc_feature 622..763 /note="similar to Mus musculus EST AI196847 (NID:g3749453) ui67e01.xl"
misc_feature 684..763 /note="match to EST BG992568 (NID:g14396638)"
misc_feature 962..1084 /note="match to EST AI656812 (NID:g4740791) tt54b06.xl"
misc_feature 967..1091 /note="match to EST AA043371 (NID:g1521226) zk53e10.rl"
misc_feature 967..1090 /note="similar to Homo sapiens EST BI114348 (NID:g14565249)"
misc_feature 967..1085

Query Match

98.5%; Score 1697; DB 9; Length 206854;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 1719; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 CCTGGCCCTCAGATCAAGAGGCTTCTTTGCTCTGTTGGCCAAAGCGTGTGCGGCGAGC 60
Db 166697 CCTGGCCCTCAGATCAAGAGGCTTCTTTGCTCTGTTGGCCAAAGCGTGTGCGGCGAGC 166638
QY 61 CCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGTGAGAGAGGCTGGGAGGTGAAG 120
Db 166637 CCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGTGAGAGAGGCTGGGAGGTGAAG 166578
QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTTACGGTGTGTTCTGGGCTGATCTCTGATAT 180
Db 166577 GGAGATGGAGAGGTGAGGGGAGATCTTTACGGTGTGTTCTGGGCTGATCTCTGATAT 166518
QY 181 ACCAAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 240
Db 166517 ACCAAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 166458
QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCGCT 300
Db 166457 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCGCT 166398
QY 301 ATGACCAAGCTGACACCTTTACCTCCGCTACTGCATGGGCCCTGTGCCATAGGTGCTTAGG 360
Db 166397 ATGACCAAGCTGACACCTTTACCTCCGCTACTGCATGGGCCCTGTGCCATAGGTGCTTAGG 166338
QY 361 AGCAATGGGGAGGAGGAGAGAAAGAGCCACCTTCTCAGGCTGTGGGGGTGCCCC 420
Db 166337 AGCAATGGGGAGGAGGAGAGAAAGAGCCACCTTCTCAGGCTGTGGGGGTGCCCC 166278
QY 421 ACTGCTCTGTCCACAGTCCCCTACTGTCTCAGACAAAGACACTGGCAGGTGGGGA 480
Db 166277 ACTGCTCTGTCCACAGTCCCCTACTGTCTCAGACAAAGACACTGGCAGGTGGGGA 166218
QY 481 GGGATCTGACCTCAACCTGCTTCCACCAAGAGCCCGGGCTGACCTCTCCCGCC 540
Db 166217 GGGATCTGACCTCAACCTGCTTCCACCAAGAGCCCGGGCTGACCTCTCCCGCC 166158
QY 541 COTCCCTGCAGGATGCTGACCATCACTGACTTTCATCTCTGTTGCTGCTACTACA 600
Db 166157 COT-CCCTGCAGGATGCTGACCATCACTGACTTTCATCTCTGTTGCTGCTACTACA 166099
QY 601 GGTCCCCCTGGTGAGAGTGGGCTGGGAATCTTATGGGCACCCAGAGGGGGGGCGG 660
Db 166098 GGTCCCCCTGGTGAGAGTGGGCTGGGAATCTTATGGGCACCCAGAGGGGGGGCGG 166039
QY 661 AGGGAGTCTCTCTGGAGCTGTGCTCCTAGAACCCACAGTCTTCTGACTTCTGGAGTC 720
Db 166038 AGGGAGTCTCTCTGGAGCTGTGCTCCTAGAACCCACAGTCTTCTGACTTCTGGAGTC 165979
QY 721 CTGTCGATGCTCTAGGTCCAGATCTATGAGATTGAACAACATAGATTGAGACCTGGAG 780
Db 165978 CTGTCGATGCTCTAGGTCCAGATCTATGAGATTGAACAACATAGATTGAGACCTGGAG 165919
QY 781 GGGTCACTGGGAGAGAAACCCGGAAAGGGCTCTTGGTGTGTTGGTGGCCAGGCTTAAG 840
Db 165918 GGGTCACTGGGAGAGAAACCCGGAAAGGGCTCTTGGTGTGTTGGTGGCCAGGCTTAAG 165860
QY 841 GTGGAGATGGGAGTGGGATGCTCTGAGTGAACAGGGAGGGACAAATAGGAGCTCG 900
Db 165859 GTGGAGATGGGAGTGGGATGCTCTGAGTGAACAGGGAGGGACAAATAGGAGCTCG 165800
QY 901 GGTGCTCAGCGAAGGAAAGCTGCCTGGGACTGCAAGGTGAGCAGGTGACCGCTCCCC 960
Db 165799 GGTGCTCAGCGAAGGAAAGCTGCCTGGGACTGCAAGGTGAGCAGGTGACCGCTCCCC 165740
QY 961 TGGCCTGACTCTGGCTCTTTCTGCGAGATCTACTCTCAAGGCTGCTTCAAGCCTCTGGT 1020
Db 165739 TGGCCTGACTCTGGCTCTTTCTGCGAGATCTACTCTCAAGGCTGCTTCAAGCCTCTGGT 165680
QY 1021 TCCTCATCTCCTAATGATAGTGGGTCTCTGCTCATTCACCTGAGCCTCTCTCTCCC 1080
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Db	165679	CTCCATCTCTCTTAATGATAGTGGTGTCTCTCTCTCAATTCACCTGAGCCTCCTCCTCCC	165620
QY	1081	ACAGTCCCTTCCCAAGTCCCACTCAGCTCTGAACCTCACTCTTCATCTAGGCGGCACA	1140
Db	165619	ACAGTCCCTTCCCAAGTCCCACTCAGCTCTGAACCTCACTCTTCATCTAGGCGGCACA	165560
QY	1141	CAGACAAGGAGCCTTGGTGCCTGCCCTCCTTTTAGGGGCTCGGATGAGGTTGTCT	1200
Db	165559	CAGACAAGGAGCCTTGGTGCCTGCCCTCCTTTTAGGGGCTCGGATGAGGTTGTCT	165500
QY	1201	CTCCCTAGGTCGCCGAGGCTCACTGCTCCATCTCTGCAGCCTGTTGAGCTGCTA	1260
Db	165459	CTCCCTAGGTCGCCGAGGCTCACTGCTCCATCTCTGCAGCCTGTTGAGCTGCTA	165440
QY	1261	CACCTCATCAAGAACCGCATCATCGCTGCCCTGCTTGTGACCGGCTGAGCAACGT	1320
Db	165439	CACCTCATCAAGAACCGCATCATCGCTGCCCTGCTTGTGACCGGCTGAGCAACGT	165380
QY	1321	ACTCCACATCCTCACACAAAGCGCTGCTCAAGTCTCTGCACATCTTTGTAAGCCTGGG	1380
Db	165379	ACTCCACATCCTCACACAAAGCGCTGCTCAAGTCTCTGCACATCTTTGTAAGCCTGGG	165320
QY	1381	CCAGGTGGGAGGAGGGGAGACCTGGCGAGTGATCAGAGGGCTGAGAGTCTTCAG	1440
Db	165319	CCAGGTGGGAGGAGGGGAGACCTGGCGAGTGATCAGAGGGCTGAGAGTCTTCAG	165260
QY	1441	CCCTAGCAGTGTGGGGAAGAGCTGGGAGCCCTCTTGAAGCTGCTGGATCCCTGATCTCC	1500
Db	165259	CCCTAGCAGTGTGGGGAAGAGCTGGGAGCCCTCTTGAAGCTGCTGGATCCCTGATCTCC	165200
QY	1501	ACCTGGTCCCATCTCAACAGGGTTCCTCTGCCCGGCCCTCCTCTCTACCGCAC	1560
Db	165199	ACCTGGTCCCATCTCAACAGGGTTCCTCTGCCCGGCCCTCCTCTCTACCGCAC	165140
QY	1561	TATCCAGATTTGGGATCGGCACATTCGGAGACTTGGCTGTGGTGGTGGAGACAGCAC	1620
Db	165139	TATCCAGATTTGGGATCGGCACATTCGGAGACTTGGCTGTGGTGGTGGAGACAGCAC	165080
QY	1621	CATCTGACTGCACTGACATCTTGTGACCGCGTGTCTGCACTGCTGCTGCTGCTCA	1680
Db	165079	CATCTGACTGCACTGACATCTTGTGACCGCGTGTCTGCACTGCTGCTGCTGCTCA	165020
QY	1681	CGAATGGTACCCACCCAGGATGAGAGGCTCGGGCTGG	1721
Db	165019	CGAATGGTACCCACCCAGGATGAGAGGCTCGGGCTGG	164979
RESULT 4			
AF214521			
LOCUS	AF214521 5888 bp DNA linear MAM 03-JUN-2000		
DEFINITION	Sus scrofa AMPK gamma subunit (PRKAG3) gene, complete cds.		
ACCESSION	AF214521		
VERSION	AF214521.1 GI:8215685		
KEYWORDS	Sus scrofa.		
SOURCE	Sus scrofa		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
REFERENCE	1 (bases 1 to 5888)		
AUTHORS	Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. and Andersson,L.		
TITLE	A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle		
JOURNAL	Science 288 (5469), 1248-1251 (2000)		
MEDLINE	20280150		
PubMed	10818001		
REFERENCE	2 (bases 1 to 5888)		
AUTHORS	Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N., Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.		
TITLE	Direct Submission		

JOURNAL	Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC Box 597, Uppsala 751 24, Sweden		
FEATURES			
source	Location/Qualifiers		
gene	1..5888		
gene	/organism="Sus scrofa"		
gene	/db_xref="taxon:9823"		
gene	/chromosome="15"		
gene	/map="15q"		
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gene	/gene="PRKAG3"		
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gene	join(1..154,515..918,1809..1890,2349..2407,2509..2554,2771..2825,3027..3153,3286..3451,4578..4615,4791..4937,5294..5410)		
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gene	/translation="NSFLQSQESRSPSRVTTSSSRHSDGDNKASRWTRQEDVREG GPPRGPGQSPRVAESTGOEATPKATPLAQAAPLAENDNPTRDILPDSCAASAS DSNTDHLDLGIEESASASGDELGLVEKPAKPCSPSEVLLPRLGHWDELQAGQVYM FMGHEHCYDAMATSKLVIFDTMLEIKAFALVANGVRAAPLMDSKKSFQGMULTI TDFLVLHRYSPRLVQIYEIEEHKIEIWEIYIQGCPKPLVSIKPNISLEFYATLI KNRHLRPLDPSGAVLHILTHKRLKLFHIFGLTLPRLPSLYRTIODLIGITFRDL AVLETAPIILTALEDIFVDRVSALPVNVTGVVLYSRFDVTHLAAQATYNHLDNV GEALRQTLCLGVLSCQPHETLGEVIDRIVREQVHRLVLDVETQHLGLVYSLDILQ ALVLSRAGIDALGA"		
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Db	1800	GGCGCTCAGATCAAGAAGGCGCTTCTTTGCTCTGTTGGGCCAACGGTGTGGGGCAGCCCT 1859	
QY	65	CTATGGGACACAGACAGACGCTTTTGGCTGAGGAGAGGCTGGGGAGGTGAAGGGAG 124	
Db	1860	TTGTGGGACACAGACAGACGCTTCTGCTGAGGAGGCGTGGGGAGG--CAGAGGTG 1918	
QY	125	ATGGAGGAGGTGAGGGGAGATCTTGTACGGTGTGTTCTGGGGCTGATCTGTGATACCA 184	
Db	1919	GTGGGAGGAGGATAGGGGACCTTGTGGGTGATCTTAGGGCGAGCTTGACACCA 1978	
QY	185	CAAGCTTGGCTTCAGGCCAACGCCAGCGGCGAGGGTGGAGAAAGTCCATCCGGAG 244	
Db	1979	CAGGCTTCAACCAAGCAGGGGCGCTGGCTGGAG--AGGGGGGAGCATTTGACCCCGGTC 2036	
QY	245	TCGTGATGCCAGCTGGGAGACCTCGGCTCAATTTCCCATCTGTGGAGCGCTATGA 304	
Db	2037	TCTGTGTGGCCAGCTGGGAGA-----TCTCACTGTAGGAGCTGTGA 2080	
QY	305	CCAGCTGACACTTTCACCTCCGCTACTGCATGGCCCTGTGCCA-----TAGTGCTAG 358	
Db	2081	CCAGCTGACCTTCCAGCTCTACTACCCCAAGTCCCTGTCGCGAGGTGTAGTAAGAAG 2140	
QY	359	GGAGCAAAATGGGGGAGGAGAGAAAGACCCCACTTCTCAGGCGTGGGGGCTGCC 418	
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QY	419	CCACTGTCTGTTCACAGTCCCACTGTGTCTCAGCACAAGGACACTGGCAGGGTGG 478	
Db	2201	ACAGGGAAGAGTAAAGAGGACAAACCCCATTTGTTCAGGCGGAGGGGCTGCCCTCTG 2260	
QY	479	GAGGGAGTCTGACCTCACTGCC-----TTCACCCCAAGGCCCCGGGCT 525	

Db	2261	TCCTCTTTTGGCCACCCCTTCAGTAAAAGGATGTGGCAGGGTGGGGGGAGGGGCCCGGGGCT	2320
QY	526	GACCTCCTCCCGCGCCCTC-CCTCGCAGGATGTGACCATCACTCAGCTTCATCTCGTGGT	584
Db	2321	GACCCCATTTGCTCCCTTCGCCCCACAGGGATGCTACCATCACAGCTTCATCTTGGTG	2380
QY	585	CTGCATCGCTACTACAGTCCCCCTGTGTGAGGATGGGCTGGGAATCTTATGGGCACC	644
Db	2381	CTGCACCGCTATTACAGTCCCCCTGTGTGAGGATGGTCTGGGGTCCCT-GGAACACC	2439
QY	645	AGAGGGCGGGGGCGAGGGAGTCTCTCTGGAGCCGTGTCCTAGAGACCCAGCTCTT	704
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QY	705	TCGTACTCTTGAGTCCCTGTGATGTCTTAGTCCAGATCTATGAGATTGAACAACATA	764
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QY	765	AGATTGAGACCTTGGAGGGGTGAGTGGGGAGAGAACCCGAAAGGGGCTGTGTGT- ----	819
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QY	875	ACAGGGAGGGACAAATAGGAGCCTCGGGTGCCTGACGGAAGGGAAGCTCCCTGGGACTG-	933
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QY	993	ACCTGCAAGGCTTTCAGGCTCTGGTCTCATCTCTCTTAATGATAGGTGGGTGCTC	1052
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QY	1113	AACTCACCTCTTTCATPCTTAGCGGCCACACAGACAGGAGGCTTGGTGCCTTGCCCTCC	1172
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QY	1173	TTTATG-GGGCTGGATGGAGGTGTCTCTCCCTAGGCTGCCCGCAGGCTCACTGTCTCC	1231
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QY	1232	CATCTCTGAGCCTGTTTGAAGCTGTCTACACCTTCATCAAGAACCGGATCCATCGCCTG	1291
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QY	1412	GGTGATCAGAGGGCTGAGGAGTCTTCAGCCCTAGCAGTCTGTG-GGGGAAGGCTGGGAG	1469
Db	3179	--CAACCTGAGTGGCTGGAAGTCTTCAGCCCTAGGATGGGGGAGGAGTACGTGGGAG	3236
QY	1470	CCCTCTTGAAGCTGTGGATCCCTGTATCTCCACCTGGTGCCTCATCAACCAAGGTTTCCC	1529
Db	3237	CCCCCTGAGGGCTAC---TCCCTCTGGCCTCACCCTGTCCCAACCAACCAAGGCAACC	3292
QY	1530	TGCTGCCCGGCCCTTCTCTACCGCACTATTCCAAGATTTGGGCATCGGCACATTTCC	1589

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Db	3353	GAGACTTGGCGTGTGGTGTGGAAACGGCGCCCATCTGACCGCACTGGACATCTTCGTGG	3412
Qy	1650	ACCGGCGTGTGTGCACTGGCTGTGGTCAACGAATGTGTACCCACCCCGCAGGATGAGA	1709
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RESULT 5	AF336381/c	227724 bp DNA linear	HTG 02-APR-2001
LOCUS	Mus musculus chromosome 1 clone PAC510; PAC457, ***	SEQUENCING IN	
DEFINITION	PROGRESS ***, 3 unordered pieces.		
ACCESSION	AF336381.1	GI:13507298	
VERSION	AF336381.1	GI:13507298	
KEYWORDS	HTG; HTGS PHASE1.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 227724)		
AUTHORS	Rump, A.; Hayes, C.; Brown, S.D.M. and Rosenthal, A.		
TITLE	Mouse chromosome 1 genomic sequence		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 227724)		
AUTHORS	Rump, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany		
COMMENT	<p>* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.</p>		
	1	17869:	contig of 17869 bp in length
	17870	17969:	gap of unknown length
	17970	32746:	contig of 14777 bp in length
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Query Match	12.2%;	Score 209.4;	DB 2; Length 227724;
Best Local Similarity	67.6%;	Pred. No. 4.4e-41;	
Matches 401;	Conservative	0; Mismatches 126;	Indels 66; Gaps 5;
Qy	1100	CCACTCAGCTCTGAACCTCACCTTTCATCTAGGCGGCACACAGACAGGAGCCTTGGT	1159
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Qy	1160	GCCCTGCCCTCCCTTTTATAGGCGGCGTGGATGGAGGTCTCTCTCCCTAGGCTGCCCGAG	1219
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Qy	1220	GCTCAGTGTGCCA-TCTCTGCAGCCTGTGTGAAGCTGTACACCTCATCAAGAACCG	1278
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* 19828 21056: contig of 1229 bp in length
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* 22213 22312: gap of unknown length
* 22313 23955: contig of 1643 bp in length
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* 36056 36155: gap of unknown length
* 36156 37400: contig of 1245 bp in length
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* 37501 39325: contig of 1825 bp in length
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* 39426 41018: contig of 1593 bp in length
* 41019 41118: gap of unknown length
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* 98382 98481: gap of unknown length
* 98482 102086: contig of 3605 bp in length
* 102087 102186: gap of unknown length
* 102187 104593: contig of 2407 bp in length
* 104594 104693: gap of unknown length
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Best Local Similarity 68.1%; Pred. No. 8.3e-38;
Matches 408; Conservative 0; Mismatches 123; Indels 68; Gaps 7;

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DB 113906 TCCTCTGGGAAGCAGAGGAGGAGGAACTTTGGTTCCTG-----TTAGGGGACC 113855
QY 1184 TGGATGAGGTTGTCTCTCCTAGGTGCCCGAGGCTCACTGC-TCCCATCTCTGCAG 1242
DB 113854 TCAGATGAGGSCCTCT--ACCATGTTGCTTCTGTCTCACTGCTTCTGTCTCCCTAAG 113798
QY 1243 CCTGTTGAAGCTGTCTACACCTCTCAAGAACCAGATCCATCCCTGCTGTCTTGA 1302
DB 113797 TCTATTTGAAGCTGTCTATGCCCTCATCAAGAACCAGATCCACCCCTGCGGTCTTGA 113738
QY 1303 CCGGTGTCAGGCAAGTACTCCATCTTCACACAAACCCCTGCTCAAGTTCTCTGCA 1362
DB 113737 CCCGTCTCTGGCAGTGTCTCTACATCTCAACAAAGAGGCTACTCAAGTTCTCTGCA 113678
QY 1363 CATCTTTGAAGCTGGGCCAGGTGGGAGGAGAGGAGAGCTGGGAGGTGATCAGAG 1422
DB 113677 TATATTTGAGCCTGGG---ATGCTGGAAGAGGAGAGCTCGGAGATGCTC--- 113625
QY 1423 GGCCTGAGGAGTCTCAGCCCTAGAGCTGCTGGGAGAGAGCTGGGAGCCCTCTTGAAGCT 1482
DB 113624 -----TAGATCCAGTGTCT 113611
QY 1483 GCTGGATCCCTGATCTCCACCTGGTCCCTCACTACACAGGTCTCCCTGTCGCCCGGCC 1542
DB 113610 TCATCTGATGAGATCACTACCTGTCCCATCCC--ACAGGCTGCCCTGTTCGCCCGGCC 113553
QY 1543 CTCCTTCTCTACCGCACTATCCAGATTTGGGATCGGCACATCCGAGACTTGGCTGT 1602
DB 113552 CTCCTTCTCTGCGCACTATCCAGACTTGGGATCGGCACATCCGAGATTAGCTGT 113493
QY 1603 GGTCTGGAGACAGCACCATCTCTGACCTGGACATCTTGTGGACGGGTGTGTC 1662
DB 113492 AGTTCTGGAACAGCTCTATCTCTGACGCGCTGGACATCTTGTGGACCGACAGGTGTC 113433
QY 1663 TGCACCTGCTGTGCTCAAGCAATGTGTGTACCCACCCAGGATGAGAGCTTCGGGTGG 1721
DB 113432 TGCACCTGCTGTGCTCAAGCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 113375

RESULT 7
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LOCUS Rattus norvegicus clone CH230-917, *** SEQUENCING IN PROGRESS ***,
54 unordered pieces.
DEFINITION AC129703
ACCESSION AC129703
VERSION AC129703.2 GI:22094278
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 190183)

AUTHORS

Muzny,D,Marie., Metzker,M, Lee., Abramson,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalbechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burtelli,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,J., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,F., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Louisedge,H., Lorzado,R.J., Lu,X., Ma,J., Maneshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhinney,S., Mcleod,M., Mcneill,T., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokeme,O., Okwuonu,G., Olatunpungoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE

JOURNAL

Unpublished

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

COMMENT

On Aug 3, 2002 this sequence version replaced gi:22038439.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GDBC
Center clone name: CH230-917
----- Summary Statistics
Sequencing vector: Plasmid:

Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 141109 bases at least Q40
Consensus quality: 148891 bases at least Q30
Consensus quality: 155675 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 54 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 2710: 2803: gap of unknown length
* 2810: 4026: contig of 1217 bp in length
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DEFINITION	Sequence 3 from Patent WO0120003.				
ACCESSION	AX099776				
VERSION	AX099776.1	GI:13538810			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 2109) Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.				
TITLE	Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof				
JOURNAL	Patent: WO 0120003-A 3 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ; Andersson, leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)				
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BASE COUNT	458 a 621 c 560 g 470 t				
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Query Match	9.8%; Score 168.2; DB 6; Length 2109;				
Best Local Similarity	95.6%; Pred. No.1e-30;				
Matches 173;	Conservative 0; Mismatches 8; Indels 0; Gaps 0;				
QY	1510 CCATCTTAACCAAGGTTTCCCTGCTGCCCGGCCCTCCCTCTCTACCGCACTATCCAAGA 1569				
Db	909 CCTGCACATCTTTGGTTCCTGCTGCCCGGCCCTCCCTCTCTACCGCACTATCCAAGA 968				
QY	1570 TTTGGCATCGGCACATTCGCAGACTTGGCTGTGGTGTGGAGACAGCACCATCTCTGAC 1629				
Db	969 TTTGGGCATCGGCACATTCGCAGACTTGGCTGTGGTGTGGAGACAGCACCATCTCTGAC 1028				
QY	1630 TGCATCGGACATCTTTGTGGACCGGGGTGTGTCTGCATCGCTGTGTCAACGAATGTGG 1689				
Db	1029 TGCATCGGACATCTTTGTGGACCGGGGTGTGTCTGCATCGCTGTGTCAACGAATGTGG 1088				
QY	1690 T 1690				
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Db	1089 T 1089				
RESULT 10					
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LOCUS	AX099802	2115 bp	DNA	linear	PAT 02-APR-2001
DEFINITION	Sequence 29 from Patent WO0120003.				
ACCESSION	AX099802				
VERSION	AX099802.1	GI:13538836			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 2115) Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.				

TITLE	Chardon,P. Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof					
JOURNAL	PATENT: WO 0120003-A 29 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ; Andersson, Lelf (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)					
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CDS	BASE COUNT 460 a 622 g 562 g 471 t ORIGIN					
Query Match	9.8%; Score 168.2; DB 6; Length 2115;					
Best Local Similarity	95.6%; Pred. No. 1e-30;					
Matches 173; Conservative	0; Mismatches 8; Indels 0; Gaps 0;					
QY	1510	CCATCCTAACAGGGTTCCTGTGCGGCCGCCCTCTTCCTACGCACATATCCAAGA	1569			
Db	915	CCTGCACATCTTTGGTTCCTGTGCGGCCGCCCTCTTCCTACGCACATATCCAAGA	974			
QY	1570	TTTGCGCATCGGCACATTCCGAGACTTGGCTGTGGTGTGGAGACAGACCACCTCTGAC	1629			
Db	975	TTTGCGCATCGGCACATTCCGAGACTTGGCTGTGGTGTGGAGACAGACCACCTCTGAC	1034			
QY	1630	TGCACCTGGACATCTTTGTGGACGGCGTGTCTGCACCTGCTGTGTCAACGAATGTGG	1689			
Db	1035	TGCACCTGGACATCTTTGTGGACGGCGTGTGTGCACCTGCTGTGTCAACGAATGTGG	1094			
QY	1690 T	1690				
Db	1095 T	1095				
RESULT 11						
LOCUS	AF214519					
DEFINITION	Homo sapiens AMP-activated protein kinase gamma subunit (PRKG3) mRNA, complete cds.					
ACCESSION	AF214519					
VERSION	AF214519.1 GI:8215681					
KEYWORDS	2115 bp mRNA linear PRI 03-JUN-2000					
SOURCE	Homo sapiens.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
AUTHORS	Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Galliard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. and Andersson,L.					
TITLE	A mutation in PRKG3 associated with excess glycogen content in pig skeletal muscle					
JOURNAL	Science 288 (5469), 1248-1251 (2000)					
MEDLINE	20280150					
PUBMED	10818001					
AUTHORS	2 (bases 1 to 2115) Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Galliard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,					

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BASE COUNT
ORIGIN

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Query Match	9.8%	Score 168.2	DB 9	Length 2115
Best Local Similarity	95.6%	Pred. No. 1e-30		
Matches 173	Conservative 0	Mismatches 8	Indels 0	Gaps 0
QY	1510	CCATCTCTAACACAGGCTTCCCTGCTGGCCGGCCCTCTTCTCTACGCACATATCCAAGA	1569	
Db	915	CCTGCACATCTTTGTTTCCCTGCTGGCCGGCCCTCTTCTCTACGCACATATCCAAGA	974	
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RESULT 12	
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DEFINITION	Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit (AMPK gamma 3 gene).
ACCESSION	AJ249977
VERSION	AJ249977.1 GI:6688200
KEYWORDS	AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Cheung,P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D.
TITLE	Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
JOURNAL	Biochem. J. 346 Pt 3, 659-669 (2000)
MEDLINE	20164049
PUBLISHED	10698692

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REFERENCE          2 (bases 1 to 2290)
AUTHORS           Carling,D.
TITLE             Direct Submission
JOURNAL           Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC
                  Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
                  London, W12 0NN, UNITED KINGDOM
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[illegible]

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DEFINITION	***, 74 unordered pieces.
ACCSSION	AC127107
VERSION	AC127107.1 GI:21743918
KEYWORDS	HTG; HTGS_PHASE1.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE	Rattus. 1 (bases 1 to 192968)
AUTHORS	Muzny,D.M., Adams,C.C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Albrooks,S.L., Anaratunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbaria,J., Benton,J.F., Bimarge,K., Blankenburg,K., Bonnin,D., Bouch,J., Bowie,S., Brivea,M., Brown,E., Brown,M., Bryant,N.P., Buyak,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

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 Weinstock, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 192968)
 Worley, K.C.
 Direct Submission
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GNHC
 Center clone name: CH230-206A13
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 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 130676 bases at least Q40
 Consensus quality: 139439 bases at least Q30
 Consensus quality: 146503 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 74 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
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 * 53798 55479: contig of 1681 bp in length
 * 55479 55579: gap of unknown length
 * 55579 57721: contig of 2142 bp in length
 * 57721 57821: gap of unknown length
 * 57821 59554: contig of 1733 bp in length
 * 59554 59654: gap of unknown length
 * 59654 62119: contig of 2465 bp in length
 * 62119 62219: gap of unknown length
 * 62219 64137: contig of 1918 bp in length

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:14:11 ; Search time 423 Seconds
(without alignments)
9167.709 Million cell updates/sec

Title: US-09-826-581-3
Perfect score: 1722
Sequence: 1 cctggccctcagatcaaga.....gatgagaggtcgtggctgga 1722

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :			
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2:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*		
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4:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*		
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21:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*		
22:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*		
23:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*		
24:	/SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
1	1722	100.0	1722 22 AAH43683 PRKAG3 intron 4 -
2	351	20.4	378 22 ABA44706 Human breast cell
3	351	20.4	378 22 ABA55162 Human foetal liver
4	351	20.4	378 22 ABA24907 Probe #3373 for ge
5	351	20.4	378 22 AAK03423 Human brain expres
6	351	20.4	378 22 AAK28874 Human bone marrow
7	351	20.4	378 22 AAK13465 Probe #3398 for ge
8	351	20.4	378 22 AAK134821 Probe #3507 used t
9	351	20.4	378 22 AA103344 Probe #3335 used t

C	10	351	20.4	378	24	ABS03407	Human genome-deriv
	11	196	11.4	547	22	ABA08485	Human AMP-activate
	12	168.2	9.8	1647	22	AAH43683	PRKAG3 cDNA. Homo
	13	168.2	9.8	2109	22	AAD03296	Human AMPK gamma s
	14	168.2	9.8	2115	22	AAD03320	Human AMPK gamma s
	15	148	8.6	1867	22	AAD03295	Pig AMPK gamma sub
	16	148	8.6	1873	22	AAD03319	Pig AMPK gamma sub
	17	148	8.6	1873	24	AAD36456	Pig wild-type PKNA
	18	148	8.6	1873	24	AAD36457	Pig PRKAG3 polymor
	19	148	8.6	1873	24	AAD36458	Pig PRKAG3 polymor
	20	148	8.6	1873	24	AAD36459	Pig PRKAG3 polymor
	21	148	8.6	1873	24	AAD36460	Pig PRKAG3 polymor
	22	148	8.6	2022	22	AAD03321	Sus scrofa PRKAG3
C	23	74.2	4.3	16525	22	AAK73303	Human immune/haema
	24	70.4	4.1	602	22	AAH35203	Human colon cancer
	25	70.4	4.1	1578	24	ABK84324	Human cDNA differe
	26	70.4	4.1	1691	21	AAC98774	Human pancreatic c
	27	70.4	4.1	1774	24	ABL39755	Human NS cDNA sequ
	28	68.8	4.0	1576	18	ABL785927	Mammalian AMPK-gam
	29	68	3.9	39651	23	ABL18856	Drosophila melanog
	30	65.8	3.8	3261	23	ABLI8857	Drosophila melanog
C	31	65	3.8	92	22	ABA49850	Human breast cell
	32	65	3.8	92	22	ABA67769	Human foetal liver
	33	65	3.8	92	22	ABA34826	Probe #13292 for g
	34	65	3.8	92	22	AAK16181	Human bone marrow
	35	65	3.8	92	22	AAK11922	Human brain expres
	36	65	3.8	92	22	AAI22692	Probe #12625 for g
	37	65	3.8	92	22	AAI47988	Probe #16674 used
	38	65	3.8	92	22	AAI08354	Probe #8345 used t
C	39	65	3.8	92	24	ABS15953	Human genome-deriv
	40	63.8	3.7	1435	20	AAH06882	Disease associated
	41	63.8	3.7	1467	23	AAH84265	DNA encoding novel
	42	63.8	3.7	2223	22	AAH14839	Human cDNA sequenc
	43	62.6	3.6	350	21	AAC01661	Human secreted pro
	44	57.2	3.3	735	22	AAH07561	Human cDNA clone (
	45	49.8	2.9	2303	23	AAH84267	DNA encoding novel

ALIGNMENTS

RESULT 1
AAH43683
ID AAH43683 standard; DNA; 1722 BP.

XX AC AAH43683;

DT 21-JAN-2002 (first entry)

XX DE PRKAG3 intron 4 - intron 10.

XX KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ds.

XX OS Homo sapiens.

Key	Location/Qualifiers
FT Intron	1..13
FT	/*tag= a
FT	/number= "Intron 4"
FT	/note= "3' portion of intron 4"
FT	14..95
FT	/*tag= b
FT	/number= "Exon 5"
FT	96..552
FT	/*tag= c
FT	/number= "Intron 5"
FT	553..611
FT	/*tag= d
FT	/number= "Exon 6"
FT	612..736
FT	/*tag= e
FT	/number= "Intron 6"

QY 1201 CTCCTAGGTCGCCGAGGCTCACTGCTCCATCTCTGCAGCCGTGTTGAGCTGTCTA 1260
Db 1201 CTCCTAGGTCGCCGAGGCTCACTGCTCCATCTCTGCAGCCGTGTTGAGCTGTCTA 1260
QY 1261 CACCTCATCAAGAACCGATCCATGCGCTGCTGTTGACCCGGTGTGAGCAACGT 1320
Db 1261 CACCTCATCAAGAACCGATCCATGCGCTGCTGTTGACCCGGTGTGAGCAACGT 1320
QY 1321 ACTCCAGTCTTCACACACAAACCGCTGCTCAAGTTCCTGTCACATCTTTGTAAGCCCTGGG 1380
Db 1321 ACTCCAGTCTTCACACACAAACCGCTGCTCAAGTTCCTGTCACATCTTTGTAAGCCCTGGG 1380
QY 1381 CCCAGGTGGGAGAGGGGAGACCTGGGAGGTGATCAGAGGCTCAGAGTCTTCAG 1440
Db 1381 CCCAGGTGGGAGAGGGGAGACCTGGGAGGTGATCAGAGGCTCAGAGTCTTCAG 1440
QY 1441 CCTPAGCAGTGTGGGAGAGCTGGGAGCCCTTTGAAGCTGCTGGATCCCTGATCTCC 1500
Db 1441 CCTPAGCAGTGTGGGAGAGCTGGGAGCCCTTTGAAGCTGCTGGATCCCTGATCTCC 1500
QY 1501 ACCGTGTCCTCATCTAACACAGGTTCCTGCTGCGCCCGCCCTCCTTCCTACCGCAC 1560
Db 1501 ACCGTGTCCTCATCTAACACAGGTTCCTGCTGCGCCCGCCCTCCTTCCTACCGCAC 1560
QY 1561 TATCCAAAGATTGGGCATCGGCACATTCGGAGACTTGGCTGTGTGGTGGAGACAGCAC 1620
Db 1561 TATCCAAAGATTGGGCATCGGCACATTCGGAGACTTGGCTGTGTGGTGGAGACAGCAC 1620
QY 1621 CATCCTGACTGCAGTGCAGACATCTTTGTGGACCGCGTGTCTGCACTGCCCTGTGGTCAA 1680
Db 1621 CATCCTGACTGCAGTGCAGACATCTTTGTGGACCGCGTGTCTGCACTGCCCTGTGGTCAA 1680
QY 1681 CGAATGTGTATCCACCCAGGATGAGAGGCTCGGCTGGA 1722
Db 1681 CGAATGTGTATCCACCCAGGATGAGAGGCTCGGCTGGA 1722
RESULT 2
ABAA4706/c
ID ID ABAA4706 standard; DNA; 378 BP.
XX AC ABAA4706;
XX AC ABAA4706;
DT 01-FEB-2002 (first entry)
DE Human breast cell single exon nucleic acid probe #3401.
XX Human breast cell single exon probe; gene expression; breast;
XX Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX Homo sapiens.
XX OS
XX PN
XX PD
XX PD
XX PF
XX PF
XX PR
XX PR
XX PR
XX PR
XX PR
XX PR
XX PR
XX PR
XX PR
XX PR
XX PA
XX PA
XX PI
XX PI
XX DR
XX DR
XX OS
XX OS
PT New spatially-addressable set of single exon nucleic acid probes,

PT useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
XX Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English.
XX The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. the method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention.
CC Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
Query Match 20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CCTGCCCCCTCAGATCAAGAAGCCCTTTGCTCTGTTGGCCCAACGGTGTGCGGGCAGC 60
Db 362 CCTGCCCCCTCAGATCAAGAAGCCCTTTGCTCTGTTGGCCCAACGGTGTGCGGGCAGC 303
QY 61 CCTCTATGGGACAGCAAGAAGCAGAGCTTTTGGGTGAGGAGAGCTGGGAGGTGAAG 120
Db 302 CCTCTATGGGACAGCAAGAAGCAGAGCTTTTGGGTGAGGAGAGCTGGGAGGTGAAG 243
QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTTACGGTTTGTCTGGGCTGATCTGTGATAT 180
Db 242 GGAGATGGAGAGGTGAGGGGAGATCTTTACGGTTTGTCTGGGCTGATCTGTGATAT 183
QY 181 ACCACAAGCTTGGCTTCAGCCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 240
Db 182 ACCACAAGCTTGGCTTCAGCCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 123
QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGTCAATTTCCCATCTGTGAGCCGCT 300
Db 122 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGTCAATTTCCCATCTGTGAGCCGCT 63
QY 301 ATGACCAAGCTGACACCTTTTCACTCCGCTTACTGTCATGSCCCTGTGTCATAGTGTAGGG 360
Db 62 ATGACCAAGCTGACACCTTTTCACTCCGCTTACTGTCATGSCCCTGTG-CATAGTGTAGGG 4
QY 361 AGC 363
Db 3 AGC 1
RESULT 3
ABAA5162/c
ID ID ABAA5162 standard; DNA; 378 BP.
XX AC ABAA5162;
XX AC ABAA5162;
DT 01-FEB-2002 (first entry)
DE Human foetal liver single exon nucleic acid probe #3467.
XX Human foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
XX OS

PN WO200157277-A2.
XX
PD
XX
PF 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX Claim 1; SEQ ID NO 3467; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: the sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCTGGCCCTCAGATCAAGAAGCCCTTTCTGCTCTGGTGGCCACGGTGTGGGGCAGC 60
DB 362 CTGGCCCTCAGATCAAGAAGCCCTTTCTGCTCTGGTGGCCACGGTGTGGGGCAGC 303

QY 61 CCTCTATGGGACAGCAAGAAGAGAGCTTTGTGGTGGAGGAGAGCTGGGGAGGTGAAG 120
DB 302 CCTCTATGGGACAGCAAGAAGAGAGCTTTGTGGTGGAGGAGAGCTGGGGAGGTGAAG 243

QY 121 GGAGATGGAGGAGGTGAGGGGAGAGATCTTGACGGTTGTTCTGGGGCTGATCTGATAT 180
DB 242 GGAGATGGAGGAGGTGAGGGGAGAGATCTTGACGGTTGTTCTGGGGCTGATCTGATAT 183

QY 181 ACCACAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGGAAGTCCATCC 240
DB 182 ACCACAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGGAAGTCCATCC 123

QY 241 GAGATCTGATGCGCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
DB 122 GAGATCTGATGCGCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63

QY 301 ATGACCAAGCTCAGACCTTTACCTCCGCTACTGATGGCCGCTGTGCCATAGTCTAGG 360
DB 62 ATGACCAAGCTCAGACCTTTACCTCCGCTACTGATGGCCGCTGTGCCATAGTCTAGG 4

QY 361 AGC 363
DB 3 AGC 1

RESULT 4
ABA24907/c
ID ABA24907 standard; DNA; 378 BP.

XX ABA24907;
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #3373 for gene expression analysis in human heart cell sample.
XX
XX Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00666.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX Claim 1; SEQ ID NO 3373; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCTGGCCCTCAGATCAAGAAGCCCTTTCTGCTCTGGTGGCCACGGTGTGGGGCAGC 60
DB 362 CTGGCCCTCAGATCAAGAAGCCCTTTCTGCTCTGGTGGCCACGGTGTGGGGCAGC 303

QY 61 CCTCTATGGGACAGCAAGAAGAGAGCTTTGTGGTGGAGGAGAGCTGGGGAGGTGAAG 120
DB 302 CCTCTATGGGACAGCAAGAAGAGAGCTTTGTGGTGGAGGAGAGCTGGGGAGGTGAAG 243

QY 121 GGAGATGGAGGAGGTGAGGGGAGAGATCTTGACGGTTGTTCTGGGGCTGATCTGATAT 180
DB 242 GGAGATGGAGGAGGTGAGGGGAGAGATCTTGACGGTTGTTCTGGGGCTGATCTGATAT 183

QY 181 ACCACAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGGAAGTCCATCC 240
DB 182 ACCACAGCTTGGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGGAAGTCCATCC 123


```
Query Match      20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCTGCCCTCAGATCAAGAAGCCCTTTCTGCTCTGTCGTCGCAAGCGTGTGCGGCAGC 60
   |||
Db 362 CCTGCCCTCAGATCAAGAAGCCCTTTCTGCTCTGTCGTCGCAAGCGTGTGCGGCAGC 303
   |||
QY 61 CCTCTATGCGACAGCAAGACAGAGCTTTTGTGGTGAGGAGAGCTGGGAGGTGAAG 120
   |||
Db 302 CCTCTATGCGACAGCAAGACAGAGCTTTTGTGGTGAGGAGAGCTGGGAGGTGAAG 243
   |||
QY 121 GGAGATGAGAGGTGAGGGGAGATCTTGTACGGTTTCTGGGGCTGATCTCTGATAT 180
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Db 242 GGAGATGAGAGGTGAGGGGAGATCTTGTACGGTTTCTGGGGCTGATCTCTGATAT 183
   |||
QY 181 ACCACAAGCTTGGCTTCAGCCCAAGCCAGCCAGCGGCGGAGGAGTGAAGTCCATCC 240
   |||
Db 182 ACCACAAGCTTGGCTTCAGCCCAAGCCAGCCAGCGGCGGAGGAGTGAAGTCCATCC 123
   |||
QY 241 GGAGTCTGATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGAGCCGCT 300
   |||
Db 122 GGAGTCTGATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGAGCCGCT 63
   |||
QY 301 ATGACAGCTGACACCTTTTCACTCGCTACTGCTGATGCGCTGTGCTATAGTGTCTAGGG 360
   |||
Db 62 ATGACAGCTGACACCTTTTCACTCGCTACTGCTGATGCGCTGTGCTATAGTGTCTAGGG 4
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QY 361 AGC 363
   |||
Db 3 AGC 1

RESULT 7
AAI13465/c
ID AAI13465 standard; DNA; 378 BP.
XX
AC AAI13465;
XX
DT 12-OCT-2001 (first entry)
XX
DE DE Probe #3398 for gene expression analysis in human cervical cell sample.
XX
KW Probe: human; microarray; gene expression; cervical epithelial cell;
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US006070.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID NO 3398; 487pp; English.
XX
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```
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match      20.4%; Score 351; DB 22; Length 378;
Best Local Similarity 99.7%; Pred. No. 9e-83;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCTGCCCTCAGATCAAGAAGCCCTTTCTGCTCTGTCGTCGCAAGCGTGTGCGGCAGC 60
   |||
Db 362 CCTGCCCTCAGATCAAGAAGCCCTTTCTGCTCTGTCGTCGCAAGCGTGTGCGGCAGC 303
   |||
QY 61 CCTCTATGCGACAGCAAGACAGAGCTTTTGTGGTGAGGAGAGCTGGGAGGTGAAG 120
   |||
Db 302 CCTCTATGCGACAGCAAGACAGAGCTTTTGTGGTGAGGAGAGCTGGGAGGTGAAG 243
   |||
QY 121 GGAGATGAGAGGTGAGGGGAGATCTTGTACGGTTTCTGGGGCTGATCTCTGATAT 180
   |||
Db 242 GGAGATGAGAGGTGAGGGGAGATCTTGTACGGTTTCTGGGGCTGATCTCTGATAT 183
   |||
QY 181 ACCACAAGCTTGGCTTCAGCCCAAGCCAGCCAGCGGCGGAGGAGTGAAGTCCATCC 240
   |||
Db 182 ACCACAAGCTTGGCTTCAGCCCAAGCCAGCCAGCGGCGGAGGAGTGAAGTCCATCC 123
   |||
QY 241 GGAGTCTGATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGAGCCGCT 300
   |||
Db 122 GGAGTCTGATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGAGCCGCT 63
   |||
QY 301 ATGACAGCTGACACCTTTTCACTCGCTACTGCTGATGCGCTGTGCTATAGTGTCTAGGG 360
   |||
Db 62 ATGACAGCTGACACCTTTTCACTCGCTACTGCTGATGCGCTGTGCTATAGTGTCTAGGG 4
   |||
QY 361 AGC 363
   |||
Db 3 AGC 1

RESULT 8
AAI34821/c
ID AAI34821 standard; DNA; 378 BP.
XX
AC AAI34821;
XX
DT 17-OCT-2001 (first entry)
XX
DE DE Probe #507 used to measure gene expression in human placenta sample.
XX
KW Probe: microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
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PN W0200157188-A2.
XX 09-AUG-2001.
PD 05-FEB-2001; 2001WO-US3800.
XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX (HYSE-) HYSEQ INC.
PI Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-457740/49.
DR P-PSDB; ABB11241.
XX Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX Claim 1; Page 429; 1963pp; English.
PS Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, and hence
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
XX novel human polypeptide of the invention.

SQ Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
Query Match 11.4%; Score 196; DB 22; Length 547;
Best Local Similarity 95.3%; Pred. No. 9.6e-42;
Matches 202; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1510 CCATCTCAACAGGTTCCCTGTCGCCCGGCCCTCTTCCTTCACCGCACTATCAAGA 1569
DB 272 CCGGACATCTTTGGTTCCCTGTCGCCCGGCCCTCTTCCTTCACCGCACTATCAAGA 331
QY 1570 TTGGGCAATCGGCACATTCGAGACTTGGCTGTGGTGGAGACAGCACCCTCTGAC 1629
DB 332 TTGGGCAATCGGCACATTCGAGACTTGGCTGTGGTGGAGACAGCACCCTCTGAC 391

QY 1630 TGCACCTGGACATCTTTGTGTGGACCGCGCTGTCTGCACCTGCTGTGTCACGAATGTGG 1689
DB 392 TGCACCTGGACATCTTTGTGTGGACCGCGCTGTCTGCACCTGCTGTGTCACGAATGTGG 451
QY 1690 TACCCACCCCAAGGATGAGAGGCTCGGGCTGG 1721
DB 452 TACCCACCCCAAGGATGAGAGGCTCGGGCTGG 483

RESULT 12
AAH43685
ID AAH43685 standard; cDNA; 1647 BP.
XX
AC AAH43685;
XX
DT 21-JAN-2002 (first entry)
XX
DE PRKAG3 CDNA.
XX
KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
KW metabolic disease; diabetes; obesity; substitution; ss.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 20..1489
FT /tag= a
FT /product= "PRKAG3"
FT variation 230
FT /tag= b
FT /label= "C230G"
FT variation 559
FT /tag= c
FT /label= "H559C"
FT /note= "Silent variation"
FT variation 1037
FT /tag= d
FT /label= "C1037T"
FT /note= "Causes R340W"
PN W0200177305-A2.
PD 18-OCT-2001.
PF 06-APR-2001; 2001WO-SE00765.
PR 07-APR-2000; 2000US-195665P.
XX (AREX-) AREXIS AB.
XX Andersson L, Luthman H, Marklund S;
PI WPI; 2001-657170/75.
DR P-PSDB; QOB47679.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX Disclosure; Fig 5; 25pp; English.
PS This sequence represents the full length cDNA encoding the human
CC AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
CC the presence of the PRKAG3 DNA, or a variant, is useful in determining
CC a risk estimate of a metabolic disease, such as diabetes or obesity,
CC in a subject. The variation may occur in exons 3, 4 or 10. In exon
CC 3 variation may be a substitution of a G for a C at nucleotide 320,
CC resulting in the amino acid substitution P71A; in exon 4 variation may
CC be a substitution of a T for a C at nucleotide 550; and in exon 10
CC variation may be a substitution of a T for a C at nucleotide 1037,

```
CC resulting in the amino acid substitution R340W. There may also be
CC nucleotide variation in intron 6. The numbering of these
CC variations is based on the full length cDNA as given, rather than on
CC position 1 of the open reading frame.
XX
SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;

Query Match          9.8%; Score 168.2; DB 22; Length 1647;
Best Local Similarity 95.6%; Pred. No. 3.3e-34;
Matches 173; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1510 CCATCTTAACACAGGTTCCCTGCTGCGCCGCGCTCTCTCTACCGCACTATCCAGA 1569
Db 1009 CCTGCACATCTTTGGTTCCTGCTGCGCCGCGCTCTCTCTACCGCACTATCCAGA 1068
Qy 1570 TTTGGGCATCGGCACATTCGGACATTCGGCTGTGGTCTGGAGACAGCACCCATCCTGAC 1629
Db 1069 TTTGGGCATCGGCACATTCGGACATTCGGCTGTGGTCTGGAGACAGCACCCATCCTGAC 1128
Qy 1630 TGCACGTGACATCTTTGTGTGACCGCGGTGTGTCTGTGCATCCCTGTGGTCAAGCATGTGG 1689
Db 1129 TGCACGTGACATCTTTGTGTGACCGCGGTGTGTCTGTGCATCCCTGTGGTCAAGCATGTGG 1188
Qy 1690 T 1690
Db 1189 T 1189

RESULT 13
AAD03296
ID AAD03296 standard; DNA; 2109 BP.
XX
AC AAD03296;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
XX
KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH 5'UTR 1..471
FT /*tag= a
FT CDS 472..1389
FT /*tag= b
FT 3'UTR /product= "Human Prkag3 protein"
FT /*tag= c
XX
PN WO200120003-A2.
XX
PD 22-MAR-2001.
XX
PF 11-SEP-2000; 2000WO-EP09896.
XX
PR 10-SEP-1999; 99EP-0402236.
PR 18-MAY-2000; 2000EP-0401388.
XX
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.
PA (LOOF/) LOOFT C.
PA (KALM/) KALM E.
XX
PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
DR WPI: 2001-244810/25.
DR P-PSDB; AAE00221.
```

```
XX New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment of disorders
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy
XX
Claim 12; Fig 2; 71pp; English.
XX
The present sequence is a cDNA encoding human adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC PRKAG3. Mutation in Prkag3 results in an altered regulation of
CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
CC useful as therapeutic for treating carbohydrate metabolism disorders such
CC as diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX
SQ Sequence 2109 BP; 458 A; 521 C; 560 G; 470 T; 0 other;

Query Match          9.8%; Score 168.2; DB 22; Length 2109;
Best Local Similarity 95.6%; Pred. No. 3.3e-34;
Matches 173; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1510 CCATCTTAACACAGGTTCCCTGCTGCGCCGCGCTCTCTCTACCGCACTATCCAGA 1569
Db 909 CTGCACATCTTTGGTTCCTGCTGCGCCGCGCTCTCTCTACCGCACTATCCAGA 968
Qy 1570 TTTGGGCATCGGCACATTCGGACATTCGGCTGTGGTCTGGAGACAGCACCCATCCTGAC 1629
Db 969 TTTGGGCATCGGCACATTCGGACATTCGGCTGTGGTCTGGAGACAGCACCCATCCTGAC 1028
Qy 1630 TGCACGTGACATCTTTGTGTGACCGCGGTGTGTCTGTGCATCCCTGTGGTCAAGCATGTGG 1689
Db 1029 TGCACGTGACATCTTTGTGTGACCGCGGTGTGTCTGTGCATCCCTGTGGTCAAGCATGTGG 1088
Qy 1690 T 1690
Db 1089 T 1089

RESULT 14
AAD03320
ID AAD03320 standard; cDNA; 2115 BP.
XX
AC AAD03320;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
XX
KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 1..1395
FT /*tag= a
FT /product= "Human complete Prkag3 protein"
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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:14:11 ; Search time 2562 seconds

(without alignments)
10885.491 Million cell updates/sec

Title: US-09-826-581-3
Perfect score: 1722
Sequence: 1 cctggccctcagatcaaga.....gatgagagctcggcgctgga 1722

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpi:*
7: em_estro:*
8: em_hic:*
9: gb_esti:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	8.6	572	13	BI344527 373008 MA
2	132.4	7.7	413	9	AA178898 2p38d10.r
3	116.8	6.8	1042	17	AL248229 Tetraodon
4	88.8	5.2	591	13	Bj495978 Bj495978
5	84.6	4.9	728	13	Bj504184 Bj504184
6	82.6	4.8	933	13	BG919314 602817782

7	82.2	4.8	633	13	BJ072114
8	81.8	4.8	536	13	BM488662
9	80.2	4.7	595	13	BM487789
10	80.2	4.7	636	12	BG713637
11	80.2	4.7	647	13	BM440762
12	80.2	4.7	649	9	AJ395115
13	80.2	4.7	687	9	AJ451523
14	78.6	4.6	758	9	AJ396118
15	76.4	4.4	576	10	AV603335
16	73	4.2	564	10	AV608257
17	71	4.1	775	13	BI833269
18	70.4	4.1	448	9	AA558845
19	70.4	4.1	450	12	BF351397
20	70.4	4.1	455	9	AA578219
21	70.4	4.1	469	9	AL047390
22	70.4	4.1	473	10	BE166881
23	70.4	4.1	508	10	BE166874
24	70.4	4.1	558	14	BM710850
25	70.4	4.1	583	10	AW379936
26	70.4	4.1	584	14	BM765123
27	70.4	4.1	586	12	BG609812
28	70.4	4.1	591	10	AA410926
29	70.4	4.1	598	10	BE148626
30	70.4	4.1	616	10	AW956906
31	70.4	4.1	634	12	BG740148
32	70.4	4.1	668	12	BG705895
33	70.4	4.1	676	14	BM782063
34	70.4	4.1	698	14	BM764743
35	70.4	4.1	708	10	AA411228
36	70.4	4.1	710	13	BI223706
37	70.4	4.1	714	14	BM783383
38	70.4	4.1	726	13	BI768590
39	70.4	4.1	742	13	BI914634
40	70.4	4.1	746	12	BF528081
41	70.4	4.1	756	13	BI859947
42	70.4	4.1	782	13	BI819312
43	70.4	4.1	782	13	BI821538
44	70.4	4.1	795	12	BE871189
45	70.4	4.1	803	14	BQ216967

ALIGNMENTS

RESULT 1	BI344527	BI344527	572 bp	mrna	linear	EST 30-JUL-2001
LOCUS	373008	MARC 2P1G	Sus	scrofa	cdna	5', mRNA sequence.
DEFINITION	BI344527					
ACCESSION	BI344527.1	GI:15037807				
VERSION	EST.					
KEYWORDS	EST.					
SOURCE	Pig.					
ORGANISM	Sus scrofa					
REFERENCE	1 (bases 1 to 572)					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. Fahrenkrug, S.C., Ereking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keeler, J.W.					
TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Smith TPL USDA, ARS, Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smithemail.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options. PCR Primers FORWARD: AGGAACACGCTATGACCAT					

RESULT 6	933 bp	mRNA	linear	EST 05-JUN-2001					
BG919314	602817787921	NCI_CGAP_Mam6	Mus musculus	cDNA clone IMAGE:4946661 5'					
LOCUS									
DEFINITION	mRNA sequence.								
ACCESSION	BG919314								
VERSION	BG919314.1	GI:14299790							
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
REFERENCE									
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
JOURNAL									
COMMENT	<p>1 (bases 1 to 933)</p> <p>NIH-MGC http://mgc.nci.nih.gov/.</p> <p>National Institutes of Health, Mammalian Gene Collection (MGC)</p> <p>Unpublished (1999)</p> <p>Contact: Robert Strausberg, Ph.D.</p> <p>Email: gqabbs-remail.nih.gov</p> <p>Tissue Procurement: Jeffrey Green M.D.</p> <p>cDNA Library Preparation: Life Technologies, Inc.</p> <p>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)</p> <p>Clone Sequencing by: Incyte Genomics, Inc.</p> <p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</p> <p>plate: LLAM10895 row: d column: 22</p> <p>High quality sequence stop: 498.</p>								
FEATURES									
source	<p>1..933</p> <p>location/Qualifiers</p> <p>organism="Mus musculus"</p> <p>strain="FVB/N"</p> <p>db_xref="taxon:10090"</p> <p>clone="IMAGE:4946661"</p> <p>clone_lib="NCI_CGAP_Mam6"</p> <p>sex="female, virgin"</p> <p>tissue_type="infiltrating ductal carcinoma"</p> <p>dev_stage="5 months"</p> <p>lab_host="DH10B"</p>								
BASE COUNT	244 a	292 c	238 g	159 t					
ORIGIN									
Query Match	4.8%	Score 82.6	DB 13	Length 933					
Best Local Similarity	52.1%	Pred. No. 5	5e-09						
Matches 232	Conservative	0	Mismatches 209	Indels 4					
Gaps	2								
Qy	1242	GCCTGTTTGAAGCTGTCATCACACCTCATCAAGAACGGATCCATCGCTGCCTGCTTCGTTGTTG	1301						
Db	7	GTCCGGTGTATGCTGCTCTCTTTATTAAATCGAAATAAGATCCACAGCTCCGATATCG	66						
Qy	1302	ACCCGGGTGCAGGCAACGTA	1302						
Db	67	ACCCAGAGTCAGCAGACACCTTGATGATCTTACTCAACGGGATCCTCAAGTTCCTCA	126						
Qy	1362	ACATCTTTTGTAAAG---CCTGGCCGAGTGGGAGGAGGAGACCTCGGACAGGTGATC	1418						
Db	127	AGTTGTTTGTAAAGTAACCTCAGGCAATCATCCGATACGTCTGTAACCTGACGACACAC	186						
Qy	1419	AGAGGGCTCAGGAGTCTTCAGCCCTAGCAGTGGTGGGGAAGAGCTGGGAGCCCTCTTGA	1478						
Db	187	AGAGCGGTTGGGGACAGAGGCGGTGTTGGTGTTCATGATTGAGCGTAGCACCTCCATG	246						
Qy	1479	AGCTGCGTGGATCCCTGATCTCCACCTGGTCCCATCCCTCAACAGGGTCCCTGCTGCCCC	1538						
Db	247	CTCT-ATCCGGAAGCACTGCAAGCAATGCCCTTCCTCAGATCACCAGGTTCCTCCCA	305						
Qy	1539	GGCCCTCTTCTCTACCGCACTATCCAAAGATTGGGATTCGGACATTCGGAGACTGG	1598						

Db	306	AGCCGGAAATTCAGTCTCCTCAGAGAGCTGCAGATTGGACCTATGCAATATTTG	365
Qy	1599	CTGTGGTGCCTGGAGACAGACACCCATCTCTGACTGCACTGGACATCTTTGTGGACCGCGCTG	1658
Db	366	CCATGGTCCGTACTACCAGCGCTGTCTACGTGGCTCTGGGCATCTTGTACAGACCCGAG	425
Qy	1659	TGCTGCGACHTGCGCTGHTGGTCAACGA	1683
Db	426	TCTCCGCTTACCTGTAGTGGATGA	450
RESULT 7			
BJ072114			
LOCUS			
DEFINITION			
BJ072114 NIBB Mochii normalized xenopus tailbud library			
laevis cDNA clone XL096j16 5', mRNA sequence.			
ACCESSION			
BJ072114			
VERSION			
BJ072114.1 GI:17502303			
KEYWORDS			
EST.			
SOURCE			
ORGANISM			
Xenopus laevis			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;			
Xenopodinae; Xenopus.			
REFERENCE			
1 (bases 1 to 633)			
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara			
Y.			
TITLE			
Expressed genes in X. laevis embryo			
JOURNAL			
Unpublished (2001)			
COMMENT			
Contact: Tadasu Shin-i			
Center For Genetic Resource Information			
National Institute of Genetics			
1111 Yata, Mishima, Shizuoka 411-8540, Japan			
Tel: 81-559-81-6856			
Fax: 81-559-81-6855			
Email: tschini@genes.nig.ac.jp.			
FEATURES			
source			
1..633			
/organism="Xenopus laevis"			
/db_xref="taxon:8355"			
/clone="XL096j16"			
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library"			
/tissue_type="whole embryo"			
/dev_stage="stage 25"			
/note="Vector: pBSRM3; Site.1: NotI; Site.2: EcoRI; cDNAs			
were oligo-dT primed and directionally cloned. Staging			
according to Nieuwkoop and Faber. Library is subtracted			
and was constructed by N. Garrett and A.M. Zorn,			
(Wellcome/CRC Institute)."			
BASE COUNT			
144 a 162 c 148 g 179 t			
ORIGIN			
Query Match 4.8%; Score 82.2; DB 13; Length 633;			
Best Local Similarity 73.4%; Pred. No. 5.8e-09;			
Matches 105; Conservative 0; Mismatches 38; Indels 0; Gaps 0;			
Qy	1228	CTCCCATCTCTGCAGCGCTGTTTGAAGCTGTCTACACCTCATCAAGACCGCTCCATCG	1287
Db	10	CTCCCCAGCAGACAGCGCTTTCCAGCTGTGTATTCACTCATCAAGAATAAGATCCACGG	69
Qy	1288	CTCGCTGTTCTTGACCCGGTGTGAGCGACGTACTCCACATCTCTCACACACAAAGCGCT	1347
Db	70	CTTACCAGTAATGAGTCCCGGTATCTGCGACATCTTGTGCATCTCTCAGCATAAAGCGCT	129
Qy	1348	GCTCAAGTTCTCGCATCTTTG	1370
Db	130	ACTCAAGTTCCTTCACCTCTTG	152
RESULT 8			
BM488662			
LOCUS			
BM488662			
DEFINITION			
Xenopus laevis			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;			

DEFINITION pgm2n.pk008.g21 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk008.g21.5' similar to gb|AAC52580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus], mRNA sequence.

ACCESSION BM488662

VERSION BM488662.1 GI:18609593

KEYWORDS EST.

SOURCE chicken.

ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

AUTHORS 1 (bases 1 to 536)

TITLE Cogburn, L.A. and Monsonego-Ornan, E.

JOURNAL ESIs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome Project

COMMENT Unpublished (2002)

CONTACT: Larry A. Cogburn

UNIVERSITY OF Delaware

TOWNSEND HALL, Newark, DE 19717, USA

TEL: 302-831-1335

FAX: 302-831-2822

EMAIL: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES

source

1..536

/organism="Gallus gallus"

/strain="Commercial broiler and Ottawa Res. Centre

Strains 90 & 21"

/db_xref="taxon:9031"

/clone="pgm2n.pk008.g21"

/cclone.lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)"

/sex="Male and Female"

/tissue.type="Breast muscle, leg muscle and epiphyseal growth plate"

/dev.stage="Breast, leg; Embryo(d19); post-hatch(1d,1,3,5,7,9,11 weeks); growth plate(1d,7d,14d post-hatch)"

/lab.host="E. coli EMDH10B"

/note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

BASE COUNT 117 a 171 c 132 g 116 t

ORIGIN

Query Match 4.8%; Score 81.8; DB 13; Length 536;

Best Local Similarity 70.1%; Pred. No. 6.7e-09;

Matches 110; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1228 CTCCTATCTCTGACGCTGTTTGAAGCTGTCTACACCTCATCAAGACCGGATCATCG 1287

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 85 CTCCTCCCAACGCCACGCTTTTGTATGCGCTCTCTCCCTGATCGGCAATAAGATCCACCG 144

QY 1288 CTGCGCTGTTCTTGACCGGTGTCAGGCAACGTACTCTACATCTCTACACACAAAGCGCT 1347

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Db 145 CTCCTCCGCTATGACCCCGACCTCTCCGCAACACTCTCTACATCTCTACCCACAAAGCAT 204

QY 1348 GCTCAAGTTCCTGCACATCTTTGTAAGCCTGGGCCCA 1384

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Db 205 CCTCAAGTTCCTCAAACTCTTTATTCGACAGGTGCCA 241

RESULT 9

BM487789

LOCUS

DEFINITION pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk005.j24.5' similar to gb|AAC52580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus], mRNA sequence.

ACCESSION BM487789

VERSION BM487789.1 GI:18608720

KEYWORDS EST.

SOURCE chicken.

ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

AUTHORS 1 (bases 1 to 595)

TITLE Cogburn, L.A. and Monsonego-Ornan, E.

JOURNAL ESIs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome Project

COMMENT Unpublished (2002)

CONTACT: Larry A. Cogburn

UNIVERSITY OF Delaware

TOWNSEND HALL, Newark, DE 19717, USA

TEL: 302-831-1335

FAX: 302-831-2822

EMAIL: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES

source

1..595

/organism="Gallus gallus"

/strain="Commercial broiler and Ottawa Res. Centre

Strains 90 & 21"

/db_xref="taxon:9031"

/clone="pgm2n.pk005.j24"

/cclone.lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)"

/sex="Male and Female"

/tissue.type="Breast muscle, leg muscle and epiphyseal growth plate"

/dev.stage="Breast, leg; Embryo(d19); post-hatch(1d,1,3,5,7,9,11 weeks); growth plate(1d,7d,14d post-hatch)"

/lab.host="E. coli EMDH10B"

/note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

BASE COUNT 126 a 199 c 137 g 133 t

ORIGIN

Query Match 4.7%; Score 80.2; DB 13; Length 595;

Best Local Similarity 69.4%; Pred. No. 1.7e-08;

Matches 109; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1228 CTCCTATCTCTGACGCTGTTTGAAGCTGTCTACACCTCATCAAGACCGGATCATCG 1287

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QY 1348 GCTCAAGTTCCTGCACATCTTTGTAAGCCTGGGCCCA 1384

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Db 409 CCTCAAGTTCCTCAAACTCTTTATTCGACAGGTGCCA 445

RESULT 10

BM487789

LOCUS

DEFINITION pgm2n.pk008.c13 Normalized Liver Library Gallus gallus cDNA clone pgm2n.pk008.c13.5' similar to gi|4506061 ref|NP_002724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens] gi|12737489 ref|Xp_006778.2| protein kinase, AMP-activated, gamma 1 non, mRNA sequence.

ACCESSION BM487789

VERSION BM487789.1 GI:14007587

KEYWORDS EST.

SOURCE chicken.

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ORGANISM      Gallus gallus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
REFERENCE      1 (bases 1 to 636)
AUTHORS        Burnside,J., Morgan,R.W. and Cogburn,L.A.
TITLE          Chicken ESTs from a normalized liver library
JOURNAL        Unpublished (2001)
COMMENT        Contact: Joan Burnside
               Molecular Endocrinology
               University of Delaware
               40 Townsend Hall, Newark, DE 19717, USA
               Tel: 302-831-1345
               Fax: 302-831-3411
               Email: joane@udel.edu, www.chickest.udel.edu.

FEATURES      1..636
               Location/Qualifiers
               /organism="Gallus gallus"
               /db_xref="taxon:9031"
               /clone="pgrln.pk008.cl3"
               /clone_lib="Normalized Liver Library"
               /sex="Male and Female"
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BASE COUNT    129 a 215 c 167 g 119 t 6 others
ORIGIN
Query Match   4.7%; Score 80.2; DB 12; Length 636;
Best Local Similarity 69.4%; Pred. No. 1.7e-08;
Matches 109; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1228 CTCCTCATCTGCGAGCGCTGTTGAAGCTGTCTACACCTCATCAAGACCGGATCCATCG 1287
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QY 1288 CTTGCGCTGTTCTGACCGGCTGTCAGGCAAGTACTCCACATCTCCACACACAAAGCGCT 1347
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QY 1348 GCTCAAGTCTCCTGCACATCTTTGTAAGCTGGGCCCA 1384
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DB 549 CCTCAAGTCTCCTCAAACTCTTTATTGCGAGAGTGCCCA 585

RESULT 11
LOCUS          BM440762
DEFINITION    pgrln.pk002.l9 Normalized Chicken Reproductive Tract cDNA Library
               (pgrln) Gallus gallus cDNA clone pgrln.pk002.l9 5' similar to
               gi|4506061 ref|NP_002724.1| protein kinase, AMP-activated, gamma 1
               non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated,
               noncatalytic, gamma-1 [Homo sapiens] gi|12737489 ref|XP_006778.2|
               protein kinase, AMP-activated, gamma 1, mRNA sequence.
ACCESSION      BM440762
VERSION        BM440762.1 GI:18471537
KEYWORDS       EST.
SOURCE         chicken.
ORGANISM       Gallus gallus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
REFERENCE      1 (bases 1 to 647)
AUTHORS        Cogburn,L.A. and Nys,Y.
TITLE          ESTs from Normalized Chicken Reproductive Tract cDNA library-
               University of Delaware and INRA, Tours-Poultry Unit Project
JOURNAL        Unpublished (2002)
COMMENT        Contact: Larry A. Cogburn
               University of Delaware
               Townsend Hall, Newark, DE 19717, USA
               Tel: 302-831-1335
               Fax: 302-831-2822
               Email: cogburn@udel.edu, www.chickest.udel.edu.

ORGANISM      Gallus gallus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
REFERENCE      1..647
               Location/Qualifiers
               /organism="Gallus gallus"
               /strain="Commercial broiler and layer"
               /db_xref="taxon:9031"
               /clone="pgrln.pk002.l9"
               /clone_lib="Normalized Chicken Reproductive Tract cDNA
               Library (pgrln)"
               /sex="Male and Female"
               /tissue_type="Testis, ovary and oviduct"
               /dev_stage="Various stages;embryonic, post-hatch, immature
               and sexually-mature"
               /lab_host="E. coli EMDH10B"
               /note="Vector: pCMVSPORT6; Library made from three total
               RNA pools from each tissue (testis 25%, ovary 25%, and
               oviduct 50% of final RNA pool); Single pass sequencing
               from 5'-end"
BASE COUNT    137 a 222 c 160 g 128 t
ORIGIN
Query Match   4.7%; Score 80.2; DB 13; Length 647;
Best Local Similarity 69.4%; Pred. No. 1.7e-08;
Matches 109; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1228 CTCCTCATCTGCGAGCGCTGTTGAAGCTGTCTACACCTCATCAAGACCGGATCCATCG 1287
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DB 393 CTCCTCATCTGCGAGCGCTGTTGAAGCTGTCTACACCTCATCAAGACCGGATCCATCG 452
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QY 1288 CTTGCGCTGTTCTGACCGGCTGTCAGGCAAGTACTCCACATCTCCACACACAAAGCGCT 1347
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DB 453 CTTGCGCTGTTCTGACCGGCTGTCAGGCAAGTACTCCACATCTCCACACACAAAGCGCT 512
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QY 1348 GCTCAAGTCTCCTGCACATCTTTGTAAGCTGGGCCCA 1384
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DB 513 CCTCAAGTCTCCTCAAACTCTTTATTGCGAGAGTGCCCA 549

RESULT 12
LOCUS          AJ395115
DEFINITION    dkfz426 Gallus gallus cDNA clone 21c2r1, mRNA sequence.
ACCESSION      AJ395115
VERSION        AJ395115.1 GI:7125706
KEYWORDS       EST.
SOURCE         chicken.
ORGANISM       Gallus gallus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
REFERENCE      1 (bases 1 to 649)
AUTHORS        Abdurakhmanov,I., Lodygin,D., Gereth,P., Arakawa,H., Law,A., Plachy
               ,J., Korn,B. and Buerstedde,J.M.
TITLE          A large database of chicken bursal ESTs as a resource for the
               analysis of vertebrate gene function
JOURNAL        Genome Res. 10 (12), 2062-2069 (2000)
MEDLINE        20568495
COMMENT        Contact: Buerstedde JM
               Cellular Immunology
               Heinrich-Pette-Institute
               Martinstr. 52, 20251 Hamburg, Germany
               Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES      1..649
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               /organism="Gallus gallus"
               /strain="CB"
               /db_xref="taxon:9031"
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               /clone_lib="dkfz426"
               /tissue_type="Bursa of Fabricius"
               /cell_type="bursal lymphocyte"
               /dev_stage="2-3 weeks old"
BASE COUNT    130 a 227 c 155 g 137 t
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AJ396118	LOCUS	AJ396118	dkfz426	Gallus gallus	clone 25f15r1, mRNA sequence.
	DEFINITION	AJ396118			
	ACCESSION	AJ396118			

JOURNAL MEDLINE	Nucleic Acids Res. 29 (22), E108 (2001)
COMMENT	21570554 Contact: Yoshikazu Sugimoto Animal Genetics Division Shirakawa Institute of Animal Genetics

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 14, 2003, 11:14:12 ; Search time 90 Seconds

(without alignments)
5867.749 Million cell updates/sec

Title: US-09-826-581-3
Perfect score: 1722
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES												
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1	68.8	4.0	1576	3	US-09-101-146-63	Sequence 63, Appl						
2	67.6	3.9	7218	1	US-08-232-463-14	Sequence 14, Appl						
3	63.8	3.7	1435	2	US-08-878-989-14	Sequence 14, Appl						
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C 8	39	2.3	53526	3	US-08-658-136-2	Sequence 2, Appl						
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12	37.4	2.2	319	4	US-09-165-264-8	Sequence 8, Appl						
13	36.2	2.1	320	4	US-09-165-264-13	Sequence 13, Appl						
14	36	2.1	320	4	US-09-165-264-11	Sequence 11, Appl						
C 15	36	2.1	2278	1	US-07-959-943-6	Sequence 6, Appl						
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	35.4	2.1	318	4	US-09-165-264-12	Sequence 12, Appl						
19	35.2	2.0	4066	3	US-09-215-966-21	Sequence 21, Appl						
20	34.6	2.0	1001	4	US-09-641-638-160	Sequence 160, App						
21	34.6	2.0	1001	4	US-09-641-638-161	Sequence 161, App						
22	34.4	2.0	707	4	US-08-998-416-876	Sequence 876, App						
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24	34.2	2.0	6306	1	US-08-467-950-3	Sequence 3, Appl						
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27	34.2	2.0	6306	1	US-08-195-487-3	Sequence 3, Appl						

28	34.2	2.0	6306	2	US-08-483-924-3	Sequence 3, Appl
29	34.2	2.0	6306	5	PCT-US93-06160-3	Sequence 3, Appl
C 30	34.2	2.0	7705	2	US-08-687-080-115	Sequence 115, App
C 31	34	2.0	2117	4	US-09-155-768-1	Sequence 1, Appl
C 32	34	2.0	6232	4	US-08-456-200B-11	Sequence 11, Appl
C 33	34	2.0	7175	1	US-08-455-543A-8	Sequence 8, Appl
C 34	34	2.0	7175	2	US-08-193-078B-8	Sequence 8, Appl
C 35	34	2.0	7175	2	US-08-223-305C-8	Sequence 8, Appl
C 36	34	2.0	7175	2	US-08-149-097D-8	Sequence 8, Appl
C 37	34	2.0	7175	3	US-08-949-386-8	Sequence 8, Appl
C 38	34	2.0	7175	4	US-08-450-562-8	Sequence 8, Appl
C 39	34	2.0	7175	4	US-08-984-709A-8	Sequence 8, Appl
C 40	34	2.0	7175	4	US-08-450-273-8	Sequence 8, Appl
C 41	34	2.0	7177	4	US-09-268-163-7	Sequence 7, Appl
C 42	34	2.0	7266	3	US-08-713-118-1	Sequence 1, Appl
C 43	34	2.0	7266	3	US-09-452-007-1	Sequence 1, Appl
C 44	34	2.0	7362	1	US-08-455-543A-7	Sequence 7, Appl
C 45	34	2.0	7362	2	US-08-193-078B-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-101-146-63
; Sequence 63, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincents Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA: US/09/101,146
; APPLICATION NUMBER: 32,257
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1576
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
US-09-101-146-63

Query Match 4.0%; Score 68.8; DB 3; Length 1576;
Best Local Similarity 67.4%; Pred. No. 4.9e-09;
Matches 97; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
OY 1240 CAGCCTGTGTTAAGCTGTCTACACCTCATCAAGACCGGATCATCGCTGCTTCT 1299
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Db 501 CAGCTTGTGATGCTGTCTCTTCAATTAATTCGACAAAGATCCACAGGCTGCCAGTTAT 560
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Db 561 TGACCCAGAAATCAGCAATACCTTTGTACATCTCACCACAAAGCGCATCTCGAAGTTCT 620
Qy 1360 GCACATCTTTGTAAGCGCTGGCC 1383
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Db 621 CAATTTGTTATCATCTAGTTCC 644

RESULT 2
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.5
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683 4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-Fls
; US-08-232-463-14

Query Match 3.9%; Score 67.6; DB 1; Length 7218;
Best Local Similarity 6.2%; pred. No. 1.9e-08;
Matches 25; Conservative 223; Mismatches 152; Indels 0; Gaps 0;

Qy 906 CTGACGGAGGAGGAGCTGCTGGGACTCGAAGGTGAGGAGGACCGGCTCCCTGGCC 965
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Db 1018 CTCACAGAAATTAATTCGAGCTTGGCTGAGTCCAGGAGCTTGGCATTTTTTTTTT 1077
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Qy 1026 TCTCTCTAATGATAGGTGGTGTCTGTCTCATTCACCTGAGCGCTCCTCCACAGT 1085
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Qy 1086 CCCTTCCCGAGTCCCACTCAGCTCTGAACCTCAGCTCTTCTCATCTAGGCGGCACACAGAC 1145
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Db 1198 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1257
Qy 1146 AAGGAGCGCTGGTGGCCCTGCCCTCCTTTTAGGGGCTGGGAGGAGGTGTCTCTCC 1305
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1258 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1317
Qy 1206 TAGGCTGCCCGAGGCTCAGCTGCCATCTCTCAGCCGTGTGAGCTGTCTACACCC 1265
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Db 1318 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1377
Qy 1266 TCATCAAGAACCGGATCCATCGCTGCCTGTCTTGACCC 1305
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RESULT 3
US-08-878-989-14
; Sequence 14, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surva K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
; US-08-878-989-14
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-658-136-2

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Best Local Similarity 52.1%; Pred. No. 2;
Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 777 GGAGGGGTGAGTGGGAGAGGAGCAACCGGAAAGGGGCTCTTGGTGATGCTGGGCCAGGGCT 836
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Db 34640 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 34581

QY 837 TAGGTGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGG 896
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; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
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; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-658-136-1

Query Match      2.3%; Score 39; DB 3; Length 53577;
Best Local Similarity 52.1%; Pred. No. 2;
Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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RESULT 10
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; Sequence 7, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: Vinavagamoorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
; FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
; US-09-165-264-7

Query Match      2.2%; Score 38.6; DB 4; Length 320;
Best Local Similarity 50.3%; Pred. No. 0.33;
Matches 95; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

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RESULT 11	
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; Sequence 14, Application US/09165264	
; Patent No. 6197510	
; GENERAL INFORMATION:	
; APPLICANT: Vinayagamoorthy, Thuraiayah	
; TITLE OF INVENTION: Multi-Loci Genomic Analysis	
; FILE REFERENCE: 44747	
; CURRENT APPLICATION NUMBER: US/09/165,264	
; CURRENT FILING DATE: 1998-10-01	
; NUMBER OF SEQ ID NOS: 14	
; SOFTWARE: PatentIn Ver. 2.1	
; SEQ ID NO 14	
; LENGTH: 320	
; TYPE: DNA	
; ORGANISM: Artificial Sequence	
; FEATURE:	
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence	
US-09-165-264-14	
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Best Local Similarity	48.8%; Pred. No. 0.33;
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Db	108 GGG 167
QY	837 TAAGGTGGAGGATGGGCAGTGGGATGTCCTGGAGTGAACAGGGGAGGACAAATAGGAGC 896
Db	168 GGG 227
QY	897 CTCGGGTGCTGACGGAAAGGAAGCTCCCTGGGGACTGC AAGGTGAGCGAGGTGACCGGCT 956
Db	228 GGG 287
QY	957 CCCTGCCTGACTCTGGCTCTTTCTGCAGAGA 989
Db	288 GGGGGGGGGGGGGGTGGCCATGTACAGAGAGA 320
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; Sequence 8, Application US/09165264	
; Patent No. 6197510	
; GENERAL INFORMATION:	
; APPLICANT: Vinayagamoorthy, Thuraiayah	
; TITLE OF INVENTION: Multi-Loci Genomic Analysis	
; FILE REFERENCE: 44747	
; CURRENT APPLICATION NUMBER: US/09/165,264	
; CURRENT FILING DATE: 1998-10-01	
; NUMBER OF SEQ ID NOS: 14	
; SOFTWARE: PatentIn Ver. 2.1	
; SEQ ID NO 8	
; LENGTH: 319	
; TYPE: DNA	
; ORGANISM: Artificial Sequence	
; FEATURE:	
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence	
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Best Local Similarity	50.3%; Pred. No. 0.68;
Matches 92; Conservative	0; Mismatches 91; Indels 0; Gaps 0;
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Db	130 GGG 189
QY	837 TAAGGTGGAGGATGGGCAGTGGGATGTCCTGGAGTGAACAGGGGAGGACAAATAGGAGC 896
Db	190 GGG 249

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Perfect score: 1722
Sequence: 1 cctggccctcagatcaaga.....gatgagagctcg99ctg9a 1722

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	168.2	9.8	1647	10	US-09-826-581-5	
3	70.4	4.1	1691	10	US-09-925-297-2	
4	68	3.9	11527	9	US-10-108-605-70	
5	65	3.8	92	10	US-09-864-761-20146	
c	7	44.2	2.6	1064	10	US-09-804-682-29
8	43	2.5	910	9	US-10-123-155-112	
c	42.4	2.5	671	9	US-10-184-644-346	
c	10	42.4	2.5	671	9	US-10-184-634-346
c	11	40.8	2.4	1512	9	US-09-984-271-18
12	40.6	2.4	671	9	US-10-184-644-346	
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c	14	40.2	2.3	1184	9	US-10-123-155-394
15	40	2.3	12733	9	US-10-032-393-47	
16	40	2.3	12739	9	US-10-032-393-8	
17	39.8	2.3	4158	10	US-09-827-998-15	
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					Sequence 3373, Ap	
					Sequence 5, Appli	
					Sequence 2, Appli	
					Sequence 70, Appli	
					Sequence 20146, A	
					Sequence 29, Appl	
					Sequence 112, App	
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					Sequence 394, App	
					Sequence 47, Appli	
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					Sequence 9, Appli	
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28	38.2	2.2	2531	9	US-10-125-540-49	Sequence 49, Appli
29	38.2	2.2	2531	10	US-09-764-870-49	Sequence 49, Appli
30	37.6	2.2	777	9	US-10-184-644-348	Sequence 348, App
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c	34	37.2	2.2	531	10	Sequence 5509, App
c	35	37.2	2.2	21423	10	Sequence 42281, A
c	36	37.2	2.2	659158	9	Sequence 2835, Ap
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c	38	36.8	2.1	440	9	Sequence 602, Appli
c	39	36.8	2.1	440	9	Sequence 202, App
c	40	36.8	2.1	1065	10	Sequence 33, Appli
41	36.6	2.1	98829	9	US-10-017-724-3	Sequence 3, Appli
c	42	36.4	2.1	765	9	Sequence 28, Appli
c	43	36.4	2.1	802	9	Sequence 312, App
c	44	36.4	2.1	802	9	Sequence 312, App
c	45	36.4	2.1	987	10	Sequence 20, Appli

ALIGNMENTS

RESULT 1

US-09-826-581-3
; Sequence 3, Application US/09826581
; Patent No.: US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 S
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3

Query Match		100.0%	Score 1722;	DB 10;	Length 1722;
Best Local Similarity		100.0%	Pred. No. 0;		
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QY	61	CCCTCTATGGGACAGCAGAGGAGGCTTTGTGGTCTAGGAGGCTGGGGAGGTGAAG	120		
DB	61	CCCTCTATGGGACAGCAGAGGAGGCTTTGTGGTCTAGGAGGCTGGGGAGGTGAAG	120		
QY	121	GGAGATGGAGAGGTGTAGGGGAGATCTTGTACGGTCTTCTGGGGCTGATCTCTGATAT	180		
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QY	181	ACCACAGCTTGGCTTCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC	240		
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QY 1561 TATCCAAAGATTGGGCATTCGGCATTCGGACATTCGGCTGTGGTGTGGAGACAGCACC 1620
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QY 1681 CGAATGTGTACCCACCCAGGATGAGAGGCTCGGGCTGGA 1722
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RESULT 2

US-09-864-761-3373/c
; Sequence 3373, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmika-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687

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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3373
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009974.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
; US-09-864-761-3373

Query Match
Best Local Similarity 20.4%; Score 351; DB 10; Length 378;
Matches 362; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCTGGCCCTCAGATCAAGAAGCGCTTCTTTGCTCTGCTGGCCAAACGGTGTGGGCGAGC 60
DB 362 CCTGGCCCTCAGATCAAGAAGCGCTTCTTTGCTCTGCTGGCCAAACGGTGTGGGCGAGC 303

QY 61 CCCTCTATGGGACAGCAAGAACAGCAGCTTTGTGGTGGAGGAGCGCTGGGGAGGTGAAG 120
DB 302 CCCTCTATGGGACAGCAAGAACAGCAGCTTTGTGGTGGAGGAGCGCTGGGGAGGTGAAG 243

QY 121 GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTGTCTCGGGGTGATCTCTGATAT 180
DB 242 GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTGTCTCGGGGTGATCTCTGATAT 183

QY 181 ACCAAGCTTGGCTTACGGCCAAAGCCAGCCAGCGGCGCAGGGTGGAGGAAGTCCATCC 240
DB 182 ACCAAGCTTGGCTTACGGCCAAAGCCAGCGGCGCAGGGTGGAGGAAGTCCATCC 123

QY 241 GGAGTCTGCATGCCAGCTGGGAGACCCCTGGGCTCAATTTCCCATCTCTGGAGCGCT 300
DB 122 GGAGTCTGCATGCCAGCTGGGAGACCCCTGGGCTCAATTTCCCATCTCTGGAGCGCT 63

QY 301 ATGACAGCTGACACCTTTACCTCCGCTACTCCATGGCCCTGTCATAGGTGCTAGGG 360
DB 62 ATGACAGCTGACACCTTTACCTCCGCTACTCCATGGCCCTGTCATAGGTGCTAGGG 4

QY 361 AGC 363
DB 3 AGC 1

RESULT 3
US-09-826-581-5
; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(1486)
; US-09-826-581-5

Query Match
Best Local Similarity 9.8%; Score 168.2; DB 10; Length 1647;
Matches 173; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1510 CCATCCTAACCAAGGTTCCCTGCTGCCCGCGCCCTCCTTCTCTACCCGACTATCAAGA 1569
DB 1009 CCTGCACATCTTTGGTTCCTGCTGCCCGCGCCCTCCTTCTCTACCCGACTATCAAGA 1068

QY 1570 TTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGGAGACAGCACCCTCTGAC 1629
DB 1069 TTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGGAGACAGCACCCTCTGAC 1128

QY 1630 TGCACCTGGACATCTTTGTGGACCGCGGTGTGTGCACTGCCTGTGGTCAACGAATGTGG 1689
DB 1129 TGCACCTGGACATCTTTGTGGACCGCGGTGTGTGCACTGCCTGTGGTCAACGAATGTGG 1188

QY 1690 T 1690
DB 1189 T 1189

RESULT 4
US-09-925-297-2
; Sequence 2, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1691
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1093)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-297-2

Query Match
Best Local Similarity 4.1%; Score 70.4; DB 10; Length 1691;
Matches 98; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1240 CAGCCTTTTGAAGCTGTCTACACCCCTCATCAGAAGCCGGATCCATCGCCTGCTTCT 1299
DB 448 CAGCTTCTTTGAGCTGTCTCTTCATTAATTCGGAACAAGATCCAGGCTGCCAGTTAT 507

QY 1300 TGACCCCGTTCAGGCAAGTACTCCATCTCTACACACCAACCGCTGCTCAAGTTCCT 1359
DB 508 TGACCCGAATCAGGCAATACTTTGTATCTCTCACCACCAAGCGCATCTCTGAAGTTCCT 567

QY 1360 GCACATCTTTGTAAGCCTGGGCC 1383
DB 568 CAATTTGTTATCATCTGAGTCCC 591
```

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RESULT 5
US-10-108-605-70
; Sequence 70, Application US/10108605
; Patent No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; FILE REFERENCE: 311336
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 11527
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-108-605-70

Query Match      3.9%; Score 68; DB 9; Length 11527;
Best Local Similarity 69.7%; Pred. No. 1e-09;
Matches 92; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1243 CCTGTTGAAGCTGTCTACACCTCATCAAGAACCGGATCCATCGCTGCTGTTCTGA 1302
Db 10193 CTTTCTTACATGCCATAAATTCATCCAGCGCATATCGCTGCGCGTCATCGA 10252

QY 1303 CCGGTGTGAGGAAAGTACTCCATCTCCACACAAACGCTGCTCAAGTTCCTGCA 1362
Db 10253 TCCGCGACGGCAATGCTCTACATCCTGACACATAAAGCATACITAGTTCCTTT 10312

QY 1363 CATCTTTGTAAG 1374
Db 10313 CCTATACGTGAG 10324

RESULT 6
US-09-864-761-20146/c
; Sequence 20146, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20146
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009974.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
; OTHER INFORMATION: NT HIT: g111430152, EVALUE 2.00e-22
; OTHER INFORMATION: EST_HUMAN HIT: BE327467.1, EVALUE 3.00e-06
; OTHER INFORMATION: SWISSPROT HIT: P54619, EVALUE 3.00e-03
US-09-864-761-20146

Query Match      3.8%; Score 65; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGCCCTCAGATCAAGAAGCCCTCTTTGCTGTGGTGGCAACGGTGTGCGGCAGC 60
Db 65 CCTGGCCCTCAGATCAAGAAGCCCTCTTTGCTGTGGTGGCAACGGTGTGCGGCAGC 6

QY 61 CCCTC 65
Db 5 CCCTC 1

RESULT 7
US-09-804-682-29/c
; Sequence 29, Application US/09804682
; Patent No. US20020106765A1
; GENERAL INFORMATION:
; APPLICANT: Kinders, Robert
; APPLICANT: Corey, Michael J.
; TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE SAME AND METHODS FOR SCREENING FOR OR
; TITLE OF INVENTION: MODULATING THE SAME
; FILE REFERENCE: 130001.406
; CURRENT APPLICATION NUMBER: US/09/804,682
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
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: LENGTH: 1064
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 5, 6, 16, 21, 24, 25, 33, 39, 72, 110, 209, 214, 231, 232,
: LOCATION: 235, 237, 238, 244, 245, 246, 256, 282, 292, 297, 306, 319,
: LOCATION: 321, 323, 330, 334, 340, 349, 354, 355, 363, 372, 376, 378,
: LOCATION: 397, 405, 432, 437, 454, 455, 457, 458, 459, 468, 470
: OTHER INFORMATION: n = A,T,C or G
: NAME/KEY: misc_feature
: LOCATION: 485, 487, 488, 494, 496, 499, 511, 524, 527, 552, 557, 562,
: LOCATION: 583, 600, 611, 613, 623, 624, 652, 654, 674, 681, 687, 691,
: LOCATION: 694, 701, 713, 716, 720, 721, 725, 731, 734, 735, 739, 743,
: LOCATION: 744, 781, 782, 785, 789, 799, 803, 821, 823, 847, 852
: OTHER INFORMATION: n = A,T,C or G
: NAME/KEY: misc_feature
: LOCATION: 858, 878, 884, 886, 896, 897, 901, 917, 926, 932, 939, 948,
: LOCATION: 957, 961, 965, 981, 991, 993, 1001, 1002, 1005, 1011, 1018,
: LOCATION: 1043, 1047, 1049, 1051, 1054, 1056
: OTHER INFORMATION: n = A,T,C or G
: US-0804-682-29

Query Match          2.6%; Score 44.2; DB 10; Length 1064;
Best Local Similarity 47.8%; Pred. No. 0.0058;
Matches 85; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy      777  CGAGGGTGACTCGGAGAGAACCCCGAAGGGCGCTGTTGTCATGCTGGCGCAGGCGCT 836
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      865  GGAGGAGGNGGANGGNGGNGGAAGGGGGGAGGAGGAAGGGGNGNGGGGGGAGGGGGG 806
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy      837  TAAGGTGGAGATGGGACGTGGGGATGCTCTGGATGAACAGGAGGGACATAGGAGC 896
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      805  GNGGNGNGGGGGGANGGNGGNGGNGGGGGGGAGGGGAGCGGNAAGGGGGGGTAGGGGGGGA 746
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy      897  CTCGGGTGCTTCAGCAGAGGGAAGCTCCCTGGGACTGCAAGGTGAGCAGGTGACCGG 954
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      745  GNGGNGGNGGNGGAGGNGGAGNGGNGGNGGAGGTGAGGGGNGGGGGGNGGNGGAGG 688
      |||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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RESULT 8
US-10-123-155-112
; Sequence 112, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See PaIm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 112
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Homo sapien

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US-10-123--155-112

Query Match          2.5%; Score 43; DB 9; Length 910;
Best Local Similarity 13.2%; Pred. No. 0.013;
Matches 48; Conservative 93; Mismatches 224; Indels 0; Gaps 0;

QY 71 GACAGCAAGACAGACAGCTTTGGTGTGAGAGAGAGCTGGGAGGTGAAGGGAGATGGAG 130
   |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : :
Db 536 GVLSPDWPQSYSPGQDCVWGWHQEBKRIILLOVELINVRGCDMLTFLFDGSPSARVLAQ 595

QY 131 GAGGTGAGGGGAGATCTTGACGTTGTCTCGGCTGATCTCTGATATATACCACAAGCT 190
   |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : :
Db 596 LGGQPRRRLLSSGPDLLIQAPPGPPNCLGQGFVLHFKEVPRNDTCEPLPPPEWGNR 655

QY 191 TGGCTTCAGCCCAAGCCAGCCAGGGGCCAGGAGGAGAAAGTCCATCCGGAGTCTGCA 250
   |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : :
Db 656 TASHGDLIRTVLYQCEPGYELLGSDILITCQNDLSWSAAPPACQKIMTCADPGETANGH 715

QY 251 TGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTGTGGAGCGCGTATGACACAGCT 310
   |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : :
Db 715 RTADAGFPVGSVHVQRCPLPGYSLEGAAMLTYSRDTGTPKMSDRVPKCALKEPCPLNPG 775

QY 311 GACACCTTCCACTCCGCTACTGTCATGCCCTGTGCCATAGTGTCTAGGAGACAATGGG 370
   |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : :
Db 776 VPENGYQLKHHYQAGESLRFYEGFELIGVITTCVPGHPQWTSQBPPLCKVQTQTD 835

QY 371 GGGAGCGAGGAGAAAGAGCCACCTTCAGCGCTGGGGGGCTGCCCACTGTCTGT 430
   |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : : |: : : :
Db 836 PSRLGEGNLALAILPLGLVLVLSGVYIYTKLQKSLFGFSGSHSYSPITVESDFSN 895

QY 431 TCCCA 435
   |: : : :
Db 896 PLYEA 900
   |: : : :

RESULT 9
US-10-184-644-346/c
; Sequence 346, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC227
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-346

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Query Match	2.5%;	Score 42.4;	DB 9;	Length 671;
Best Local Similarity	5.3%;	Pred.No. 0.018;		
Matches	20;	Conservative 151;	Mismatches 206;	Indels 0; Gaps 0;
QY	924	CCTGGGACTCGAAGTGAGGCAGGTGACCGGCTCCCGCTGGGCTGACCTGCTGCTTTCTCG	983	
		: : : :	: : : :	
DB	515	M...SAB..AC...TN.GYMBH.SBHM.T.M..SD.M.M..BS..MMH.BMYHKS.C456		
		: : : :	: : : :	
QY	984	CAGAGATCTACCTCGCAAGGCTGCTTCAAGGCTCTGGTCTCCATCTCTCTCAATGATAGT	1043	

Db 455 SYMFAY.BMB.MT..M...YBYM.M.C.MYT..ASSS..MMTSMMT.Y...T...SHSS 396
QY 1044 GGGTGTCTCTCTCATTACCTGAGCCCTCTCTCTCCACAGTCCCTTCCCTCCACAGTCCAC 1103
Db 395 S..CYCYCMYCYMB..HH.Y..HCSSCCSY.T.CYHTY.YYY.M..M...Y.YY.... 336
QY 1104 TCAGCTGTGAACCTCACTCTTCTATCTAGCGGGGACACAGACAGAGGAGCTTGGTGCCC 1163
Db 335 ..YYVYT...YYVT.HYYMW.S.YHB.HSHSHSSSS..Y..M.MYCY.M...M.T.MYC 276
QY 1164 TCGCCTCTCTTTAGGGGCTGGGATGGAGGTCTCTCTCTCTAGCTGCCCGAGGCTC 1223
Db 275 Y..MMBSHSHSSSSSSSSSTSYTKTB...MTCHSTMSHSHSTS.TMMMYCC..CY 216
QY 1224 ACTGCTCCATCTCTCAGCCTGTTTGAAGCTGTCTACACCTCATCAAGACCGGATCC 1283
Db 215 .TYBTMM..A.H.HSAM.S.SSS.SN...S.SBST.H.HSSTMYTMSBSKM.T.AMYM 156
QY 1284 ATCGCTGCTCTGTCTT 1300
Db 155 .CSNHSSMHSHSHS.KY 139

RESULT 10

US-10-184-634-346/c
; Sequence 346, Application US/10184634
; Publication No. US2003006864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Paim
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-346

Query Match 2.5%; Score 42.4; DB 9; Length 671;
Best Local Similarity 5.3%; Pred. No. 0.018;
Matches 20; Conservative 151; Mismatches 206; Indels 0; Gaps 0;

QY 924 CTGGGACTGCAAGGTGAGCAGGTGACGGCTCCCTGCGCTGACTGTGGCTTCTTCTG 983
Db 515 M...SAB..AC....TN.GYMBH.SBEM.T.M..SD.M.M..BS..MM.BMYHKS.C 456
QY 984 CAGAGATCTACTGCAAGGCTGCTTCAAGCCTCTGTCTCCATCTCTCTCTAATGATAGT 1043
Db 455 SYMFAY.BMB.MT..M...YBYM.M.C.MYT..ASSS..MMTSMMT.Y...T...SHSS 396
QY 1044 GGGTGTCTCTCTCATTACCTGAGCCTCTCTCTCCACAGTCCCTTCCCGAGTCCAC 1103
Db 395 S..CYCYCMYCYMB..HH.Y..HCSSCCSY.T.CYHTY.YYY.M..M...Y.YY.... 336
QY 1104 TCAGCTGTGAACCTCACTCTTCTATCTAGCGGGGACACAGACAGAGGAGCTTGGTGCCC 1163
Db 335 ..YYVYT...YYVT.HYYMW.S.YHB.HSHSHSSSS..Y..M.MYCY.M...M.T.MYC 276

QY 1164 TCCCTCTCTTTTAGGGGCTGGGATGGAGGTCTCTCTCTCTAGCTGCCCGAGGCTC 1223
Db 275 Y..MMBSHSHSSSSSSSSSTSYTKTB...MTCHSTMSHSHSTS.TMMMYCC..CY 216
QY 1224 ACTGCTCCATCTCTCAGCCTGTTTGAAGCTGTCTACACCTCATCAAGACCGGATCC 1283
Db 215 .TYBTMM..A.H.HSAM.S.SSS.SN...S.SBST.H.HSSTMYTMSBSKM.T.AMYM 156
QY 1284 ATCGCTGCTCTGTCTT 1300
Db 155 .CSNHSSMHSHSHS.KY 139

RESULT 11

US-09-984-271-18/c
; Sequence 18, Application US/09984271
; Publication No. US20030040088A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/984,271
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (207)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE
; LOCATION: (209)
; OTHER INFORMATION: n equals a.t.g, or c
; NAME/KEY: SITE
; LOCATION: (521)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-984-271-18

Query Match 2.4%; Score 40.8; DB 9; Length 1512;
Best Local Similarity 49.1%; Pred. No. 0.062;
Matches 105; Conservative 1; Mismatches 108; Indels 0; Gaps 0;

QY 386 AAGAGCCCACTCTTCAGGCGCTGGGGGCTGCCCACTGTCTCTTCCACAGTCCCCAC 445
Db 1286 AAGTGTGGCAGACAGAGGAGGAGGCGAGGGCTCCTGCGCTGCTGCGAGTCTTGG 1227
QY 446 TGTGTCTCAGCACAGACACTGGCAGGGGTGGGGAGGGGATCTGACCTCAACCTGCTT 505
Db 1226 GAGGGGAAGGCTAGGAACCTCCAGCAGAGGAGGGGTTTGGACCCACTATGACAGT 1167
QY 506 CCACCAAGGCCCGGGCTGACCTCTCTCCCGGCCCTCCCTGCGAGGATGTGACCAT 565
Db 1166 CCTCACAGGCCAGGAGTTACCCCGTTCCACCACTCTCTGCGCTGCTGCGGGGCC 1107
QY 566 CACTGACTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
Db 1106 CACACTCTCTCTCTCATATATACATATCATCTCC 1073

RESULT 12

```
US-10-184-644-346
; Sequence 346, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-346

Query Match      2.4%; Score 40.6; DB 9; Length 671;
Best Local Similarity 7.5%; Pred. No. 0.059;
Matches 25; Conservative 135; Mismatches 173; Indels 0; Gaps 0;

QY 644 CAGAGGGCGGGCGGAGGAGTCTCTCTGAGCCCTGGTGCCTAGAGCCACGCTCT 703
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 89 HASYSAPPVSSDSEAPENADGSDADEDDRGVMVAVTAVTATAASDRMESDSDK 148
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 704 TTCTGACTTCTGGAGTCTCTGTCGATCTCTAGTCCAGATCTATGAGATTGAACAACAT 763
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 149 SSDNSGLKRTKTPALKMSVSKRARKASSDLDOASVSPSEENSESSSEKTSDDQFTPEK 208
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 764 AAGATTGACCTGGAGGGGTGAGTGGGAGAGAACCCGGAAGGGGCTGTGGTGATG 823
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 209 KAAVRAPRRGPLGRKKKAPSASDSKSDGAKPEPVAMARSASSSSSSSSSDSDV 268
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 824 GTGGCCAGCGCTTAAGTGTGGAGGTGGCAGTGGGATGCTCTGGAGTGAACAGGGAG 883
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 SVKKPPRGKPAEKPLPKPRGKPKPERPPSSSSSDSDSDVDRISFWKRRDEARRRELE 328
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 884 GGACAATAGGAGCTCGGGTGCCTGACGGAAGGAAGCTGCCTGGGACTGCAAGGTGAGG 943
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 329 ARRRREQEELRLRLREQEKERRERADRGAEERGSGSSGDELREDDPEPVKKRGRKG 388
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 944 CAGGTGACCGGCTCCCTCGCTGACTCTGGCT 976
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 389 RGRPPSSSDSEPAELEAREAKKSARKKQSSST 421
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-10-184-634-346
; Sequence 346, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

```
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-346

Query Match      2.4%; Score 40.6; DB 9; Length 671;
Best Local Similarity 7.5%; Pred. No. 0.059;
Matches 25; Conservative 135; Mismatches 173; Indels 0; Gaps 0;

QY 644 CAGAGGGCGGGCGGAGGAGTCTCTCTGAGCCCTGGTGCCTAGAGCCACGCTCT 703
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 89 HASYSAPPVSSDSEAPENADGSDADEDDRGVMVAVTAVTATAASDRMESDSDK 148
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 704 TTCTGACTTCTGGAGTCTCTGTCGATCTCTAGTCCAGATCTATGAGATTGAACAACAT 763
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 149 SSDNSGLKRTKTPALKMSVSKRARKASSDLDOASVSPSEENSESSSEKTSDDQFTPEK 208
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 764 AAGATTGACCTGGAGGGGTGAGTGGGAGAGAACCCGGAAGGGGCTGTGGTGATG 823
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 209 KAAVRAPRRGPLGRKKKAPSASDSKSDGAKPEPVAMARSASSSSSSSSSDSDV 268
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 824 GTGGCCAGCGCTTAAGTGTGGAGGTGGCAGTGGGATGCTCTGGAGTGAACAGGGAG 883
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 SVKKPPRGKPAEKPLPKPRGKPKPERPPSSSSSDSDSDVDRISFWKRRDEARRRELE 328
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 884 GGACAATAGGAGCTCGGGTGCCTGACGGAAGGAAGCTGCCTGGGACTGCAAGGTGAGG 943
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 329 ARRRREQEELRLRLREQEKERRERADRGAEERGSGSSGDELREDDPEPVKKRGRKG 388
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 944 CAGGTGACCGGCTCCCTCGCTGACTCTGGCT 976
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 389 RGRPPSSSDSEPAELEAREAKKSARKKQSSST 421
    |: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-10-123-155-394/c
; Sequence 394, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 394
; LENGTH: 1184
```

```
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-153-394

Query Match      2.3%; Score 40.2; DB 9; Length 1184;
Best Local Similarity 8.8%; Pred. No. 0.089;
Matches 57; Conservative 175; Mismatches 412; Indels 1; Gaps 1;

QY 1021 CTCGATCTCTCTAATGATAGGTTGGTGTCTCTGCTCATTCACCTGAGCCCTCTCTCC 1080
   ||| : : : : | : ||| : : : : | : : : : | : : : : | : : : : |
Db 1085 Y...ATTTT.S.BNHYENAA...S.YTKWT.H.TS.YH.T.CAS.H..SS.....MBS 1026

QY 1081 ACAGTCCCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1140
   : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 1025 .H...H..C.....HA..CCYTS..CHAH..TSYSC..MT..RMICYDN..M....C.D..S. 966

QY 1141 CAGACAAAGGAGCCTTGGTGCCTCGCCTCCCTCTTTTATAGGGCCCTGGATGGAGTGT-C 1199
   : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 965 ..S...B..SHBA...B.NY.T.TTBS.YB.SY...Y.CS.M..SBMCN.DY.YY.ATSS 906

QY 1200 TCTCCCTAGGTGCCCCGAGGCTCAGTCTGCTCCATCTCTGACGCTGTTTGAAGCTGTCT 1259
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 905 T..Y..T..SC.HCT.YCA..SCTBM..YSY..CAT.....N.N.YSTNY.Y.DN...NB 846

QY 1260 ACACCTCATCAAGAACCGGATCCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1319
   | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 845 AH..B.YS.T.TC.NC.NY.AYR.A.A.D..T..G.HWCT.KKT.MHBHDS..CB.G..C 786

QY 1320 TACTCCACATCTCACACAAAGCGCTGCTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1379
   | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 785 T..CY..B.B.D..HTM..DM..YM...YRAS.T.YGNRTYNHMM.AYG.SK..T...C..C. 726

QY 1380 GCCCAGGTGGGAGAGGGGAGACCTGGCGAGGTGATCAGAGGGCTGAGGAGTCTTCA 1439
   : : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 725 .BT.G.BA.KSKS..TC.MYTSY.DHBSAB..KBY..TYA....SC.H.BB....W.SC... 666

QY 1440 GCCCTAGCAGTGTGGGGAAGAGCTGGGAGCGCTTGAAGCTGCTGCTGCTGCTGCTGCTGCT 1499
   : : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 665 SSTNABNB...CAP.N...DT.NCNY.SR...CNTCSHHTYB.AA.....YSSDAT... 606

QY 1500 CACCTGGTCCCTCCCTCAACAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1559
   ||| : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 605 AHACT.C.CN.A...B..DCASTNB..BS.STMCHS.B..BB..TNHNTH..SBWBSBSST 546

QY 1560 CTAATCAAGATTGGGCATCGGCACATTCGAGACTGGCTGCTGCTGCTGCTGCTGCTGCTG 1619
   : | : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 545 .K..CSH.T.B....CTK..RN.SY.TAB.CANSH.TB.DTB.SH..YRSBMCN.C.HTH 486

QY 1620 CGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1664
   : : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 485 DTW.A..D.S..NN.YASB.RYSM...B.TNIN.IS...S...MNTS 441

RESULT 15
US-10-032-393-47
; Sequence 47, Application us/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Molly
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITRA.010A
; CURRENT APPLICATION NUMBER: US/10/032,393
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/259,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 47
; LENGTH: 12733
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector pPEPF14
US-10-032-393-47

Query Match      2.3%; Score 40; DB 9; Length 12733;
Best Local Similarity 49.5%; Pred. No. 0.18;
Matches 103; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 777 GGAGGGGTGAGTGGGGAGAGAACCCGGAAGGGGCTGTGTTGTTGATGTTGGCCAGGGCT 836
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5178 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 5237

QY 837 TAAGTGTGAGGATGGGCGAGTGGGGATGTCCTGGAGTGAACAGGGGAGGACAATAGGAGC 896
   || || || || || || || || || || || || || || || || || || || || ||
Db 5238 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 5297

QY 897 CTCGGGTGCTTGACGGAAGGAAGTGCCTGGGACTGCAAGGTGAGGCAGGTGACCGGCT 956
   |||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5298 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 5357

QY 957 CCCCTGGCCTGACTCTGGCTCTTTCTGC 984
   |||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5358 GCCTTGAGAGCCCTCAACCCAGCTCAGC 5385

Search completed: June 14, 2003, 20:47:11
Job time : 292 secs
```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 01:49:14 ; Search time 192.613 Seconds
(without alignments)
9216.782 Million cell updates/sec

Title: US-09-826-581-3_Copy_612_672
Perfect score: 61
Sequence: 1 gtagaggagtgctgggaat.....ggggggggaggagtcctc 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.or.*
- 21: em.os.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pla.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sv.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	61	100.0	1722	6	AX281580	Sequence
c 2	61	100.0	206854	9	AC009974	AX281580 Homo sapi
c 3	59.4	97.4	152129	2	AC027416	AC027416 Homo sapi
c 4	30.4	49.8	91247	2	AC106624	AC106624 Rattus no
c 5	29.8	48.9	127181	2	AC118404	AC118404 Rattus no
c 6	29.2	47.9	281000	10	MMU276505	AJ276505 Mus muscu
c 7	29	47.5	140819	10	AC121886	AC121886 Mus muscu
c 8	28.8	47.2	117082	2	AC126076	AC126076 Rattus no
c 9	28.8	47.2	155645	2	AC094964	AC094964 Rattus no
c 10	28.6	46.9	899	11	G75185	G75185 MARC 11245-
c 11	28.6	46.9	945	11	G74939	G74939 MARC 11247-
c 12	28.6	46.9	215046	2	AF354168	AF354168 Ovis arie
c 13	28.4	46.6	184454	2	AC128911	AC128911 Rattus no
c 14	28.2	46.2	164800	2	AC113756	AC113756 Rattus no
c 15	27.8	45.6	170476	2	AC111883	AC111883 Rattus no
c 16	27.8	45.6	191720	2	AC109982	AC109982 Rattus no
c 17	27.6	45.2	653	11	PM7F7B	AL685186 Penicilli
c 18	27.6	45.2	127794	9	AL138688	AL138688 Human DNA
c 19	27.6	45.2	214971	2	AC094543	AC094543 Rattus no
c 20	27.4	44.9	48489	8	AC091776	AC091776 Chlamydom
c 21	27.4	44.9	65932	8	AP004938	AP004938 Lotus jap
c 22	27.4	44.9	68736	2	AC090435	AC090435 Chlamydom
c 23	27.4	44.9	69660	2	AC106670	AC106670 Rattus no
c 24	27.4	44.9	134366	2	AC119661	AC119661 Rattus no
c 25	27.4	44.9	161951	2	CNS07YPU	AL713951 Oryza sat
c 26	27.4	44.9	166007	2	AP004862	AP004862 Oryza sat
c 27	27.4	44.9	183450	2	AC115443	AC115443 Rattus no
c 28	27.4	44.9	207374	9	CNS07YFU	AL583722 Human chr
c 29	27.4	44.9	292136	2	AC103544	AC103544 Rattus no
c 30	27.4	44.9	300605	2	AC098460	AC098460 Rattus no
c 31	27.2	44.6	36582	2	AC103128	AC103128 Rattus no
c 32	27.2	44.6	113633	2	AC094512	AC094512 Rattus no
c 33	27.2	44.6	116239	2	AC117323	AC117323 Rattus no
c 34	27.2	44.6	143899	2	AC013606	AC013606 Homo sapi
c 35	27.2	44.6	143899	6	AX411543	AX411543 Sequence
c 36	27.2	44.6	154126	2	AC010758	AC010758 Homo sapi
c 37	27.2	44.6	157437	2	AC021669	AC021669 Homo sapi
c 38	27.2	44.6	164290	2	AC096454	AC096454 Rattus no
c 39	27.2	44.6	165314	2	AC103081	AC103081 Rattus no
c 40	27.2	44.6	165434	2	AC087505	AC087505 Homo sapi
c 41	27.2	44.6	177107	2	AC109908	AC109908 Rattus no
c 42	27.2	44.6	177433	9	AC011747	AC011747 Homo sapi
c 43	27.2	44.6	178000	9	AP002893	AP002893 Homo sapi
c 44	27.2	44.6	178744	2	AC117508	AC117508 Homo sapi
c 45	27.2	44.6	184668	2	AC096340	AC096340 Rattus no

ALIGNMENTS

RESULT 1
AX281580
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Andersson,L., Luthman,H. and Marklund,S.
Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: WO 0177305-A 3 18-OCT-2001;

AX281580
Sequence
AX281580
AX281580.1
Sequence
3 from Patent WO0177305.
1722 bp
DNA
linear
PAT 03-NOV-2001


```

FEATURES             Location/Qualifiers
     source           1..1722
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT          321 a 504 c 534 g 363 t
ORIGIN

Query Match          100.0%; Score 61; DB 6; Length 1722;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGAGAGTGGCTGGGAATCTTATGGCACCCAGAGCGCGGCGGAGGAGTCT 60
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Db      612 GTGAGAGTGGCTGGGAATCTTATGGCACCCAGAGCGCGGCGGAGGAGTCT 671

QY      61 C 61
        |
Db      672 C 672

RESULT 2
AC009974/c
LOCUS               AC009974               206854 bp    DNA    linear    PRI 09-JAN-2002
DEFINITION          Homo sapiens BAC clone RP11-459I19 from 2, complete sequence.
ACCESSION            AC009974
VERSION              AC009974.9  GI:16799058
KEYWORDS              HTG.
SOURCE               Homo sapiens.
ORGANISM              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS              Sulston, J.E. and Waterston, R.
TITLE                Toward a complete human genome sequence
JOURNAL              Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE              99063792
PUBMED               9847074
REFERENCE
AUTHORS              Harris, A. and Cotton, M.
TITLE                The sequence of Homo sapiens BAC clone RP11-459I19
JOURNAL              Unpublished (2001)
REFERENCE
AUTHORS              Waterston, R.H.
TITLE                Direct Submission
JOURNAL              Submitted (08-SEP-1999) Genome Sequencing Center, Washington
                      University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                      MO 63108, USA
                      Waterston, R.H.
                      (bases 1 to 206854)
REFERENCE
AUTHORS              University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                      MO 63108, USA
                      (bases 1 to 206854)
TITLE                Direct Submission
JOURNAL              Submitted (08-NOV-2001) Genome Sequencing Center, Washington
                      University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                      MO 63108, USA
                      (bases 1 to 206854)
REFERENCE
AUTHORS              Waterston, R.H.
TITLE                Direct Submission
JOURNAL              Submitted (09-JAN-2002) Genome Sequencing Center, Washington
                      University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                      MO 63108, USA
                      (bases 1 to 206854)
REFERENCE
AUTHORS              Waterston, R.
TITLE                Direct Submission
JOURNAL              Submitted (09-JAN-2002) Department of Genetics, Washington
                      University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                      On Nov 8, 2001 this sequence version replaced gi:13431203.
COMMENT
-----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
-----
Summary Statistics
-----
Center project name: H_NH0459119

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459I19; actual end is at base position 206854 of RP11-459I19.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

```

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/clone_lib="RPCI-11"

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misc_feature      1..37
                  /note="match to EST AW880850 (NID:g8042860)"
misc_feature      1..37
                  /note="match to EST BE047599 (NID:g8364652) tz39c01.yl"
misc_feature      1..37
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misc_feature      4..37
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Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGAGGAGTGGCTGGGAATCTTATGGCACCACCCAGAGGGCGGGGAGGAGTCT 60
|||||
Db 166087 GTGAGGAGTGGCTGGGAATCTTATGGCACCACCCAGAGGGCGGGGAGGAGTCT 166028
Qy 61 C 61
Db 166027 C 166027
RESULT 3
AC027416/c
LOCUS AC027416 152129 bp DNA linear HTG 07-JUN-2000
DEFINITION Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
unordered pieces.
ACCESSION AC027416
VERSION AC027416.2 GI:8317289
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 152129)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-504G11
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 152129)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferrel,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenca,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessile,H., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7458
Center clone name: 504_G11
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: phrap; version 0.960731
 Consensus quality: 43576 bases at least Q40
 Consensus quality: 44364 bases at least Q30
 Consensus quality: 445653 bases at least Q20
 Insert size: 161000; agarose-fp
 Insert size: 149029; sum-of-contigs
 Quality coverage: 3.1 in Q20 bases; agarose-fp
 Quality coverage: 3.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1005:	contig of 1005 bp in length
1105:	gap of 100 bp
12402:	contig of 1297 bp in length
2502:	gap of 100 bp
3623:	contig of 1321 bp in length
3923:	gap of 100 bp
5020:	contig of 1097 bp in length
5120:	gap of 100 bp
6161:	contig of 1041 bp in length
6261:	gap of 100 bp
7547:	contig of 1286 bp in length
7647:	gap of 100 bp
9983:	contig of 2336 bp in length
10083:	gap of 100 bp
12556:	contig of 2473 bp in length
12656:	gap of 100 bp
15043:	contig of 2387 bp in length
15143:	gap of 100 bp
17123:	contig of 1980 bp in length
17223:	gap of 100 bp
19466:	contig of 2243 bp in length
19566:	gap of 100 bp
21928:	contig of 2362 bp in length
22028:	gap of 100 bp
24319:	contig of 2291 bp in length
24419:	gap of 100 bp
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27159:	gap of 100 bp
30170:	contig of 3011 bp in length
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33968:	contig of 3698 bp in length
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38179:	contig of 4111 bp in length
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42366:	contig of 4087 bp in length
42466:	gap of 100 bp
46365:	contig of 3899 bp in length
46465:	gap of 100 bp
51285:	contig of 4820 bp in length
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55871:	contig of 4486 bp in length
55971:	gap of 100 bp
60595:	contig of 4624 bp in length
60695:	gap of 100 bp
66595:	contig of 5900 bp in length
66695:	gap of 100 bp
73218:	contig of 6523 bp in length
73318:	gap of 100 bp
77115:	contig of 3797 bp in length
77215:	gap of 100 bp
85022:	contig of 7807 bp in length
85122:	gap of 100 bp
93314:	contig of 8192 bp in length
93414:	gap of 100 bp
101193:	contig of 7779 bp in length

JOURNAL

Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20162777.
----- Genome Center

COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GUIR
Center clone name: CH230-150G18
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 65762 bases at least Q40
Consensus quality: 72462 bases at least Q30
Consensus quality: 77125 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 56 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 2656 4350: contig of 1695 bp in length
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* 4451 5648: contig of 1198 bp in length
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* 5749 7176: contig of 1428 bp in length
* 7177 7276: gap of unknown length
* 7277 8374: contig of 1098 bp in length
* 8375 8474: gap of unknown length
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* 9628 9727: gap of unknown length
* 9728 11357: contig of 1630 bp in length
* 11358 11457: gap of unknown length
* 11458 12462: contig of 1005 bp in length
* 12463 12562: gap of unknown length
* 12563 13840: contig of 1278 bp in length
* 13841 13940: gap of unknown length
* 13941 15505: contig of 1565 bp in length
* 15506 15605: gap of unknown length
* 15606 17067: contig of 1462 bp in length
* 17068 17167: gap of unknown length
* 17168 19112: contig of 1945 bp in length
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* 27138 27237: gap of unknown length
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* 28298 28397: gap of unknown length
* 28398 29809: contig of 1412 bp in length
* 29810 29909: gap of unknown length
* 29910 32067: contig of 2158 bp in length
* 32068 32167: gap of unknown length
* 32168 34176: contig of 2009 bp in length

* 34177 34276: gap of unknown length
* 34277 35685: contig of 1409 bp in length
* 35686 35785: gap of unknown length
* 35786 37408: contig of 1623 bp in length
* 37409 37508: gap of unknown length
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* 39966 40065: gap of unknown length
* 40066 41967: contig of 1902 bp in length
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* 42068 43856: contig of 1789 bp in length
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* 47074 47173: gap of unknown length
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* 50302 50401: gap of unknown length
* 50402 52400: contig of 1999 bp in length
* 52401 52500: gap of unknown length
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* 53734 56087: contig of 2354 bp in length
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* 56188 57598: contig of 1412 bp in length
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* 59845 61551: contig of 1708 bp in length
* 61552 63065: contig of 1414 bp in length
* 63066 63165: gap of unknown length
* 63166 65040: contig of 1875 bp in length
* 65041 65140: gap of unknown length
* 65141 66783: contig of 1643 bp in length
* 66784 66883: gap of unknown length
* 66884 68892: contig of 2009 bp in length
* 68893 68992: gap of unknown length
* 68993 70919: contig of 1927 bp in length
* 70920 73482: contig of 2463 bp in length
* 73483 73582: gap of unknown length
* 73583 75995: contig of 2413 bp in length
* 75996 76095: gap of unknown length
* 76096 78998: contig of 2903 bp in length
* 78999 79098: gap of unknown length
* 79099 81131: contig of 2033 bp in length
* 81132 81231: gap of unknown length
* 81232 85493: contig of 4262 bp in length
* 85494 85593: gap of unknown length
* 85594 87634: contig of 2041 bp in length
* 87635 87734: gap of unknown length
* 87735 90259: contig of 2525 bp in length
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* 90360 93882: contig of 3523 bp in length
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* 93983 98284: contig of 4302 bp in length
* 98285 98384: gap of unknown length
* 98385 102361: contig of 3977 bp in length
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* 107146 107245: gap of unknown length
* 107246 112070: contig of 4825 bp in length

Query Match 48.9%; Score 29.8; DB 2; Length 127181;
Best Local Similarity 70.2%; Pred. No. 13;
Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGAATCTATGGGACCCAGAGGGCGGGGGGAGT 57

DB 33643 GCGAGGGTGGGGCGGGGAGGGGTGGATCCCGAGGGCGGGGGCGGT 33587

RESULT 6

MMU276505

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

MMU276505 281000 bp DNA linear ROD 06-MAR-2002
Mus musculus genomic fragment, 281000 bp, chromosome 7.
A276505
A276505.2 GI:12583595
cars gene; cdkn1c gene; cyclin-dependent kinase inhibitor 1C;
cysteinyl-ERNA-synthetase; IPL gene; Itm gene; Nap114 gene;
nucleosome assembly protein 1-like 4 protein; Obphi gene; oxysterol
binding protein; Tnfrh1 gene; Tnfrh2 gene; tumor necrosis factor
receptor p60 homolog 1; tumor necrosis factor receptor p60
homologue 2; tumor suppressing subtransferable candidate 5.
western European house mouse.

SOURCE

ORGANISM

Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Engemann, S., Strodicke, M., Paulsen, M., Franck, O., Reinhardt, R.,
Lane, N., Reik, W. and Walter, J.
Sequence and functional comparison in the Beckwith-Wiedemann
region: implications for a novel imprinting centre and extended
imprinting

TITLE

Hum. Mol. Genet. 9 (18), 2691-2706 (2000)
20519229
11063728

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Jan 27, 2001 this sequence version replaced gi:11191799.
related accession numbers AJ300452-AJ300460
has a 1000 bp overlap with AJ271885.

FEATURES

source

1. 281000
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/strain="129 SV"
/sub_species="domesticus"
/db_xref="taxon:10092"
/chromosome="7"
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1431..28364
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gene

mRNA

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17790..17888,21514..21610,21996..22086,22181..22317,
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CDS

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Direct Submission
Unpublished
2 (bases 1 to 117082)
Worley, K. C.

Direct Submission
Submitted (03-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 117082)
Worley, K. C.

Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 5, 2002 this sequence version replaced gi:21696820.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: G2TG
Center clone name: CH230-143P6
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 55139 bases at least Q40
Consensus quality: 61060 bases at least Q30
Consensus quality: 64630 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 63 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1055: contig of 1055 bp in length
* 1056 1155: gap of unknown length
* 1156 2165: contig of 1010 bp in length
* 2166 2265: gap of unknown length
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11638 11737: gap of unknown length
11738 13085: contig of 1348 bp in length
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13187 14617: contig of 1432 bp in length
14618 16407: contig of 1690 bp in length
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19309 21017: contig of 1710 bp in length
21018 22172: contig of 1055 bp in length
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29856 31657: contig of 1802 bp in length
31658 33595: contig of 1838 bp in length
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33696 35198: contig of 1503 bp in length
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37641 37740: gap of unknown length
37741 39003: contig of 1263 bp in length
39004 39103: gap of unknown length
39104 41305: contig of 2202 bp in length
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41406 42620: contig of 1215 bp in length
42621 42720: gap of unknown length
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43941 44040: gap of unknown length
44041 45996: contig of 1956 bp in length
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49552 50801: contig of 1250 bp in length
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52982 54499: contig of 1518 bp in length
54500 54599: gap of unknown length
54600 56034: gap of unknown length
56035 58138: contig of 2104 bp in length
58139 58238: gap of unknown length

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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* 59733	59832:	gap of unknown length
* 59833	61285:	contig of 1453 bp in length
* 61286	61385:	gap of unknown length
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* 62881	62980:	gap of unknown length
* 62981	64930:	contig of 1950 bp in length
* 64931	65030:	gap of unknown length
* 65031	66998:	contig of 1968 bp in length
* 66999	67098:	gap of unknown length
* 67099	69768:	contig of 2670 bp in length
* 69769	69868:	gap of unknown length
* 69869	72122:	contig of 2254 bp in length
* 72123	72222:	gap of unknown length
* 72223	74144:	contig of 1922 bp in length
* 74145	74244:	gap of unknown length
* 74245	75957:	contig of 1713 bp in length
* 75958	76057:	gap of unknown length
* 76058	78577:	contig of 2520 bp in length
* 78578	78677:	gap of unknown length
* 78678	80255:	contig of 1578 bp in length
* 80256	80355:	gap of unknown length
* 80356	82593:	contig of 2238 bp in length
* 82594	82693:	gap of unknown length
* 82694	84585:	contig of 1992 bp in length
* 84586	84785:	gap of unknown length
* 84786	86448:	contig of 1663 bp in length
* 86449	86548:	gap of unknown length
* 86549	87884:	contig of 1336 bp in length
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Best Local Similarity 47.2%; Score 28.8; DB 2; Length 117082;		
Matches 39; Conservative 0; Mismatches 17; Indels 0; Gaps 0;		
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Db	45287	GGGGGGGGGGGGCGCGTGTATGCGCCCGGGGGGGGGGGGGGAG 45342
RESULT 9		
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LOCUS	79 unordered pieces.	
DEFINITION	AC094964.3 GI:22450519	
VERSION	HTG; HTGS_PHASE1.	
KEYWORDS	Norway rat.	
SOURCE	Rattus norvegicus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
REFERENCE	1 (bases 1 to 155645)	
AUTHORS	Muzny,D,Marie,, Metzker,M,Iee,, Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Ayoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalto,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhaq,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,	

Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpthy,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.I., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhera,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., Mcleod,M., Mcneill,T., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokemele,O., Okwuonu,G., Olanpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Poindester,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczek,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.	Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
REFERENCE	3 (bases 1 to 155645)	
AUTHORS	Rat Genome Sequencing Consortium.	
TITLE	Direct Submission	
JOURNAL	Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	
COMMENT	On Aug 23, 2002 this sequence version replaced gi:21716685.	
----- Genome Center		
Center: Baylor College of Medicine		
Center code: BCM		
Web site: http://www.hgsc.bcm.tmc.edu/		
Contact: hgsc-help@bcm.tmc.edu		
----- Project Information		
Center project name: GSUZ		
Center clone name: CH230-6L21		
----- Summary Statistics		
Sequencing vector: Plasmid;		
Chemistry: Dye-terminator Big Dye: 100% of reads		
Assembly program: Phrap; version 0.990329		
Consensus quality: 96145 bases at least Q40		
Consensus quality: 105750 bases at least Q30		
Consensus quality: 111678 bases at least Q30		

* NOTE: Estimated insert size may differ from sequence length		
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).		
* NOTE: This is a 'working draft' sequence. It currently		
consists of 79 contigs. the true order of the pieces		
is not known and their order in this sequence record is		
arbitrary. Gaps between the contigs are represented as		
runs of N, but the exact sizes of the gaps are unknown.		
* This record will be updated with the finished sequence		
as soon as it is available and the accession number will		
be preserved.		
* 1 1071: contig of 1071 bp in length		
* 1072 1171: gap of unknown length		
* 1172 2289: contig of 1118 bp in length		
* 2290 2389: gap of unknown length		

Consensus quality: 151052 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 70 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1006: contig of 1006 bp in length
1007 1106: gap of unknown length
1107 2160: contig of 1054 bp in length
2161 2260: gap of unknown length
2261 3707: contig of 1447 bp in length
3708 3807: gap of unknown length
3808 4904: contig of 1097 bp in length
4905 5004: gap of unknown length
5005 6398: contig of 1394 bp in length
6399 6498: gap of unknown length
6499 7523: contig of 1025 bp in length
7524 7624: gap of unknown length
7624 8788: contig of 1165 bp in length
8789 8888: gap of unknown length
8889 10114: contig of 1226 bp in length
10115 10214: gap of unknown length
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11380 11479: gap of unknown length
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12545 12644: gap of unknown length
12645 14706: contig of 2062 bp in length
14707 14806: gap of unknown length
14807 17053: contig of 2257 bp in length
17054 17163: gap of unknown length
17164 18248: contig of 1085 bp in length
18249 18348: gap of unknown length
18349 19912: contig of 1564 bp in length
19913 20012: gap of unknown length
20013 21555: contig of 1543 bp in length
21556 21655: gap of unknown length
21656 22967: contig of 1312 bp in length
22968 23067: gap of unknown length
23068 24534: contig of 1467 bp in length
24535 24634: gap of unknown length
24635 25905: contig of 1271 bp in length
25906 26005: gap of unknown length
26006 27235: contig of 1230 bp in length
27236 27335: gap of unknown length
27336 29168: contig of 1833 bp in length
29169 29288: gap of unknown length
29289 30590: contig of 1322 bp in length
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30691 32623: contig of 1933 bp in length
32624 32723: gap of unknown length
32724 33865: contig of 1142 bp in length
33866 33965: gap of unknown length
33966 35087: contig of 1122 bp in length
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36558 36657: gap of unknown length
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38206 38305: gap of unknown length
38306 40591: contig of 2286 bp in length
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40692 41703: contig of 1012 bp in length
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41804 44051: contig of 2248 bp in length
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44152 45165: contig of 1014 bp in length
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49074 49174: gap of unknown length
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50895 50995: gap of unknown length
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52766 54888: contig of 2123 bp in length
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57959 60027: contig of 2069 bp in length
60028 60128: gap of unknown length
60129 62566: contig of 2439 bp in length
62567 64939: gap of unknown length
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65040 67402: contig of 2363 bp in length
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67503 70175: contig of 2673 bp in length
70176 70275: gap of unknown length
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72929 73028: gap of unknown length
73029 75454: contig of 2426 bp in length
75455 75554: gap of unknown length
75555 78626: contig of 3072 bp in length
78627 78726: gap of unknown length
78727 83316: contig of 4590 bp in length
83317 83417: gap of unknown length
83417 86097: contig of 2680 bp in length
86097 86197: gap of unknown length
86197 88902: contig of 2706 bp in length
88903 92100: contig of 3098 bp in length
92101 92201: gap of unknown length
92201 95523: contig of 3329 bp in length
95523 95623: gap of unknown length
95623 98686: contig of 3057 bp in length
98687 98787: gap of unknown length
98787 101890: contig of 3104 bp in length
101891 101990: gap of unknown length
101991 106105: contig of 4115 bp in length
106106 106205: gap of unknown length
106206 108982: contig of 2777 bp in length
108983 109083: gap of unknown length
109083 113320: contig of 4238 bp in length
113321 113420: gap of unknown length
113421 116544: contig of 3124 bp in length
116545 116644: gap of unknown length
116645 120403: contig of 3759 bp in length
120404 120503: gap of unknown length

Query Match 46.6%; Score 28.4; DB 2; Length 184454;
Best Local Similarity 76.1%; Pred. No. 34;
Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 8 GTGGCTGGGAATCTTATGGCCACCGAGGGGGGGGGGGGGGGGG 53

Db 7049 GCGGTTGGATAGTCATGGCCCTTGAGGGGGGGGGGGGGGG 7094

RESULT 14
AC113756/c

LOCUS

DEFINITION

AC113756

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AC113756 164800 bp DNA linear HTG 17-JUL-2002
Rattus norvegicus clone CH230-195D20, *** SEQUENCING IN PROGRESS
***, 79 unordered pieces.
AC113756
AC113756.3 GI:21744532
HTG; HTGS_PHASE1.
Norway rat.
Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE AUTHORS

1 (bases 1 to 164800)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Anaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delanaye,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lied,C., Lucier,R., Luna,R., Ma,J., Lozada,R.J., Lu,X., Lucier,A., Lucier,R., Liu,J., Liu,W., Loulsegad,H., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Maxwell,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenko,S., Oguh,M., Okunnu,G., Otaguaye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Roife,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I., Sodergren,E., Sonaite,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,K., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 164800)
Worley,K.C.

Direct Submission
Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 164800)
Worley,K.C.

Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence version replaced gi:19525921.

COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GSES
Center clone name: CH230-195D20

Summary Statistics

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 96892 bases at least Q40
Consensus quality: 103381 bases at least Q30

Consensus quality: 108963 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 79 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1648: contig of 1648 bp in length
* 1649 1748: gap of unknown length
* 1749 2982: contig of 1234 bp in length
* 2983 3082: gap of unknown length
* 3083 4545: contig of 1463 bp in length
* 4546 4645: gap of unknown length
* 4646 5832: contig of 1187 bp in length
* 5833 5932: gap of unknown length
* 5933 7111: contig of 1179 bp in length
* 7112 8227: contig of 1016 bp in length
* 8228 8328: gap of unknown length
* 8329 9534: contig of 1207 bp in length
* 9535 9635: gap of unknown length
* 9636 11087: contig of 1452 bp in length
* 11088 11186: gap of unknown length
* 11187 12505: contig of 1319 bp in length
* 12506 12605: gap of unknown length
* 12606 13936: contig of 1331 bp in length
* 13937 14036: gap of unknown length
* 14037 15243: contig of 1207 bp in length
* 15244 15343: gap of unknown length
* 15344 17223: contig of 1880 bp in length
* 17224 17323: gap of unknown length
* 17324 18400: contig of 1077 bp in length
* 18401 18500: gap of unknown length
* 18501 19843: contig of 1343 bp in length
* 19844 19943: gap of unknown length
* 19944 21185: contig of 1242 bp in length
* 21186 21285: gap of unknown length
* 21286 22817: contig of 1532 bp in length
* 22818 22917: gap of unknown length
* 22918 24380: contig of 1463 bp in length
* 24381 24480: gap of unknown length
* 24481 25864: contig of 1384 bp in length
* 25865 27030: contig of 1066 bp in length
* 27031 27130: gap of unknown length
* 27131 28270: contig of 1140 bp in length
* 28271 29967: contig of 1597 bp in length
* 29968 30068: gap of unknown length
* 30069 32159: contig of 2091 bp in length
* 32159 32258: gap of unknown length
* 32259 33379: contig of 1121 bp in length
* 33380 33479: gap of unknown length
* 33480 34945: contig of 1466 bp in length
* 34946 35046: gap of unknown length
* 35046 36947: contig of 1902 bp in length
* 36948 37047: gap of unknown length
* 37048 38123: contig of 1076 bp in length
* 38124 38223: gap of unknown length
* 38224 39818: contig of 1595 bp in length
* 39819 39918: gap of unknown length
* 39919 41249: contig of 1331 bp in length
* 41250 41349: gap of unknown length
* 41350 43061: contig of 1712 bp in length
* 43062 43161: gap of unknown length
* 43162 44775: contig of 1614 bp in length
* 44776 46481: gap of unknown length
* 46481 46876: contig of 1606 bp in length

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* 46482 46581: gap of unknown length
* 46582 48396: contig of 1815 bp in length
* 48397 48496: gap of unknown length
* 48497 49592: contig of 1096 bp in length
* 49593 51037: gap of unknown length
* 51038 51137: contig of 1345 bp in length
* 51138 52743: gap of unknown length
* 52744 52843: contig of 1606 bp in length
* 52844 54340: gap of unknown length
* 54341 54640: contig of 1697 bp in length
* 54641 56806: gap of unknown length
* 56807 56906: contig of 2166 bp in length
* 56907 58706: gap of unknown length
* 58707 59848: contig of 1700 bp in length
* 59849 61308: gap of unknown length
* 61309 61409: contig of 1142 bp in length
* 61409 62678: gap of unknown length
* 62679 64805: contig of 1270 bp in length
* 64806 64905: gap of unknown length
* 64906 67563: contig of 2027 bp in length
* 67564 67663: gap of unknown length
* 67664 69361: contig of 2658 bp in length
* 69362 69461: gap of unknown length
* 69462 71667: contig of 1698 bp in length
* 71667 73763: gap of unknown length
* 73764 76437: contig of 2205 bp in length
* 76438 76537: gap of unknown length
* 76538 78086: contig of 1997 bp in length
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* 84862 84961: contig of 1732 bp in length
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* 88702 91014: contig of 1772 bp in length
* 91014 91014: contig of 1868 bp in length

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Query Match
Best Local Similarity 46.2%; Score 28.2; DB 2; Length 164800;
Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GTGAGGAGTGGCTGGGAATCTTATGGCCACCCAGAGCGGCGGAGGGGAGT 57
    ||| ||||| ||||| ||| ||| ||| ||||| ||||| ||||| |||||
Db 9180 GTGGGAGTGGATTGGCGGCGGTGATGGATCGGAGAGGGGGGTGGGGGGGAGT 9124

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RESULT 15

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AC111883 170476 bp DNA linear HTG 17-JUL-2002
LOCUS Rattus norvegicus clone CH230-26L15, *** SEQUENCING IN PROGRESS
DEFINITION *** 94 unordered pieces.
ACCESSION AC111883
VERSION AC111883.2 GI:21743819
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
          1 (bases 1 to 170476)
REFERENCE Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
          Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T.,
          Barbara,J., Benton,J., Bimage,K., Blankenburg,K., Bonnini,D.,

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Bouck,J., Bowie,S., Brieve,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J.J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
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Rivas,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoshitari,N., Sisson,I.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Stanley,H., Stone,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczky,K., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,X.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
2 (bases 1 to 170476)
Worley,K.C.
Direct Submission
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 170476)
Worley,K.C.
Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence version replaced gi:18701729.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GOKO
Center clone name: CH230-26L15
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 103990 bases at least Q40
Consensus quality: 112822 bases at least Q30
Consensus quality: 119677 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 94 contigs. The true order of the pieces
* is not known and their order in this sequence record is

```


* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1	1103:	contig	of 1103	bp in length
1104	1203:	gap of unknown	length	
1204	2210:	contig of 1007	bp in length	
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7253	9379:	contig of 2027	bp in length	
9280	9379:	gap of unknown	length	
9380	11053:	contig of 1674	bp in length	
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13599	13698:	gap of unknown	length	
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15026	15125:	gap of unknown	length	
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16378	17396:	contig of 1019	bp in length	
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17497	19368:	contig of 1872	bp in length	
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20594	21607:	contig of 1014	bp in length	
21608	21707:	gap of unknown	length	
21708	22743:	contig of 1036	bp in length	
22744	22843:	gap of unknown	length	
22844	24218:	contig of 1375	bp in length	
24219	24318:	gap of unknown	length	
24319	25319:	contig of 1001	bp in length	
25320	25419:	gap of unknown	length	
25420	26893:	contig of 1474	bp in length	
26894	26993:	gap of unknown	length	
26994	28558:	contig of 1565	bp in length	
28559	28658:	gap of unknown	length	
28659	29266:	contig of 1068	bp in length	
29270	29272:	gap of unknown	length	
29271	30867:	contig of 1041	bp in length	
29827	30967:	gap of unknown	length	
30968	31968:	contig of 1031	bp in length	
31969	32098:	gap of unknown	length	
32099	33304:	contig of 1206	bp in length	
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34502	34601:	gap of unknown	length	
34602	36165:	contig of 1364	bp in length	
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36266	37316:	contig of 1051	bp in length	
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38596	39850:	contig of 1355	bp in length	
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42855	42954:	gap of unknown	length	
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44378	45718:	contig of 1341	bp in length	
45719	45818:	gap of unknown	length	

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 01:37:39 ; Search time 22.1613 Seconds
(without alignments)
6198.732 Million cell updates/sec

Title: US-09-826-581-3_COPY_612_672

Perfect score: 61
Sequence: 1 gtgaggagtggctgggaat.....ggggggcggaggagtcctc 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002.*

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- 24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	61	100.0	1722	AAH43683	PRKAG3 intron 4 -
2	27.2	44.6	143899	AAI38336	Genomic sequence e
3	26	42.6	17761	AAK79415	Human immune/haema
4	26	42.6	17761	ABK42709	Genomic sequence #
5	25.8	42.3	112414	ABL59091	Nucleotide sequenc
6	25.6	42.0	14070	AAK70465	Human immune/haema
7	25.2	41.3	686	AAH08414	Human cDNA clone (
8	25.2	41.3	1030	AAK77940	Human cancer assoc
9	25.2	41.3	1105	AAK77880	Human ATFX coding

c 10	25.2	41.3	1374	22	AAH18673	Human cDNA sequenc
c 11	25.2	41.3	5938	23	ABK42266	Genomic sequence #
c 12	25.2	41.3	9305	24	ABL54634	Human p53AIP1 asso
13	25	41.0	275	24	ABN96428	Gene #2926 used to
14	25	41.0	303	21	AAAI4998	cDNA encoding a hu
c 15	25	41.0	541	20	AAK37383	Human secreted pro
16	25	41.0	1351	24	AAK99401	DNA of APP related
17	24.8	40.7	563	24	ABL93040	Rat metastatic tum
18	24.8	40.7	1727	23	AAK83596	DNA encoding novel
19	24.8	40.7	1991	22	ABK46174	Human breast cell
20	24.8	40.7	1991	22	ABA26334	Probe #4800 for ge
21	24.8	40.7	1991	22	AAK04847	Human brain expres
22	24.8	40.7	1991	22	AAK30374	Human bone marrow
23	24.8	40.7	1991	22	AAI36331	Probe #5017 used t
24	24.8	40.7	1991	24	ABK04972	Human genome-deriv
25	24.8	40.7	2837	22	ABA51286	Human breast cell
26	24.8	40.7	2837	22	ABA36219	Probe #14665 for g
27	24.8	40.7	2837	22	AAK17578	Human brain expres
28	24.8	40.7	2837	22	AAK43391	Human bone marrow
29	24.8	40.7	2837	22	AAI49460	Probe #18146 used
30	24.8	40.7	2837	24	ABK17483	Human genome-deriv
c 31	24.8	40.7	5849	24	ABK17335	Human Rb-interacti
c 32	24.8	40.7	5868	17	AAI18020	Human RIZ allelele D
c 33	24.8	40.7	5868	21	AAA60104	Human RIZ allelele D
c 34	24.8	40.7	5868	21	AAA60123	Human RIZ allelele E
c 35	24.8	40.7	5868	21	AAA60124	Human mutant RIZ a
c 36	24.8	40.7	5868	24	AAK18781	DNA sequence encod
c 37	24.6	40.3	498	15	AAK078112	Hepatitis C virus
c 38	24.6	40.3	573	17	AAI16646	Hepatitis C virus
c 39	24.6	40.3	573	17	AAI16647	Hepatitis C virus
c 40	24.6	40.3	24843	24	AAK17764	Human Genomic DNA
41	24.4	40.0	231	22	ABA73753	Human foetal liver
42	24.4	40.0	231	22	ABA38943	Probe #17409 for g
43	24.4	40.0	231	22	AAK22202	Human brain expres
44	24.4	40.0	231	22	AAK48368	Human bone marrow
45	24.4	40.0	231	22	AAI26223	Probe #16156 for g

ALIGNMENTS

RESULT 1

AAH43683

ID AAH43683 standard; DNA; 1722 Bp.

XX AC AAH43683;

XX DT 21-JAN-2002 (first entry)

XX PRKAG3 intron 4 - intron 10.

XX DE PRKAG3 intron 4 - intron 10.

XX KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;

XX KW metabolic disease; diabetes; obesity; substitution; ds.

XX OS Homo sapiens.

XX FH Key

XX FH Location/Qualifiers

FT intron 1..13

FT /tag= a

FT /number= "Intron 4"

FT /note= "3' portion of intron 4"

FT exon 14..95

FT /tag= b

FT /number= "Exon 5"

FT intron 96..552

FT /tag= c

FT /number= "Intron 5"

FT exon 553..611

FT /tag= d

FT /number= "Exon 6"

FT intron 612..736

FT /tag= e

FT /number= "Intron 6"

```
FT exon 737..782
FT /*tag= f
FT /number= "Exon 7"
FT intron 783..986
FT /*tag= g
FT /number= "Intron 7"
FT exon 987..1041
FT /*tag= h
FT /number= "Exon 8"
FT intron 1042..1242
FT /*tag= i
FT /number= "Intron 8"
FT exon 1243..1369
FT /*tag= j
FT /number= "Exon 9"
FT intron 1370..1522
FT /*tag= k
FT /number= "Intron 9"
FT exon 1523..1688
FT /*tag= l
FT /number= "Exon 10"
FT intron 1689..1722
FT /*tag= i
FT /number= "Intron 10"
FT /*note= "5' portion of intron 10"
XX
PN WO200177305-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-SE00765.
XX
XX 07-APR-2000; 2000US-195665P.
XX
XX (AREX-) AREXIS AB.
XX
XX Andersson L, Luthman H, Marklund S;
XX WPI; 2001-657170/75.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
XX Example 1; Fig 3; 25pp; English.
XX
XX The sequences given in AAH43681-84 represents genomic fragments
CC encoding the human AMP-activated protein kinase gamma 3 subunit
CC (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
CC is useful in determining a risk estimate of a metabolic disease,
CC such as diabetes or obesity, in a subject. The variation may occur
CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of
CC a G for a C at nucleotide 320, resulting in the amino acid
CC substitution P71A; in exon 4 variation may be a substitution of a
CC T for a C at nucleotide 550; and in exon 10 variation may be a
CC substitution of a T for a C at nucleotide 1037, resulting in the
CC amino acid substitution R340W. There may also be nucleotide variation
CC in intron 6.
XX
XX Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0 other;
SQ
Query Match 100.0%; Score 61; DB 22; Length 1722;
Best Local Similarity 100.0%; Pred. No. 5.le-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGAGGAGTGGGCTGGGAATCTTATGGGCACCCAGAGGGGGGGGGAGGAGTCTCT 60
Db |
612 GTGAGGAGTGGGCTGGGAATCTTATGGGCACCCAGAGGGGGGGGGAGGAGTCTCT 671
QY 61 C 61
Db 672 C 672
```

```
RESULT 2
AAL38336
ID AAL38336 standard; DNA; 143899 BP.
XX
XX AC AAL38336;
XX
XX 15-AUG-2002 (first entry)
XX
XX Genomic sequence encoding a human Ngr2 protein.
XX
XX Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;
KW Ngr2; Ngr3; axonal growth; central nervous system; CNS; cerebral injury;
KW spinal cord injury; stroke; demyelinating disease; multiple sclerosis;
KW monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;
KW multifocal leukoencephalopathy; panencephalitis; Spongy degeneration;
KW Alexander's disease; Canavan's disease; metachromatic leukodystrophy;
KW Krabbe's disease; immune; bait protein; genetic mapping; gene therapy;
KW transgenic animal; unregulated cellular growth; cancer; tumour; human;
KW gene; ds.
XX
XX Homo sapiens.
XX
XX WO200229059-A2.
XX
XX 11-APR-2002.
XX
XX 06-OCT-2001; 2001WO-US31488.
XX
XX 06-OCT-2000; 2000US-238361P.
XX
XX (UYIA ) UNIV YALE.
XX
XX (BIOG ) BIOGEN INC.
XX
XX Strittmatter SM, Cate RL, Sah DW;
XX WPI; 2002-416677/44.
XX
XX Novel Nogo receptor homolog polypeptide, Ngr2 or Ngr3, useful for
PT treating central nervous system disorder, cerebral injury, spinal cord
PT injury, stroke, and demyelinating diseases -
XX
XX Example 2; Page 176-214; 277pp; English.
XX
XX The invention relates to a Nogo receptor homologue polypeptide, Ngr2 or
CC Ngr3, comprising a 50 amino acid LRRC sequence, a 284 amino acid NTLRRCT
CC sequence, or a 420, 461 or 392 amino acid sequence, all given in the
CC specification. The Ngr3 protein or its binding antibody is useful for
CC decreasing inhibition of axonal growth of a central nervous system (CNS)
CC neuron, by contacting the neuron Ngr3 or its antibody, and for treating
CC CNS disease, disorder or injury. Ngr3 or a vector comprising Ngr3 is
CC useful for treating cerebral injury, spinal cord injury, stroke,
CC demyelinating diseases, e.g. multiple sclerosis, monophasic
CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,
CC panencephalitis, Marchiafava-Bignami disease, Spongy degeneration,
CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy and
CC Krabbe's disease. Ngr3 is useful for inducing an immune response in a
CC mammal against Ngr3, as a bait protein in a two-hybrid or three-hybrid
CC assay, and as a research tool for identification, characterisation and
CC purification of interacting, regulatory proteins. The nucleotide
CC sequences of the invention are useful for screening for RFLP associated
CC with certain disorders, for genetic mapping, and for gene therapy. The
CC vector containing Ngr3 is useful for producing non-human transgenic
CC animals. The Ngr3 binding antibody is useful for isolating and purifying
CC Ngr3, for localisation and/or quantitation of Ngr3, and for diagnostic
CC and therapeutic purposes. The sequences of the invention, vectors and
CC antibodies are useful for treating or preventing unregulated cellular
CC growth such as cancer and tumour growth. This polynucleotide sequence
CC represents the genomic sequence encoding a human Ngr2 protein of the
XX invention.
XX
XX Sequence 143899 BP; 36346 A; 35277 C; 35318 G; 35657 T; 1301 other;
SQ
```



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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
DR
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 34227; 3071pp + Sequence Listing; English.
PS
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 17761 BP; 3137 A; 5132 C; 5595 G; 3837 T; 0 other;
SQ
Query Match 42.6%; Score 26; DB 22; Length 17761;
Best Local Similarity 65.5%; Pred. No. 50;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GTGAGGAGTGGCTGGGATCTATGCGCACCCAGAGGGCGGGCGGAGGGGAGTC 58
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1563 GTGAGGTGTGGCTGGGTATTCTGTGGGTTCAGAAAGCCCTGCGCTGTGGATC 1620
RESULT 4
ABK42709
ID ABK42709 standard; DNA; 17761 BP.
XX
XX AC ABK42709;
XX
XX 21-MAY-2002 (first entry)
XX
XX Genomic sequence #608 encoding novel human connective tissue polypeptide.
DE
XX
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KW Human; connective tissue related disorder; cancer; gene therapy;
KW cytostatic; gene; ds.
XX
XX Homo sapiens.
XX
XX WO200155343-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01322.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180828.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
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XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231413.
XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
XX 14-SEP-2000; 2000US-0232398.
XX 14-SEP-2000; 2000US-0232399.
XX 14-SEP-2000; 2000US-0232400.
XX 14-SEP-2000; 2000US-0232401.
XX 14-SEP-2000; 2000US-0233063.
XX 14-SEP-2000; 2000US-0233064.
XX 14-SEP-2000; 2000US-0233065.
XX 21-SEP-2000; 2000US-0234223.
XX 21-SEP-2000; 2000US-0234274.
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PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
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PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
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PR 13-OCT-2000; 2000US-0239935.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
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PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.

PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-565190/63.
XX Nucleic acid encoding novel connective tissue associated polypeptides,
PT used in diagnosing, preventing, treating or ameliorating a disorder
PT such as cancer or rheumatoid arthritis -
XX Disclosure; SEQ ID No 1596; 673pp; English.
XX The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
CC (cDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s), including
CC cancer. The polynucleotide sequences of the invention are also useful
CC in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding
CC the novel human connective tissue related polypeptides.
CC Note: the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 17761 BP; 3197 A; 5132 C; 5595 G; 3837 T; 0 other;
SQ

Query Match 42.6%; Score 26; DB 23; Length 17761;
Best Local Similarity 65.5%; Pred. No. 50;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GTGAGGAGTGGCTGGGAATCTTATGGCACCCAGAGGGCGGGCGGAGGAGTC 58
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1563 GTGAGGTGTGGCTGGGTATTGTCTGGGTTCCAGAAAGCCTGTGCCGTGGAGTC 1620

RESULT 5
ABL59091/c
ID ABL59091 standard; DNA; 112414 BP.
XX
AC ABL59091;
XX
DT 20-AUG-2002 (first entry)
XX
DE Nucleotide sequence of Ehime-1 strain of Red sea bream iridovirus.
XX
KW Neutralisation; Chrysophrys major iridovirus; antigen; RSIV; ss.
XX
OS Red sea bream iridovirus.
XX
PN JP2002101895-A.
XX
XX 09-APR-2002.
XX
PF 27-SEP-2000; 2000JP-0294991.
XX
XX 27-SEP-2000; 2000JP-0294991.
XX
XX (NORQ) NORINSUISANSHO YOSHOKU KENKYU.
XX (KURI/) KURITA J.
XX
XX WPI; 2002-440455/47.
XX
XX A DNA encoding a protein related to neutralization and infection
PT prevention of Chrysophrys major iridovirus -
XX
XX Example 1; Page 13-51; 65pp; Japanese.
XX
XX The specification describes proteins related to neutralisation and
CC infection prevention of Chrysophrys major iridovirus. The protein
CC encoded by the DNA is useful as an antigen for preventing infection
CC of Chrysophrys major iridovirus. The present sequence represents the

CC nucleotide sequence of the Ehime-1 strain of Red sea bream iridovirus
CC (RSIV).
XX
SQ Sequence 112414 BP; 26205 A; 29684 C; 30351 G; 26174 T; 0 other;
Query Match 42.3%; Score 25.8; DB 24; Length 112414;
Best Local Similarity 73.3%; Pred. No. 67;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 10 GGCTGGGAACCTTATGGCCACAGAGGGGGGGGGGGAGGGG 54
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 18391 GGGTGGCGATCTGATGGGTGACAAAGAGGGGCTGTAGCCAGGGG 18347
RESULT 6
AAK70465
ID AAK70465 standard; DNA; 14070 BP.
AC
XX AAK70465;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25277.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX
PN W0200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225274.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0244675.
PR 08-NOV-2000; 2000US-0244676.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.


```

XX 08-FEB-2001 (first entry)
XX Human cancer associated gene sequence SEQ ID NO:334.
XX
XX Human; cancer associated gene; cancer antigen; detection; cancer;
XX diagnosis; cytostatic; proliferative; vulnery; immunomodulator;
XX antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
XX antinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
XX dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
XX vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
XX immune disorder; hematopoietic cell disorder; autoimmune disorder;
XX allergic reaction; graft versus host disease; organ rejection;
XX haemostatic; thrombolytic; cardiovascular disorder; infection;
XX neurological disease; drug screening; ss.
XX
XX Homo sapiens.
XX
XX WO200055350-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05882.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI: 2000-587533/55.
XX
XX P-PSDB; AAB43731.
XX
XX Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer -
XX
XX Claim 1; Page 886; 2352pp; English.
XX
XX AAC77607 to AAC78448 encode the human cancer associated proteins given
XX in AAB43398 to AAB44239. The proteins can have activities based on the
XX tissues and cells the genes are expressed in. Example of activities
XX include: cytostatic; proliferative; vulnery; immunomodulator;
XX antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
XX antinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
XX dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
XX nootropic; vasotropic; antipsoriatic and antiangiogenic. The
XX polynucleotides and polypeptides can be used for preventing, treating or
XX ameliorating medical conditions and diagnosing pathological conditions.
XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from
XX the present invention may be used to treat immune disorders by activating
XX or inhibiting the proliferation, differentiation or mobilisation of
XX immune cells, to treat disorders of hematopoietic cells, autoimmune
XX disorders, allergic reactions, graft versus host disease and organ
XX rejection, modulate haemostatic or thrombolytic activity, modulate
XX inflammation, cancers, cardiovascular disorders, neurological disease and
XX bacterial or viral infections. The peptides, nucleotides, antibodies,
XX agonists and antagonists may be also be used in drug screens. AAC78449 to
XX AAC78457 and AAB44240 represent sequences used in the exemplification of
XX the present invention.
XX
XX Sequence 1030 BP; 175 A; 362 C; 287 G; 195 T; 11 other;
XX
XX Query Match 41.3%; Score 25.2; DB 21; Length 1030;
XX Best Local Similarity 66.7%; Pred. No. 72;
XX Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
XX
XX Oy 4 AGGAGTGGCTGGGAATCTATGGCACCACAGGGCGGGCGGAGGAGT 57
XX ||| | | | | | | | | | | | | | | | | | | | | |
XX Db 418 AGGGCTCCCAAGACCTCATAGGAGCCAGGGGGGCGAGGGGGGAGT 365
XX
XX RESULT 9
XX AAC77880/c

```

```

ID AAF77880 standard; cDNA; 1105 BP.
XX
XX AAC77880;
XX
XX 30-MAY-2001 (first entry)
XX
XX Human ATFX coding sequence with 5' extension.
XX
XX Human; ATFX; gamma aminobutyric acid B receptor; GABA B receptor;
XX transcription factor; ss.
XX
XX Homo sapiens.
XX
XX WO200116596-A2.
XX
XX 08-MAR-2001.
XX
XX 31-AUG-2000; 2000WO-GB03361.
XX
XX 31-AUG-1999; 99GB-0020569.
XX
XX 12-JAN-2000; 2000GB-0000516.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX White J, Wise A, Marshall F;
XX
XX WPI: 2001-265904/27.
XX
XX P-PSDB; AAB80896.
XX
XX Identifying modulators of gamma aminobutyric acid(GABA)-B receptor
XX mediated activity by monitoring the interaction between GABAB receptor
XX and the CREB/ATF transcription factors in the presence of a test
XX substance -
XX
XX Claim 17; Fig 9; 71pp; English.
XX
XX The present invention relates to a method for identifying a modulator of
XX gamma aminobutyric acid_B (GABA_B) receptor-mediated activity, by
XX monitoring the interaction between a CREB/ATF transcription factor
XX capable of binding to GABA_B receptor. The present sequence is the coding
XX sequence for human ATFX, which was used in the method of the present
XX invention. ATFX is a member of the CREB/ATF family of transcription
XX factors. ATFX contains a bZIP domain, by which it interacts with the
XX coiled coil domain of GABA_B receptor. Modulators of GABA_B receptor
XX activity are useful for treating central nervous system or peripheral
XX nervous system disorders. The present sequence encodes an ATFX protein
XX with a N-terminal extension (compared to AAB80892).
XX
XX Sequence 1105 BP; 198 A; 399 C; 308 G; 200 T; 0 other;
XX
XX Query Match 41.3%; Score 25.2; DB 22; Length 1105;
XX Best Local Similarity 66.7%; Pred. No. 72;
XX Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
XX
XX Oy 4 AGGAGTGGCTGGGAATCTATGGCACCACAGGGCGGGCGGAGGAGT 57
XX ||| | | | | | | | | | | | | | | | | | | | | |
XX Db 190 AGGGCTCCCAAGACCTCATAGGAGCCAGGGGGGCGAGGGGGGAGT 137
XX
XX RESULT 10
XX AAC77880/c
XX
XX AAC77880 standard; cDNA; 1374 BP.
XX
XX AAC77880;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human cDNA sequence SEQ ID NO:18921.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX Homo sapiens.
XX

```


XX Sequence 303 BP; 67 A; 85 C; 110 G; 41 T; 0 other;
SQ Query Match 41.0%; Score 25; DB 21; Length 303;
Best Local Similarity 64.9%; Pred. No. 75;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 5 GGATGGCTGGGAATCTTATGGGCACCCAGAGGGGGCGGGAGGAGTCTCTC 61
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 GGAGCGGATCGAAGGAGCGGACACCATGAAGAGAGCGGCGGCGGAGTTCTC 155
RESULT 15
AAX37383/C
ID AAX37383 standard; cDNA; 541 BP.
XX
AC AAX37383;
XX
DT 06-JUL-1999 (first entry)
XX
DE Human secreted protein cDNA fragment containing gene 15.
XX
KW Human; secreted protein; prevention; treatment; protein therapy;
KW gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder;
KW developmental abnormality; foetal deficiency; blood disorder; lymphoma;
KW leukemia; immune system disorder; autoimmune disease; hepatic disease;
KW renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS;
KW Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;
KW arthritis; psoriasis; digestive; endocrine; infection; ss.
XX
OS Homo sapiens.
XX
PN W09909155-A1.
XX
PD 25-FEB-1999.
XX
PF 18-AUG-1998; 98WO-US17044.
XX
PR 16-JUN-1998; 98US-0092956.
PR 15-JUL-1998; 98US-0092956.
PR 19-AUG-1997; 97US-0056368.
PR 19-AUG-1997; 97US-0056369.
PR 19-AUG-1997; 97US-0056535.
PR 19-AUG-1997; 97US-0056555.
PR 19-AUG-1997; 97US-0056556.
PR 19-AUG-1997; 97US-0056628.
PR 19-AUG-1997; 97US-0056629.
PR 19-AUG-1997; 97US-0056726.
PR 19-AUG-1997; 97US-0056728.
XX
(HUMA-) HUMAN GENOME SCI INC.
XX
PI Brewer LA, Duan R, Ebner R, Endress GA, Feng P;
PI Florence C, Florence KA, Komatsoulis GA, Lafleur DW;
PI Moore PA, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR;
PI Young PE;
XX
WPI: 1999-150160/16.
DR P-PSDB; AAY07758.
XX
PT New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1a; Page 198; 280pp; English.
XX
CC This invention describes novel isolated human secreted proteins and
CC their encoding nucleic acid sequences. The products of the invention
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also pathological conditions can be
CC diagnosed by determining the presence or amount of expression of
CC the new polypeptides in a sample or by determining the presence or
CC absence of mutations in the new polynucleotides. Specific uses are

CC described for each of the 70 polynucleotides, based on which tissues
CC they are most highly expressed in, and include developing products for
CC the diagnosis or treatment of cancer, tumours, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC asthma, sepsis, diabetes, Alzheimer's and cognitive disorders,
CC schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine
CC disorders, infections and AIDS. The human secreted proteins of the
CC invention are represented in AAY07744-Y07850 and the encoding nucleic
CC acids are represented in AAX37369-X37441.
XX
SQ Sequence 541 BP; 118 A; 135 C; 131 G; 155 T; 2 other;
Query Match 41.0%; Score 25; DB 20; Length 541;
Best Local Similarity 69.4%; Pred. No. 79;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 12 GCTGGGAATCTTATGGGCACCCAGAGGGGGCGGGAGGAGGAGTCTCT 60
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 GATGGGTAAGATCTGGAGACAGATGGGGGGGGGGGGGGGAGTCTCT 14
Search completed: June 13, 2003, 02:59:50
Job time : 23.1613 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:37:44 ; Search time 151.839 Seconds
(without alignments)
6506.409 Million cell updates/sec

Title: US-09-826-581-3_COPY_612_672

Perfect score: 61
Sequence: 1 9t9agggagtggtgggaat.....ggggggcggaggagtcctc 61

Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_plo:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	32.2	52.8	354	10	AW026388	AW026388 w12f05.x
c 2	30.4	49.8	1208	14	BQ433885	BQ433885 AGENCOURT
c 3	29.8	48.9	1056	14	BM600472	BM600472 AGENCOURT
c 4	29.2	47.9	688	9	AL514251	AL514251 AL514251
c 5	28.8	47.2	1084	14	BQ708179	BQ708179 AGENCOURT
c 6	28.4	46.6	872	9	AL530561	AL530561 AL530561

7	28.2	46.2	735	12	BG309093	BG309093 HVSMEC000
c 8	28.2	46.2	1729	14	BM909483	BM909483 AGENCOURT
c 9	28	45.9	403	14	BQ521472	BQ521472 NISC_n11
c 10	28	45.9	530	14	BQ038856	BQ038856 pgn1c_pk0
c 11	27.8	45.6	653	17	AG122806	AG122806 Pan trogl
c 12	27.8	45.6	712	17	AG090162	AG090162 Pan trogl
c 13	27.8	45.6	1434	14	BQ648687	BQ648687 AGENCOURT
c 14	27.6	45.2	493	17	BH756447	BH756447 SALK_0536
c 15	27.6	45.2	1242	13	B1489045	B1489045 AG03021030
c 16	27.6	45.2	1293	14	BM912901	BM912901 AGENCOURT
c 17	27.4	44.9	272	10	BF195192	BF195192 BB195192
c 18	27.4	44.9	576	12	BF430892	BF430892 OG05G06T3
c 19	27.4	44.9	740	13	B1955582	B1955582 HVSME002
c 20	27.4	44.9	901	17	AZ200974	AZ200974 SP_0055_A
c 21	27.4	44.9	1386	12	BE963498	BE963498 601657281
c 22	27.2	44.6	212	9	AU256222	AU256222 AU256222
c 23	27.2	44.6	733	17	AG180340	AG180340 Pan trogl
c 24	27.2	44.6	883	17	AZ527770	AZ527770 ENTD480T
c 25	27.2	44.6	886	12	BF272027	BF272027 GA_Eb001
c 26	27.2	44.6	894	13	B1953428	B1953428 HVSME001
c 27	27.2	44.6	912	12	BG191779	BG191779 RST10875
c 28	27.2	44.6	926	12	BE890765	BE890765 601431204
c 29	27.2	44.6	997	14	BQ675584	BQ675584 AGENCOURT
c 30	27.2	44.6	1097	14	BM801525	BM801525 AGENCOURT
c 31	27.2	44.6	1101	17	CNS00DDA	AL067198 DTOSOPH11
c 32	27.2	44.6	1327	13	BM464195	BM464195 AGENCOURT
c 33	27	44.3	211	10	BB379140	BB379140 BB379140
c 34	27	44.3	442	13	BM116323	BM116323 L0834C09-
c 35	27	44.3	833	10	BE559614	BE559614 601347308
c 36	27	44.3	1015	12	BF215427	BF215427 601880953
c 37	27	44.3	1066	14	BQ066683	BQ066683 AGENCOURT
c 38	26.8	43.9	282	9	AA872225	AA872225 oh71b02.s
c 39	26.8	43.9	443	10	BB858755	BB858755 BB858755
c 40	26.8	43.9	943	12	BE744657	BE744657 601577506
c 41	26.8	43.9	1099	14	BQ878976	BQ878976 AGENCOURT
c 42	26.8	43.9	1555	14	BM923470	BM923470 AGENCOURT
c 43	26.6	43.6	243	10	BB038623	BB038623 BB038623
c 44	26.6	43.6	392	10	AW081866	AW081866 xb56c05.x
c 45	26.6	43.6	659	13	B1954751	B1954751 HVSME001

ALIGNMENTS

RESULT 1
AW026388/c 354 bp mRNA linear EST 09-MAR-2000
LOCUS w12f05.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529345 3',
DEFINITION similar to contains element MSK1 repetitive element ; , mRNA
sequence.
ACCESSION AW026388
VERSION AW026388.1 GI:5879918
KEYWORDS EST,
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 354)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.lnl.gov/bbrp/image/image.html
 Insert Length: 1245 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 338.
 Location/Qualifiers

FEATURES

source

1. 334
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2529345"
 /clone_lib="NCL CGAP Brn23"
 /tissue_type="glioblastoma (pooled)"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lstr strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 72 a 104 c 89 g 88 t 1 others

ORIGIN

Query Match 52.8%; Score 32.2; DB 10; Length 354;
 Best Local Similarity 74.1%; Pred. No. 19;
 Matches 40; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 8 GTGGCGCTGGGAATCTTATGGCACCCAGAGGGCGGGGGAGGAGTCTCT 61

Db 213 GGGGGGGGGGATCTTTGGAAACCCNGGGGGGGGGGGGGAGCCCC 160

RESULT 2

BQ433885/c

LOCUS

DEFINITION AGENCOURT_7751176 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6062177
 5', mRNA sequence.

ACCESSION

VERSION BQ433885.1 GI:21172961

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1333 row: d column: 18

High quality sequence stop: 135.

Location/Qualifiers

1. 1208

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6062177"

/clone_lib="NIH_MGC_72"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

BASE COUNT 182 a 536 c 129 g 360 t 1 others

ORIGIN

Query Match 49.8%; Score 30.4; DB 14; Length 1208;
 Best Local Similarity 71.4%; Pred. No. 69;
 Matches 40; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 2 TGAGGAGTGGCTGGGAATCTTATGGCACCCAGAGGGCGGGGGAGGAGT 57

Db 1118 TGAGGAGGGCTCTGGGGAGATCAGGGGGAATAGAGGGGGGGGGGAGAGAAT 1063

RESULT 3

BM800472/c

LOCUS

DEFINITION BM800472 1056 bp mRNA linear EST 05-MAR-2002
 AGENCOURT_6419113 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5534991
 5', mRNA sequence.

ACCESSION

VERSION BM800472.1 GI:19117295

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1056)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12222 row: f column: 16

High quality sequence stop: 635.

Location/Qualifiers

1. 1056

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5534991"

/clone_lib="NIH_MGC_71"

/tissue_type="leiomyosarcoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pCMV-Sport6; Site_1: NotI;
 Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 2.1 kb."

BASE COUNT 238 a 334 c 277 g 207 t

ORIGIN

Query Match 48.9%; Score 29.8; DB 14; Length 1056;
 Best Local Similarity 70.2%; Pred. No. 1e+02;
 Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CTGAGGAGTGGCTGGGAATCTTATGGCACCCAGAGGGCGGGGGAGGAGT 57

Db 983 GAGGGGGAGGGCTTGGGAATCTTATGGTGAACATGAGGGGGGGCGCGCGATT 927

RESULT 4

AL514251

LOCUS

DEFINITION AL514251 LTI_NFL006_PL2 Homo sapiens cDNA clone CLOB0062G02 3
 prime, mRNA sequence.

ACCESSION

VERSION AL514251.1 GI:12777745

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS      Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. .688
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="CL0BB006ZG02"
   /clone_lib="LTI_NFL006_PL2"
   /tissue_type="placenta"
   /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
   was primed with a NotI-oligo(dT) primer. Five prime end
   enriched, double-stranded cDNA was digested with Not I and
   cloned into the Not I and Eco RV sites of the pCMVSPORT 6
   vector. Library was normalized. Library was constructed by
   Life Technologies. Contact : Feng Liang Life Technologies,
   a division of Invitrogen 9800 Medical Center Drive
   Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
   Email : fliang@lifetech.com URL :
   http://fulllength.invitrogen.com"

BASE COUNT   201 a   99 c  163 g  145 t   80 others
ORIGIN

Query Match      47.9%; Score 29.2; DB 9; Length 688;
Best Local Similarity 55.7%; Pred. No. 1.4e+02;
Matches 34; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 GTGAGGAGTGGGCTGGGAATCTTATGGCACCCAGAGGGGGGGGGGAGGAGTCT 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 379 GGGGGGGGGGGGGAAGAAWNYTTKSCCSCGGGGGGGGGGGGGGGGGGGCC 438

QY 61 C 61
   |
Db 439 C 439

RESULT 5
BQ708179/c
LOCUS        BQ708179      1084 bp      mRNA      linear      EST 16-JUL-2002
DEFINITION   AGENCOURT_8292191 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280902
5', mRNA sequence.
ACCESSION    BQ708179
VERSION      BQ708179.1 GI:21847078
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM2472 row: n column: 07
High quality sequence stop: 415.
Location/Qualifiers
1. .1084
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="IMAGE:6280902"

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/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT   139 a   421 c   311 g   213 t
ORIGIN

Query Match      47.2%; Score 28.8; DB 14; Length 1084;
Best Local Similarity 69.6%; Pred. No. 1.9e+02;
Matches 39; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GTGAGGAGTGGGCTGGGAATCTTATGGCACCCAGAGGGGGGGGGGAGGAG 56
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 834 GTGAGGAGGCTCGGGCAGCCGACGTCGACGCGGAGGGGGGGGGGGGGG 779

RESULT 6
AL530561
LOCUS        AL530561      872 bp      mRNA      linear      EST 13-FEB-2001
DEFINITION   AL530561 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD007Y022 5
prime, mRNA sequence.
ACCESSION    AL530561
VERSION      AL530561.1 GI:12794054
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .872
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="CS0DD007Y022"
   /clone_lib="LTI_NFL001_NBC4"
   /sex="male"
   /tissue_type="neuroblastoma cells"
   /lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT   195 a   189 c   337 g   38 t   113 others
ORIGIN

Query Match      46.6%; Score 28.4; DB 9; Length 872;
Best Local Similarity 55.2%; Pred. No. 2.4e+02;
Matches 32; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 GTGAGGAGTGGGCTGGGAATCTTATGGCACCCAGAGGGGGGGGGGAGGAGTC 58
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 379 GGGAGGAGKGAAGAAKGAAGKGGKGCACAGKGGCGGGGGKCGKAGCGGCC 436

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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
1. (bases 1 to 403)
NIH-XGC http://image.llnl.gov/image/html/xenopuslib_info.shtml.
National Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
Unpublished (2002)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
CDNA Library Preparation:
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
  DNA Sequencing by: National Institutes of Health Intramural
  Sequencing Center (NISC)
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  info@image.llnl.gov
Plate: L1AM1853 row: F column: 1
Seq primer: -21M13 forward primer (ABI).
FEATURES
    source
        1..403
            /organism="Silurana tropicalis"
            /db_xref="taxon:8364"
            /clone="IMAGE:5336064"
            /clone_lib="NICHG_XGC Emb7"
            /tissue_type="tailbud"
            /dev_stage="embryo, stages 20-27"
            /lab_host="DH10B (phage-resistant)"
            /note="Vector: pCMV-SPORT6.cdb; Site:1: NotI; Site:2:
            EcoRV; Cloned unidirectionally. Primer: Oligo dt. Average
            insert size 2.1 kb. Constructed by Invitrogen. Note: This
            is a Xenopus Gene Collection (XGC) library."
BASE COUNT      68 a 123 c 69 g 143 t
ORIGIN
Query Match      45.9%; Score 28; DB 14; Length 403;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY      2 TGAGAGTGGCTGGGAACTTATGGCCACCCAGAGGGCGGGCGGAGGGAGTCTCTC 61
Db      11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
26 TGGGGGGGGGGGGGGAATCTTCCAAAGGGCGGGGGGGAAGGGGCCCCCCCC 167

RESULT 10
BQ038856
LOCUS      530 bp mRNA linear EST 01-MAY-2002
DEFINITION      pgnlc.pk010.k15 normalized chicken lymphoid cDNA library Gallus
                gallus clone pgnlc.pk010.k15 5' similar to no significant hits
                (plog(P) 4), mRNA sequence.
ACCESSION      BQ038856
VERSION      BQ038856.2 GI:20383618
KEYWORDS      EST.
SOURCE      Chicken.
ORGANISM      Gallus gallus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                Phasianinae; Gallus.
REFERENCE      1 (bases 1 to 530)
AUTHORS      Morgan,R.W. and Burnside,J.
TITLE      Chicken lymphoid ESTs
JOURNAL      Unpublished (2001)
COMMENT      On Mar 27, 2002 this sequence version replaced gi:19772396.
                Contact: Joan Burnside
                Molecular Endocrinology
                University of Delaware
                40 Townsend Hall, Newark, DE 19717, USA
                Tel: 302 831-1345
                Fax: 302-831-3411
                Email: joan@udel.edu, www.chickest.udel.edu.
FEATURES
    source
        1..530
            /location/Qualifiers
            /organism="Gallus gallus"
            /db_xref="taxon:9031"

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/clone="pgnlc.pk010.k15"
/clone_lib="normalized chicken lymphoid cDNA library"
/sex="Male and Female"
/tissue_type="thymus, bursa, spleen, PBL, bone marrow"
/lab_host="E.coli EMDH10B"
/note="Vector: pCMVSPORT 6"
BASE COUNT      80 a 149 c 142 g 126 t
ORIGIN
Query Match      45.9%; Score 28; DB 14; Length 530;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY      2 TGAGAGTGGCTGGGAACTTATGGCCACCCAGAGGGCGGGCGGAGGGAGTCTCTC 61
Db      11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
107 TGTGGGTGGGCTGTGCATCGGGGCCACGCGGAGCAGCAGCGAGGGGGTCTTC 166

RESULT 11
AG122806/c
LOCUS      653 bp DNA linear GSS 04-NOV-2001
DEFINITION      Pan troglodytes DNA, clone: PTB-132E07.R, genomic survey sequence.
ACCESSION      AG122806
VERSION      AG122806.1 GI:16651971
KEYWORDS      GSS.
SOURCE      Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
                BAC Library clone:PTB-132E07.R.
ORGANISM      Pan troglodytes
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE      1
AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
                Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      BAC end sequences of Library PTB
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 653)
AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
                Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                (E-mail:chimbases@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
                Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT      Clones are derived from the chimpanzee BAC library PTB This BAC end
                was generated during the Rad process and may have higher chance of
                clone tracking errors.
                PRIMERS
                Sequencing: M13Rev
                LIBRARY
                Vector : pKS145
                R.Site 1 : SacI
                R.Site 2 : SacI.
FEATURES
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        1..653
            /location/Qualifiers
            /organism="Pan troglodytes"
            /db_xref="taxon:9598"
            /clone="PTB-132E07.R"
            /sex="male"
            /cell_type="lymphoblast"
            /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      140 a 258 c 82 g 173 t
ORIGIN
Query Match      45.6%; Score 27.8; DB 17; Length 653;
Best Local Similarity 69.1%; Pred. No. 3.4e+02;
Matches 38; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY      3 GAGAGTGGGCTGGGAATCTTATGGCCACCCAGAGGGCGGGCGGAGGGAGT 57
Db      11 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
495 GAGGAGTGGGATAGGAATAGAGGGCGGCGGAGTGTGTGGGGTGGGTAGT 441

```

RESULT 12
AG090162/c
LOCUS
DEFINITION Pan troglodytes DNA, clone: PTB-089K05.R, genomic survey sequence.
ACCESSION AG090162
VERSION AG090162.1 GI:16641964
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC library clone:PTB-089K05.R.
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki.Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 712)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe.H. and Sakaki.Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimbegscgsc.riken.go.jp, URL:http://bgp.gsc.riken.go.jp/, Tel.:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS Sequencing: MJ3Rev
LIBRARY Vector : pKS145 R.Site 1 : SacI R.Site 2 : SacI. Location/Qualifiers 1..712 /organism="Pan troglodytes" /db_xref="taxon:9598" /clone="PTB-089K05.R" /sex="male" /cell_type="lymphoblast" /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 126 a 230 c 205 g 150 t 1 others
ORIGIN
Query Match 45.6%; Score 27.8; DS 17; Length 712; Best Local Similarity 69.1%; Pred. No. 3.5e+02; Matches 38; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 7 ACTGGCTGGGAATCTTATGCCACCACAGCGGGCGGGCCGAGGGGACTCCTC 61
Dd 688 ACTCGTGCGCATATAACAGAAACAACGCGGACTGGAGTGGGAAGGAGTCCTC 634
RESULT 13
BQ648687/c
LOCUS BQ648687
DEFINITION AGENCOURT_8297851 NIH_MGC_100 Homo sapiens cdNA clone IMAGE:6270062 5', mRNA sequence.
ACCESSION BQ648687
VERSION BQ648687.1 GI:21772859
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D. Email: ccapbs-re@mail.nih.gov
COMMENT

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:39:09 ; Search time 4.64516 seconds
(without alignments)
4027.262 Million cell updates/sec

Title: US-09-826-581-3_COPY_612_672

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	SUMMARIES			ID	Description
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C 1	24.8	40.7	5183	1	US-08-459-568-3
C 2	24.8	40.7	5183	2	US-08-399-411-3
C 3	24.8	40.7	5868	3	US-08-516-859A-3
C 4	24.8	40.7	5868	4	US-09-586-472-3
C 5	24.8	40.7	5868	4	US-09-528-706-3
C 6	24.6	40.3	573	2	US-08-290-665A-139
C 7	24.6	40.3	573	2	US-08-290-665A-140
C 8	24.6	40.3	573	5	PCT-US95-10398-139
C 9	24.6	40.3	573	5	PCT-US95-10398-140
C 10	24.4	40.0	957	4	US-08-836-075A-17
C 11	24.4	40.0	4403765	4	US-09-103-840A-2
C 12	24.4	40.0	4411529	4	US-09-103-840A-1
C 13	24.2	39.7	31571	1	US-08-323-443B-1
C 14	24.2	39.7	53526	3	US-08-658-136-2
C 15	24.2	39.7	53577	3	US-08-658-136-1
C 16	24	39.3	739	4	US-08-943-731-136
C 17	24	39.3	24183	4	US-08-943-731-3
C 18	23.4	38.4	393	3	US-09-188-930-26
C 19	23.4	38.4	601	4	US-09-336-536-74
C 20	23.4	38.4	728	4	US-09-336-536-2
C 21	23.4	38.4	1001	3	US-09-188-930-218
C 22	23.4	38.4	1015	3	US-09-188-930-30
C 23	23.4	38.4	1338	4	US-09-336-536-1
C 24	23.4	38.4	1347	4	US-09-140-804-1
C 25	23.4	38.4	2543	1	US-08-555-669-11
C 26	23.4	38.4	2543	3	US-09-073-663-11
C 27	23.2	38.0	1701	3	US-09-264-737-3

Sequence 1, Appli
Sequence 1, Appli
Sequence 135, App
Sequence 136, App
Sequence 137, App
Sequence 138, App
Sequence 139, App
Sequence 144, App
Sequence 135, App
Sequence 136, App
Sequence 137, App
Sequence 138, App
Sequence 144, App
Sequence 3, Appli
Sequence 85, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-08-459-568-3/C
; Sequence 3, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..5158
US-08-459-568-3

Query Match 40.7%; Score 24.8; DB 1; Length 5183;
Best Local Similarity 67.3%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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QY      3 GAGGACTGGCTGGCGAAATCTATTGGCCACCACCCAGAGGGCGGGCGCGAGGGG 54
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Db     3002 GAAGAGGGGGCTGGGAAGAGGTACGGTAGGAAGAGGAGGGGAGGGCGGAGTGG 2951

RESULT 2
US-08-399-411-3/C
; Sequence 3, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,411
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..5158
; US-08-399-411-3

Query Match 40.7%; Score 24.8; DB 2; Length 5183;
Best Local Similarity 67.3%; Pred.No.12;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY      3 GAGGAGTGCGCTGGCGAAATCTATTGGCCACCACCCAGAGGGCGGGCGCGAGGGG 54
       || ||| ||||| | || ||| ||||| ||||| ||||| ||||| ||||| ||
Db     3002 GAAGAGGGGGCTGGGAAGAGGTACGGTAGGAAGAGGAGGGGAGGGCGGAGTGG 2951

RESULT 3
US-08-516-859A-3/c
; Sequence 3, Application US/08516859A
; Patent No. 6069231
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

```

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;
; FILING DATE: 06-MAR-1995
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 4130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5868 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..5278
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-586-472-3

Query Match      40.7%; Score 24.8; DB 4; Length 5868;
Best Local Similarity 67.3%; Pred. No. 13;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY  3 GAGAGTGGGCTGGGAATCTTATGGGCACCCAGAGGGGGGGGGGGAGGGG 54
    || || || || || || || || || || || || || || || || || ||
Db  3122 GAAGAGGGGGCTGGAAGAGGACGTACGTTAGGAAGAGGGGGGGGGAGTGG 3071

RESULT 5
US-09-528-706-3/c
; Sequence 3, Application US/09528706
; Patent No. 6468985
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5868 base pairs
; TYPE: nucleic acid
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;
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..5278
US-09-528-706-3

Query Match      40.7%; Score 24.8; DB 4; Length 5868;
Best Local Similarity 67.3%; Pred. No. 13;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY  3 GAGAGTGGGCTGGGAATCTTATGGGCACCCAGAGGGGGGGGGGGAGGGG 54
    || || || || || || || || || || || || || || || || || ||
Db  3122 GAAGAGGGGGCTGGAAGAGGACGTACGTTAGGAAGAGGGGGGGGGAGTGG 3071

RESULT 6
US-08-290-665A-139/C
; Sequence 139, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
; APPLICANT: BURK, J., MILLER, R.H. AND
; APPLICANT: PURCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: 24
US-08-290-665A-139

Query Match      40.3%; Score 24.6; DB 2; Length 573;
Best Local Similarity 70.2%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY  12 GCTGGGAATCTTATGGGCACCCAGAGGGGGGGGGGGAGGGGAGTC 58
    || || || || || || || || || || || || || || || || || ||
Db  340 GCCTGGGATCATTTGGGCCCAAGATGGCGGAGAGCCGCGAGGAGAC 294
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RESULT 7
US-08-290-665A-140/C
; Sequence 140, Application US/08290665A
; Patent No. 5802852
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PORCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,665A
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: 28
US-08-290-665A-140

Query Match          40.3%; Score 24.6; DB 2; Length 573;
Best Local Similarity 70.2%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      12 GCTGGGAATCTTATGGCCACCGAGGGCGGGCGGAGGGGAGTC 58
        || || || || || || || || || || || || || || || ||
DB      340 GCCGGGGATCATTTGGGCCCCAAGACGGTCGAGAGCCGCGGGGAC 294

RESULT 8
PCT-US95-10398-139/C
; Sequence 139, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PORCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
```

```
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10398
; FILING DATE: 15-AUG-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29 JUNE 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290/665
; FILING DATE: 15 AUGUST 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: 24
PCT-US95-10398-139

Query Match          40.3%; Score 24.6; DB 5; Length 573;
Best Local Similarity 70.2%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      12 GCTGGGAATCTTATGGCCACCGAGGGCGGGCGGAGGGGAGTC 58
        || || || || || || || || || || || || || || || ||
DB      340 GCCGGGGATCATTTGGGCCCCAAGATGCCGAGAGCCGCGAGGAGAC 294

RESULT 9
PCT-US95-10398-140/C
; Sequence 140, Application PC/TUS9510398
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; APPLICANT: PORCELL, R.H.
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
; TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
; TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
; TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10398
; FILING DATE: 15-AUG-1995
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; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 957 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-836-075A-17

Query Match 40.0%; Score 24.4; DB 4; Length 957;
Best Local Similarity 68.0%; Pred. No. 14;
Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 9 TGGGCTGGGAATCTATTGGCCACCAGAGGGGGGGGGGAGGAGGAGTC 58
Db 343 TGTGGCGGGGGCTGCTTTTGGCCCCCAGAGGGGGGAGAGCCCGGGGGGAC 294

RESULT 11
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: FRASER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 40.0%; Score 24.4; DB 4; Length 4403765;
Best Local Similarity 63.8%; Pred. No. 30;
Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 3 GAGGAGTGGCTGGGAATCTATTGGCCACCAGAGGGGGGGGGGAGGAGGAGTCCT 60
Db 3958304 GAAGGTTGTCGACGAAGTTTGTGGCGCCCGACAGATCGTTCGAGCGCATGGACCT 3958247

RESULT 12
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: FRASER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

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; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      40.0%; Score 24.4; DB 4; Length 4411529;
Best Local Similarity 63.8%; Pred. No. 30;
Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 3 GAGGAGTGGCTGGGAATCTTATGGCACCAGAGGGCGGGCGGAGGGAGTCTCT 60
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Db 3966215 GAAGGGTGTGAGCAAGTTTCTGGGCCCCACATCGGTGGCAGCGATGACACCT 3966159

RESULT 13
US-08-323-443B-1
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0372/OA462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match      39.7%; Score 24.2; DB 1; Length 31571;
Best Local Similarity 62.3%; Pred. No. 24;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GTGAGGAGTGGCTGGGAATCTTATGGCACCAGAGGGCGGGCGGAGGGAGTCTCT 60
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Db 16436 GTCACTCGTGGGAGGGTGACACCTGGGGAAGTAGAGCCCTGGCAGGAGTGAAGCCT 16495
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QY 61 C 61
Db 16496 C 16496

RESULT 14
US-08-658-136-2
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GENA-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match      39.7%; Score 24.2; DB 3; Length 53526;
Best Local Similarity 62.3%; Pred. No. 26;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GTGAGGAGTGGCTGGGAATCTTATGGCACCAGAGGGCGGGCGGAGGGAGTCTCT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 17422 GTCACTCGTGGGAGGGTGACACCTGGGGAAGTAGAGCCCTGGCAGGAGTGAAGCCT 17481

QY 61 C 61
Db 17482 C 17482

RESULT 15
US-08-658-136-1
; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
```

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; APPLICANT:  CONNORS, TIMOTHY D
; APPLICANT:  DACKOWSKI, WILLIAM
; APPLICANT:  GERMINO, GREGORY
; APPLICANT:  QIAN, FENG
; TITLE OF INVENTION:  POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES:  58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  GENZYME CORPORATION
; STREET:  ONE MOUNTAIN ROAD
; CITY:  FRAMINGHAM
; STATE:  MASSACHUSETTS
; COUNTRY:  USA
; ZIP:  01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/658,136
; FILING DATE:
; CLASSIFICATION:  435
; ATTORNEY/AGENT INFORMATION:
; NAME:  LASSEN, ELIZABETH
; REGISTRATION NUMBER:  31,845
; REFERENCE/DOCKET NUMBER:  GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  508-872-8400
; TELEFAX:  508-872-5415
; INFORMATION FOR SEQ ID NO:  1:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  53577 base pairs
; TYPE:  nucleic acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; MOLECULE TYPE:  DNA (genomic)
US-08-658-136-1

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Query Match      39.7%; Score 24.2; DB 3; Length 53577;
Best Local Similarity 62.3%; Pred. No. 26;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      1 GTGAGGAGTGGGCTGGGAATCTTATGGCACCCAGAGGGCGGGGGGAGGAGTCCT 60
      |||  ||||| |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      17421 GTCACCTGCTGGGAGGGTGACACCTGGGGAAAGTAGAGGCCCGTGGCAGGAGGTGAGGCCT 17480

QY      61 C 61
      |
Db      17481 C 17481

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Search completed: June 13, 2003, 06:00:55
Job time : 13.6452 secs

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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
(without alignments)
4579.068 Million cell updates/sec

Title: US-09-826-581-3_COPY_612_672
Perfect score: 61
Sequence: 1 GTGAGGAGTGGCTGGGAAT.....GGGGGCGAGGGAGTCTCTC 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	61	100.0	1722	10	US-09-826-581-3
2	26	42.6	17761	9	US-10-092-154-1596
3	26	42.6	17761	10	US-09-764-847-1596
c 4	25.2	41.3	1030	10	US-09-925-301-324
c 5	25.2	41.3	5938	9	US-10-092-154-1153
c 6	25.2	41.3	5938	10	US-09-764-847-1153
7	25	41.0	275	10	US-09-880-107-2925
c 8	25	41.0	541	9	US-10-144-929-25
9	25	41.0	1351	9	US-09-964-859-30
10	25	41.0	1847	12	US-10-044-090-338
11	24.8	40.7	1991	10	US-09-864-761-4800
12	24.8	40.7	2837	10	US-09-864-761-21539
c 13	24.8	40.7	5868	9	US-10-024-450-3
c 14	24.6	40.3	498	9	US-09-899-046-193
c 15	24.6	40.3	498	9	US-09-878-281-193
16	24.4	40.0	231	10	US-09-864-761-24263
17	24.4	40.0	550	10	US-09-864-761-7558
c 18	24.4	40.0	957	9	US-09-851-138-17
19	24.4	40.0	1155	9	US-10-126-279-14

c 20	24.4	40.0	3367	9	US-10-223-085-33	Sequence 33, Appl
c 21	24.4	40.0	3367	9	US-10-223-084-33	Sequence 33, Appl
c 22	24.4	40.0	3367	9	US-10-223-088-33	Sequence 33, Appl
c 23	24.4	40.0	3367	9	US-10-223-090-33	Sequence 33, Appl
c 24	24.4	40.0	3889	9	US-10-037-270-400	Sequence 400, App
c 25	24.4	40.0	174566	9	US-10-020-141-1	Sequence 1, Appl
c 26	24.2	39.7	53522	9	US-09-904-968A-1	Sequence 1, Appl
c 27	24	39.3	13862	9	US-09-764-891-5477	Sequence 5477, Ap
c 28	24	39.3	13862	9	US-09-764-891-10204	Sequence 10204, A
c 29	23.8	39.0	606	9	US-09-738-626-1796	Sequence 1796, Ap
c 30	23.8	39.0	1074	9	US-09-738-626-1795	Sequence 1795, Ap
c 31	23.8	39.0	3309400	9	US-09-738-626-1	Sequence 1, Appl
c 32	23.6	38.7	383	10	US-09-867-701-10278	Sequence 10278, A
c 33	23.6	38.7	540	9	US-09-822-846-553	Sequence 553, App
c 34	23.6	38.7	4241	9	US-10-171-581-213	Sequence 213, App
c 35	23.6	38.7	4711	12	US-10-044-090-210	Sequence 210, App
c 36	23.6	38.7	4720	9	US-09-822-846-158	Sequence 158, App
c 37	23.6	38.7	22452	9	US-09-764-868-1487	Sequence 1487, Ap
c 38	23.6	38.7	22452	9	US-09-764-868-1489	Sequence 1489, Ap
c 39	23.4	38.4	100	10	US-09-969-373-114	Sequence 114, App
c 40	23.4	38.4	393	9	US-10-152-661-26	Sequence 26, Appl
c 41	23.4	38.4	393	9	US-09-866-050A-26	Sequence 26, Appl
c 42	23.4	38.4	1001	9	US-10-152-661-218	Sequence 218, App
c 43	23.4	38.4	1001	9	US-09-866-050A-218	Sequence 218, App
c 44	23.4	38.4	1015	9	US-10-152-661-30	Sequence 30, Appl
c 45	23.4	38.4	1015	9	US-09-866-050A-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-826-581-3
; Sequence 3, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Marklund, Stefan
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-3

Query Match 100.0%; Score 61; DB 10; Length 1722;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGAGGAGTGGCTGGGATCTTATGGCACCAGAGGGGGGGGAGGAGTCTCT 60
Db 612 GTGAGGAGTGGCTGGGATCTTATGGCACCAGAGGGGGGGGAGGAGTCTCT 671
QY 61 C 61
Db 672 C 672

RESULT 2
US-10-092-154-1596
; Sequence 1596, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

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; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; OTHER INFORMATION: n equals a,t,g, or c
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1596
; LENGTH: 17761
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1596

Query Match          42.6%; Score 26; DB 9; Length 17761;
Best Local Similarity 65.5%; Pred. No. 2.3;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGAATCTTATGGGCACCCAGAGGGCGGGCGGAGGGAGTC 58
||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 1563 GTGAGGTGTGGCTGGGTATGTCTGGGTTCAGAAAGCCTGTGCCGTCTGGAGTC 1620

RESULT 3
US-09-764-847-1596
; Sequence 1596, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1596
; LENGTH: 17761
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1596

Query Match          42.6%; Score 26; DB 10; Length 17761;
Best Local Similarity 65.5%; Pred. No. 2.3;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGAATCTTATGGGCACCCAGAGGGCGGGCGGAGGGAGTC 58
||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 1563 GTGAGGTGTGGCTGGGTATGTCTGGGTTCAGAAAGCCTGTGCCGTCTGGAGTC 1620

RESULT 4
US-09-925-301-334/c
; Sequence 334, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL06
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; Prior Application Number: PCT/US00/05882
; Prior Filing Date: 2000-03-08
; Prior Application Number: 60/124,270
; Prior Filing Date: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 334
; LENGTH: 1030
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: misc_feature
; LOCATION: (989)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1006)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1023)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-334

Query Match          41.3%; Score 25.2; DB 10; Length 1030;
Best Local Similarity 66.7%; Pred. No. 5.3;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 4 AGGAGTGGCTGGGAATCTTATGGGCACCCAGAGGGCGGGCGGAGGGAGT 57
||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 418 AGGGCTCCCCCAAGACCTCATAGGAGCCAGGGGGCGGGCGGGGAGT 365

RESULT 5
US-10-092-154-1153/c
; Sequence 1153, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1153
; LENGTH: 5938
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1153

Query Match          41.3%; Score 25.2; DB 9; Length 5938;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGAATCTTATGGGCACCCAGAGGGCGGGCGGAGGGG 54
||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 1855 GAGGGGACAGAGCTAGGAGAGGGAGGGGAGCCAGCAAGAGCGAGGGTGCAGGGG 1802

RESULT 6
US-09-764-847-1153/c
; Sequence 1153, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1153
; LENGTH: 5938
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1153

Query Match          41.3%; Score 25.2; DB 10; Length 5938;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 GTGAGAGTGGCTGGGAATCTTATGGGCACCCAGAGGGCGGGCGGAGGGG 54
||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 1855 GAGGGGACAGAGCTAGGAGAGGGAGGGGAGCCAGCAAGAGCGAGGGTGCAGGGG 1802
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Db 1855 GAGGGACAGACTAGGAGAGGGGAGGCGAGCCAGAGGGCGAGGGGTGCAGGGG 1802

RESULT 7
US-10-144-929-25
; Sequence 2925, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2925
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 R62519
; NAME/KEY: unsure
; LOCATION: (1)..(275)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-2925

Query Match 41.0%; Score 25; DB 10; Length 275;
Best Local Similarity 75.6%; Pred. No. 6.9;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 17 GAATCTTATGGCCACCCAGAGGGGGGGGGGGGGGGGAGT 57
Db 148 GGACCTCATAGGGAGCCAGGGGGGCGAGGGGGGGGAGT 188

RESULT 8
US-10-144-929-25/c
; Sequence 25, Application US/10144929
; Publication No. US20030069405A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2014P1
; CURRENT APPLICATION NUMBER: US/10/144,929
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/251,329
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: PCT/US98/17044
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-144-929-25

Query Match 41.0%; Score 25; DB 9; Length 541;

Best Local Similarity 69.4%; Pred. No. 6.6;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 12 GCTGGGAATCTTATGGGACCCAGAGGGGGGGGGGAGGAGTCTCT 60
Db 62 GATGGGTAAGATCTGGAGAGACATGGGGGGGGGGGGGATTCTCT 14

RESULT 9
US-09-964-899-30
; Sequence 30, Application US/09964899
; Patent No. US20020174446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1351
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-964-899-30

Query Match 41.0%; Score 25; DB 9; Length 1351;
Best Local Similarity 64.9%; Pred. No. 6.2;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 5 GGAGTGGCTGGGAATCTTATGGGACCCAGAGGGGGGGGGGAGTCTCT 61
Db 42 GGAGCGGATGCGAGGAGCGGACCATGAGAGGAGCGCGCGGAGTTCTC 98

RESULT 10
US-10-044-090-338
; Sequence 338, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 338
; LENGTH: 1847
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 344297.3
US-10-044-090-338

Query Match 41.0%; Score 25; DB 12; Length 1847;
Best Local Similarity 64.9%; Pred. No. 6;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 5 GGAGTGGCTGGGAATCTTATGGGACCCAGAGGGGGGGGGGAGTCTCT 61
Db 99 GGAGCGGATGCGAGGAGCGGACCATGAGAGGAGCGCGCGGAGTTCTC 155

RESULT 11
US-09-864-761-4800
; Sequence 4800, Application US/09864761

; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4800
; LENGTH: 1991
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031277.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.98
US-09-864-761-4800

Query Match 40.7%; Score 24.8; DB 10; Length 1991;
Best Local Similarity 67.3%; Pred. No. 7;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 GAGGAGTGGCTGGGAATCTTATGGCACCCAGAGGGCGGGCGGAGGGG 54

Db 1022 GAAGAGGGGCTGGGAAGAGGTACGTAGGAAGAGGGCGGGCGGAGTGG 1073

RESULT 12

US-09-864-761-21539
; Sequence 21539, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21539
; LENGTH: 2837
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031277.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.98
; OTHER INFORMATION: NT HIT: g11423021, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: 061116, EVALUATE 1.00e-09
; OTHER INFORMATION: EST_HUMAN HIT: BB885438.1, EVALUATE 0.00e+00
US-09-864-761-21539

Query Match 40.7%; Score 24.8; DB 10; Length 2837;
Best Local Similarity 67.3%; Pred. No. 6.9;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 GAGGAGTGGCTGGGAATCTTATGGCACCCAGAGGGCGGGCGGAGGGG 54

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Db      1926 GAAGAGGGGCTGGGAAGAGGTACGTTAGGAGAGGGGAGGGGGCGGAGTGG 1977
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RESULT 13
US-10-024-450-3/c
; Sequence 3, Application US/10024450
; Publication No. US20030032606A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; APPLICANT: Chadwick, Robert B.
; TITLE OF INVENTION: Methods of Detecting and Treating
; TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ
; FILE REFERENCE: P-LJ 5101
; CURRENT APPLICATION NUMBER: US/10/024,450
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/256,582
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5868
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (121)...(5277)
US-10-024-450-3
Query Match 40.7%; Score 24.8; DB 9; Length 5868;
Best Local Similarity 67.3%; Pred. No. 6.5;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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||||| ||||||| || ||| ||||||| ||||||| ||||||| ||
Db      3122 GAAGAGGGGCTGGGAAGAGGTACGTTAGGAGAGGGGAGGGGGCGGAGTGG 3071
||||| ||||||| || ||| ||||||| ||||||| ||||||| ||
RESULT 14
US-09-899-046-193/c
; Sequence 193, Application US/09899046
; Publication No. US20030008274A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: New sequences of hepatitis C virus
; TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
; NUMBER OF SEQUENCES: 270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,046
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/362,455
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..498
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..495

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GenCore version 5.1.6
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(without alignments)
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Perfect score: 1647
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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32: em_htg_other.*
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39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1647	100.0	1647	6	AX281582 Sequence
2	1590	96.5	2290	9	HSA249977 Homo sapi
3	1453	88.2	2115	6	AX099802 Sequence
4	1453	88.2	2115	9	AF214519 Homo sapi
5	1447	87.9	2109	6	AX099776 Sequence
6	1172.8	71.2	2022	6	AX099804 Sequence
7	1142	69.3	1873	6	AX398333 Sequence
8	1140.4	69.2	1873	4	AF214520 Sus scrofa
9	1140.4	69.2	1873	6	AX099800 Sequence
10	1140.4	69.2	1873	6	AX398331 Sequence
11	1138.8	69.1	1873	6	AX398335 Sequence
12	1138.8	69.1	1873	6	AX398337 Sequence
13	1138.8	69.1	1873	6	AX398339 Sequence
14	1134.4	68.9	1867	6	AX099774 Sequence
15	414.8	25.2	1328	10	RNAMEPKGAM U42413 Rattus norv
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17	407.2	24.7	989	6	AX281579 Sequence
18	396.8	24.1	1623	10	AF036535 Mus muscu
19	395.4	24.0	3132	10	BC015283 Mus muscu
20	395.2	24.0	20854	9	AC009974 Homo sapi
21	393.4	23.9	1578	9	HSU42412 Human 5'-AM
22	393.4	23.9	1677	9	BC000358 Homo sapi
23	367.2	22.3	1774	6	AX364914 Sequence
24	366.6	22.3	1167	9	AB025580 Homo sapi
25	366.6	22.3	1435	6	AR139104 Sequence
26	366.6	22.3	2194	9	AF087875 Homo sapi
27	366.6	22.3	2203	9	BC020540 Homo sapi
28	366.6	22.3	2223	9	AK001887 Homo sapi
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36	278.8	16.9	152129	2	AC027416 Homo sapi
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39	254.6	15.5	146577	2	AC128070 Rattus no
40	254.6	15.5	190183	2	AC129703 Rattus no
41	254.6	15.5	192968	2	AC127107 Rattus no
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43	168.2	10.2	1722	6	AX281580 Sequence
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ALIGNMENTS

RESULT 1	AX281582	AX281582	1647 bp	DNA	linear	PAT 02-NOV-2001
LOCUS	Sequence 5	from Patent	WO0177305.			
DEFINITION	Sequence 5	from Patent	WO0177305.			
ACCESSION	AX281582					
VERSION	AX281582.1	GI:16608833				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					

REFERENCE 1
AUTHORS Andersson L., Luthman, H. and Marklund, S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 5 18-OCT-2001;

FEATURES	Arexis AB (SE)	
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	LVANGVRAAPLWDSKOSFYGMILITDFILVLHRYTRSP.LQVIEIEQKHIEFWREY	
	LQGCPRPLVSPINDSLFEAVYTLIKNRILRPVLDPVSGNVLRHLTHRLKLFHLIF	
	GSLRPFSLYRTTLDIGIGTFRDLAVULETAPILTAIDIPVDRVRSALPVPVNECGOV	
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Best Local Similarity 100.0%; Pred. No. 0;		
Matches 1647; Conservative 0; Mismatches 0; Indels 0; gaps 0;		
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Db	61	CTGAGCAGCCTTTGGGGTTCTGAGCATCAAGAGATGAGCTTCCTAGAGCAAGAAACAG 120
QY	121	CAGCTCATGCGCATCACCAGCTGTGACCGACACTCAGAAAGATTCCTGGGAAAGCGAG 180
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QY	181	GGCCAAAGCCTTGAGATGGACAAGCAGAGTCGGTGAGAGGAGGGAGGCCACACAGTCA 240
Db	181	GGCCAAAGCCTTGAGATGGACAAGCAGAGTCGGTGAGAGGAGGGAGGCCACACAGTCA 240
QY	241	GGGGAAAGTTCCTCCGCTCCAGCCAGCTGTGAGTCCACCGGGCTGGAGGCCACATTCCT 300
Db	241	GGGGAAAGTTCCTCCGCTCCAGCCAGCTGTGAGTCCACCGGGCTGGAGGCCACATTCCT 300
QY	301	CAAGACACACCTTTGGCTTCAAGCTGATTCCTCCGGGGTGGGCATCTCCACCAACAGGGTG 360
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QY	361	GGACTGCTCCCTCTGACTGTACAGCTCAGCTGCAGGCTCCAGCAGAGATGATGTGGA 420
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Db	661	GGCCTTCTTTGCTCTGGTGGCCACAGGTTGGGGGAGGCCCTCTATGGGACACCAAGAA 720

RESULT 2
HSA249977
LOCUS
DEFINITION
Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
(AMPK gamma 3 gene).
ACCESSION
AJ249977
VERSION
AJ249977.1 GI:6688200

2290 bp mRNA linear PRI 07-APR-2000

721 GCAGAGCTTTGGGGATGCTGACCATCACTGACTTCATCTCGTGGTGTGATCGCTACTA 780
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1021 TGGTTCCTGCTGCCCGGCCCTCTTCTTACCCGACATATCCAAAGATTTGGGCATCG 1080
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Db 1562 CTTCATCTTCCGCCACCCCAATTTGCTGCTCAGCTATGATTCAGGTCTTTCAGGCC 1619

RESULT 3
AX099802
LOCUS AX099802 2115 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 29 from Patent WO0120003.
ACCESSION AX099802
VERSION AX099802.1 GI:13538836
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2115)
AUTHORS Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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BASE COUNT 460 a 622 c 562 g 471 t
ORIGIN

Query Match 88.2%; Score 1453; DB 6; Length 2115;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1501; Conservative 0; Mismatches 35; Indels 7; Gaps 2;

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Db 121 GTGGAGGAAGGGAGCCACACGAGTCAGGGGGAAGGTCCCGGTCCAGGCCAACTGCTGAG 180

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Db	1440	CAATGAAGGAATTGAGA-----ACAGCTTCATTTCCCGCAACCCCAATTTGCTGGTTGAG	1493
QY	1595	CTATGATTCAGGTAGGCTCTGCCCTGGGCCATGACACACAGCCT	1637
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RESULT 4			
LOCUS	AF214519	2115 bp mRNA linear PRI 03-JUN-2000	
DEFINITION	Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3) mRNA, complete cds.		
ACCESSION	AF214519		
VERSION	AF214519.1	GI:8215681	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 2115) Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Galliard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P. and Andersson,L.		
TITLE	A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle		
JOURNAL	Science 288 (5469), 1248-1251 (2000)		
MEDLINE	20280150		
PUBMED	10818001		
REFERENCE	2 (bases 1 to 2115) Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Galliard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N., Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.		
AUTHORS	Direct Submission		
TITLE	Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24, Sweden		
JOURNAL			
FEATURES	Location/Qualifiers		
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ORIGIN			

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DEFINITION Sequence 3 from Patent WO0120003.
ACCESSION AX099776
VERSION AX099776.1 GI:13538810
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ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2109)
AUTHORS Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
JOURNAL Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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Best Local Similarity 97.3%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 35; Indels 7; Gaps 2;
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    Chardon,P.
    Variants of the gamma chain of ampk, dna sequences encoding the
    same, and uses thereof
    JOURNAL
    INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
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Rothschild, M. F., Ciobanu, D. C., Malek, M. and Piastow, G.
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LOCUS
DEFINITION Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)

ACCESSION AF214520
VERSION AF214520.1 GI:8215683
KEYWORDS mRNA, complete cds.

SOURCE Sus scrofa.
ORGANISM Sus scrofa.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE 1 (bases 1 to 1873)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Galliard,C., Paul,S., Iannuccelli,N., Resk,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Geilun,J., Kalm,E., Roy,P.L., Chardon,P.
and Andersson,L.
TITLE A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle

JOURNAL Science 288 (5469), 1248-1251 (2000)
MEDLINE 20280150
PUBMED 10818001

REFERENCE 2 (bases 1 to 1873)
AUTHORS Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Galliard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission

TITLE Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
JOURNAL University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden

FEATURES Location/Qualifiers
Source 1. .1873
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gene 1. .1873
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CDS 1. .1395

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Best Local Similarity 85.7%; Pred. No. 2.8e-252;
Matches 1315; Conservative 0; Mismatches 211; Indels 8; Gaps 4;
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RESULT 9
AX099800
LOCUS AX099800 1873 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 27 from Patent WO0120003.
ACCESSION AX099800
VERSION AX099800.1 GI:13538834
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE
1 (bases 1 to 1873)
AUTHORS
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Geillin, J., le Roy, P., and
Chardon, P.
TITLE
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL
Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;

Andersson, Looft, Christian (DE) ; Kalm, Ernst (DE)
Location/Qualifiers
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1..1395
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ORIGIN

Query Match 69.2%; Score 1140.4; DB 6; Length 1873;
Best Local Similarity 85.7%; Pred. No. 2.8e-252;
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VERSION	AX398331.1 GI:21261106		
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SOURCE	Sus scrofa		
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REFERENCE	1		
AUTHORS	Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.		
TITLE	Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits		

JOURNAL	Patent: WO 0220850-A 1 14-MAR-2002:		
FEATURES	Iowa State University Research Foundation, Inc. (US)		
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RESULT 12
AX398337
LOCUS AX398337 1873 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 7 from Patent W00220850.
ACCESSION AX398337
VERSION AX398337.1 GI:21261112
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.

Novel prka3 alleles and use of the same as genetic markers for reproductive and meat quality traits
Patent: WO 0220850-A 7 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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Best Local Similarity 85.7%; Pred. No. 6.6e-252;
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RESULT 14
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LOCUS AX099774 1867 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 1 from Patent WO0120003.
ACCESSION AX099774
VERSION AX099774.1 GI:13538808
KEYWORDS
SOURCE .
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 1867)
AUTHORS Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Lelf (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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Query Match 68.9%; Score 1134.4; DB 6; Length 1867;
Best Local Similarity 85.7%; Pred. No. 6.8e-251;
Matches 1309; Conservative 0; Mismatches 211; Indels 8; Gaps 4;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 01:37:39 ; Search time 598.355 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES			
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2	1453	88.2	2115 22 AAD03320 Human AMPK gamma s
3	1447	87.9	2109 22 AAD03296 Human AMPK gamma s
4	1172.8	71.2	2022 22 AAD03321 Sus scrofa PRKAG3
5	1142	69.3	1873 22 AAD36457 Pig PRKAG3 polymor
6	1140.4	69.2	1873 22 AAD03319 Pig AMPK gamma sub
7	1140.4	69.2	1873 24 AAD36456 Pig wild-type PRK
8	1138.8	69.1	1873 24 AAD36458 Pig PRKAG3 polymor
9	1138.8	69.1	1873 24 AAD36459 pig PRKAG3 polymor

10	1138.8	69.1	1873	24	AAD36460	Pig PRKAG3 polymor
11	1134.4	68.9	1867	22	AAD03295	Pig AMPK gamma sub
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13	407.2	24.7	989	22	AAH43682	PRKAG3 intron 2 -
14	393.4	23.9	1578	24	ABK84324	Human cDNA differe
15	393.4	23.9	1691	21	AAK98774	Human pancreatic c
16	390.2	23.7	1576	18	AAK985927	Mammalian AMPK-gam
17	367.2	22.3	1774	24	AB139755	Human NS cDNA sequ
18	366.6	22.3	1435	20	AAK06882	Disease associated
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24	188.4	11.4	602	22	AAH35203	Human colon cancer
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40	85	5.2	378	22	AAK28874	Human bone marrow
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ALIGNMENTS

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ID AAH43685 standard; cDNA; 1647 BP.

AC AAH43685;
XX

DT 21-JAN-2002 (first entry)
XX

DE PRKAG3 CDNA.

KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
KW metabolic disease; diabetes; obesity; substitution; ss.

OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 20..1489

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XX FT /note= "Causes R340W"

FN W0200177305-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-SE00765.
XX 07-APR-2000; 2000US-195665P.
XX (AREX-) AREXIS AB.
XX Andersson L, Luthman H, Marklund S;
XX P-PSDB; Q0847679.
XX WPI: 2001-657170/75.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
XX associated with a metabolic disease e.g. diabetes or obesity and method
XX for determining a risk estimate of diseases in subject by detecting the
XX variant -
XX
XX Disclosure; Fig 5; 25pp; English.
XX
XX This sequence represents the full length cDNA encoding the human
XX AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
XX the presence of the PRKAG3 DNA, or a variant, is useful in determining
XX a risk estimate of a metabolic disease, such as diabetes or obesity,
XX in a subject. The variation may occur in exons 3, 4 or 10. In exon
XX 3 variation may be a substitution of a G for a C at nucleotide 320,
XX resulting in the amino acid substitution P71A; in exon 4 variation may
XX be a substitution of a T for a C at nucleotide 550; and in exon 10
XX variation may be a substitution of a T for a C at nucleotide 1037,
XX resulting in the amino acid substitution R340W. There may also be
XX nucleotide variation in intron 6. The numbering of these
XX variations is based on the full length cDNA as given, rather than on
XX position 1 of the open reading frame.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 301 CAAGACACACACCTTGGCTCAAGCTGATCCTGCCGGGTGGGCACTCCACCAACAGGGTG 360

QY 361 GGACTGCTCCCTCTGACTGTACAGCTCAGCTGCAAGGTCCAGCAGCAGATGATGTGA 420
DB 361 GGACTGCTCCCTCTGACTGTACAGCTCAGCTGCAAGGTCCAGCAGCAGATGATGTGA 420

QY 421 GCTGCCACAGGNTTCCACCCACAGAGCCCTGGGAGTGTGAGCTAGAGGGCTCTCTGA 480
DB 421 GCTGCCACAGGNTTCCACCCACAGAGCCCTGGGAGTGTGAGCTAGAGGGCTCTCTGA 480

QY 481 AGAGAGGCGCTGCCCTGTGCCTGTCCCGCAGGCCGCCATTTCCAAAGCTGGGCTGGGATGA 540
DB 481 AGAGAGGCGCTGCCCTGTGCCTGTCCCGCAGGCCGCCATTTCCAAAGCTGGGCTGGGATGA 540

QY 541 CGAACTGGGAAACCCGGGCCAGATCTACATCGGCTTCATGACAGGACACACTCTCTA 600
DB 541 CGAACTGGGAAACCCGGGCCAGATCTACATCGGCTTCATGACAGGACACACTCTCTA 600

QY 601 CGATGCCATGCAACTAGCTCCAAAGCTAGTCTTCGACACACATGCTGGAGATCAAGAA 660
DB 601 CGATGCCATGCAACTAGCTCCAAAGCTAGTCTTCGACACACATGCTGGAGATCAAGAA 660

QY 661 GGCCTTTCTTGTCTGTGGTGGCCAAAGGCTGCGGGCAGCCCTCTATGGGACACAAGAA 720
DB 661 GGCCTTTCTTGTCTGTGGTGGCCAAAGGCTGCGGGCAGCCCTCTATGGGACACAAGAA 720

QY 721 GCAGAGCTTTGTGGGATGCTGACCATCAGTCTTCCATCTGCTGGTCTGATCTACTA 780
DB 721 GCAGAGCTTTGTGGGATGCTGACCATCAGTCTTCCATCTGCTGGTCTGATCTACTA 780

QY 781 CAGGTCCCGCTGGTCCAGATCTATGAGATTGAACAACATAGATTGAGACTGGAGGA 840
DB 781 CAGGTCCCGCTGGTCCAGATCTATGAGATTGAACAACATAGATTGAGACTGGAGGA 840

QY 841 GATCTACCTGCAAGGCTGCTTCAAGCCTCTGCTCTCCATCTCTCCTTAATGATACCTGTT 900
DB 841 GATCTACCTGCAAGGCTGCTTCAAGCCTCTGCTCTCCATCTCTCCTTAATGATACCTGTT 900

QY 901 TGAAGCTGTCTACACCTCATCAAGAACGGATCCATCGCCTGCTTCTTGTGACCCGGT 960
DB 901 TGAAGCTGTCTACACCTCATCAAGAACGGATCCATCGCCTGCTTCTTGTGACCCGGT 960

QY 961 GTCAGGCAAGTACTTCACATCTCACAACAAGGCTGCTCAAGTTCCTGCAACATCTT 1020
DB 961 GTCAGGCAAGTACTTCACATCTCACAACAAGGCTGCTCAAGTTCCTGCAACATCTT 1020

QY 1021 TGGTTCCTGCTGCCCGGCTCTCTCTACGCACTATCCAGATTTGGGATCGG 1080
DB 1021 TGGTTCCTGCTGCCCGGCTCTCTCTACGCACTATCCAGATTTGGGATCGG 1080

QY 1081 CACATTCGAGACTTGGCTGTGTGCTGGAGACAGCACCCTCTGACTGCACTGGACAT 1140
DB 1081 CACATTCGAGACTTGGCTGTGTGCTGGAGACAGCACCCTCTGACTGCACTGGACAT 1140

QY 1141 CTTTGTGACCGGGTGTGTGCTGCACTGCTTGGTCAAGAAATGTGTGAGTCTGGG 1200
DB 1141 CTTTGTGACCGGGTGTGTGCTGCACTGCTTGGTCAAGAAATGTGTGAGTCTGGG 1200

QY 1201 CCTCTATTCCCGCTTTGATGTATTACCTGGCTGCCAGCAAACTACAAACCTCTGGA 1260
DB 1201 CCTCTATTCCCGCTTTGATGTATTACCTGGCTGCCAGCAAACTACAAACCTCTGGA 1260

QY 1261 CATGAGTGTGGGAGAACCTCTGAGGAGAGGACACTATGCTTGGAGGGAGTCTTCTCTG 1320
DB 1261 CATGAGTGTGGGAGAACCTCTGAGGAGAGGACACTATGCTTGGAGGGAGTCTTCTCTG 1320

QY 1321 CCAGCCCCACAGAGCTTGGGGAGAGTGTATCGACAGATTTGCTGCGGAGGAGTACACAG 1380
DB 1321 CCAGCCCCACAGAGCTTGGGGAGAGTGTATCGACAGATTTGCTGCGGAGGAGTACACAG 1380

QY 1381 GCTGTGTAGTGTGACGAGACCCAGCATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCT 1440
DB 1381 GCTGTGTAGTGTGACGAGACCCAGCATCTCTTGGGCGTGGTCTCCCTCTCCGACATCCT 1440

QY 1441 TCAGGCACTGTGTCTAGCCCTGCTGGCATCGATGCCCTCGGGGCTGAGAAGATCTGAG 1500
DB 1441 TCAGGCACTGTGTCTAGCCCTGCTGGCATCGATGCCCTCGGGGCTGAGAAGATCTGAG 1500

QY 1501 TCTCAATCCCAAGCCACTGTCACACCTCGAAGCCATGAAGGACTGGAGACTCAGC 1560
DB 1501 TCTCAATCCCAAGCCACTGTCACACCTCGAAGCCATGAAGGACTGGAGACTCAGC 1560

QY	1561	CTTCATCTTCCCCACACCCCAATTTGCTTGCTTACGCTATGATTCAGGTAGGCTCTGCCCTG	1620
Db	1561	CTTCATCTTCCCCACACCCCAATTTGCTTGCTTACGCTATGATTCAGGTAGGCTCTGCCCTG	1620
QY	1621	GGCCATGACACACGAGCTCTTAGTCTTC	1647
Db	1621	GGCCATGACACACGAGCTCTTAGTCTTC	1647
RESULT 2			
AA003320			
ID	AA003320	standard; cDNA; 2115 BP.	
XX	AA003320;		
AC	AA003320;		
XX	DT	(first entry)	
XX	13-JUN-2001		
DE	Human AMPK	gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.	
KW	Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;		
KW	PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;		
KW	genetic testing; carbohydrate metabolism disorder; skeletal muscle;		
KW	cystathione beta synthase; CBS; cardiant; gene therapy; ss.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FH	CDS	1..1395	
FT	FT	/tag= a	
FT	FT	/product= "Human complete Prkag3 protein"	
XX	WO200120003-A2.		
XX	22-MAR-2001.		
XX	11-SEP-2000;	2000WO-EP09896.	
PF	10-SEP-1999;	99EP-0402236.	
PR	18-MAY-2000;	2000EP-0401388.	
XX	(ING) INRA INST NAT RECH AGRONOMIQUE.		
PA	(ANDE/) ANDERSSON L.		
PA	(LOOF/) LOOFT C.		
PA	(KALM/) KALM E.		
XX	Andersson L, Loof C, Kaim E, Milan D, Robic A, Rogel-Gaillard C;		
PI	Iannuccelli N, Gellin J, Le Roy P, Chardon P;		
PI	WPI: 2001-244810/25.		
DR	P-PSDB: AAE00223.		
XX	New variants of the gamma subunit of vertebrate adenosine		
PT	monophosphate-activated kinase for diagnosis or treatment of disorders		
PT	associated with energy metabolism such as diabetes, obesity, and		
PT	myopathy		
XX	Claim 12; Page 65-68; 7ipp; English.		
XX	The present sequence is a cDNA encoding human adenosine monophosphate		
CC	(AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,		
CC	complete PRKAG3. Mutation in prkag3 results in an altered regulation of		
CC	carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is		
CC	useful as therapeutic for treating carbohydrate metabolism disorders such		
CC	as diabetes, obesity, and disorders associated with muscle metabolism		
CC	such as myopathy and cardiovascular diseases, to modulate AMPK		
CC	activity, and for restoring a normal AMPK function. PRKAG3 sequence		
CC	and its functionally altered mutants are useful for the diagnostic		
CC	evaluation, genetic testing and prognosis of a metabolic disorder,		
CC	preferably a carbohydrate metabolism disorder. Primers that can detect		
CC	a genetic polymorphic marker linked to a sequence encoding PRKAG3, are		
CC	useful for detecting a dysfunction of carbohydrate metabolism resulting		
CC	from the expression of a functionally altered allele of PRKAG3.		
CC	Transgenic animal and host cell transformed with PRKAG3 or a		

CC	heterotrimeric AMPK consisting of PRKA3 or its mutant, are useful for
CC	screening compounds able to modulate AMPK activity. Nucleic acid
CC	encoding PRKA3 is useful for detecting mutations in a prka3 gene, or
CC	in a sequence encoding the first cystathione beta synthase (CBS) domain
CC	of PRKA3 and is useful in gene therapy.
XX	
SQ	Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
	Query Match 88.2%; Score 1453; DB 22; Length 2115;
	Best Local Similarity 97.3%; Pred. No. 0;
	Matches 1501; Conservative 0; Mismatches 35; Indels 7; Gaps 2;
QY	95 ATGAGCTTCCTAGACGAAGAAAACAGCAGGTCTATGCCATCACCAAGTGTGACCAGCAGC 154
DB	1 ATGAGCTTCCTAGACGAAGAAAACAGCAGGTCTATGCCATCACCAAGTGTGACCAGCAGC 60
QY	155 TCACAAAGATCCGTGGGAACAGAGGGCCAAAGCCTTGAGATGGAACAAGCGAGAAGTCG 214
DB	61 TCACAAAGATCCGTGGGAACAGAGGGCCAAAGCCTTGAGATGGAACAAGCGAGAAGTCG 121
QY	215 GTGAGGACAGGGGAGCCACCAAGGTCAGGGGAAGGTCCC CGGTCCAGGCCACAGTGCCTGAG 274
DB	121 GTGAGGACAGGGGAGCCACCAAGGTCAGGGGAAGGTCCC CGGTCCAGGCCACTGCTGAG 180
QY	275 TCCACCGGGTGGAGGGCCACATTCCCCAAGACACACACCCTTTGGTCAAGCTGATCCTGCC 334
DB	181 TCCACCGGGTGGAGGGCCACATTCCCCAAGACACACACCCTTTGGTCAAGCTGATCCTGCC 240
QY	335 GGGGTGGCACTCCACCAACAGGTTGGGACTGGCTCCCTCTGACTGTACAGCCTCAAGCT 394
DB	241 GGGGTGGCACTCCACCAACAGGTTGGGACTGGCTCCCTCTGACTGTACAGCCTCAAGCT 300
QY	395 GCAGGCTTCCACGACAGATGATGTGGAGCTGGCCACAGGAGTCCCAGCCACAGAGGCGCTGG 454
DB	301 GCAGGCTTCCACGACAGATGATGTGGAGCTGGCCACAGGAGTCCCAGCCACAGAGGCGCTGG 360
QY	455 GAGTGTGAGCTAGAAGGCGCTGCTGGAAGAGAGGCGCTTGCCCTGTGCCGTCCCGCAGGCC 514
DB	361 GAGTGTGAGCTAGAAGGCGCTGCTGGAAGAGAGGCGCTTGCCCTGTGCCGTCCCGCAGGCC 420
QY	515 CCATTTCCCAAGCTGGGCTGGGATGACGAACTCGGAAACCGCGGCGCCAGATCTACATG 574
DB	421 CCATTTCCCAAGCTGGGCTGGGATGACGAACTCGGAAACCGCGGCGCCAGATCTACATG 480
QY	575 GCGTTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTGCATC 634
DB	481 GCGTTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCAAGCTAGTGCATC 540
QY	635 TTCGACACCATGCTGGAGATCAAGAAGCGCTTTGTTGGCTCTGGTGGCCAACGCTGTGGGG 694
DB	541 TTCGACACCATGCTGGAGATCAAGAAGCGCTTTGTTGGCTCTGGTGGCCAACGCTGTGGGG 600
QY	695 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGGATGCTGACCACTACTGAC 754
DB	601 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGGATGCTGACCACTACTGAC 660
QY	755 TTCACTCTGTGTGCTGCTGCTACTACAGTGCCTCCCTGCTCCAGTCCAGATCATGAGATTGAA 814
DB	661 TTCACTCTGTGTGCTGCTGCTACTACAGTGCCTCCCTGCTCCAGTCCAGATCATGAGATTGAA 720
QY	815 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTTCAAGCCTCTGGTGC 874
DB	721 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTTCAAGCCTCTGGTGC 780
QY	875 TCCATCTCTCTTAATGATAGCTGTTTGAAGCTGTCTACACCCCTCATCAAGAACCGGATC 934
DB	781 TCCATCTCTCTTAATGATAGCTGTTTGAAGCTGTCTACACCCCTCATCAAGAACCGGATC 840
QY	935 CATGCCCTGCGCTGCTTCTTGACCCGGTGTCAAGCAAGCTACTTCCATCTCTACACACAAA 994
DB	841 CATGCCCTGCGCTGCTTCTTGACCCGGTGTCAAGCAAGCTACTTCCATCTCTACACACAAA 900
QY	995 GCGCTGCTCAAGTTCCTGTCACATCTTTGTTGGTTCCTGCTGGCCCGCGGCTCTTTCCTCTAC 1054

Db 901 GCGCTGCTCAAGTCTCTGCACATCTTTGGTTCCCTGCTGCCCCGGCCCTCTCTCTAC 960
QY 1055 GGCATATCCAAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTCTCGGAGACA 1114
Db 961 GGCATATCCAAGATTGGGCATCGGCACATTCGAGACTTGGCTGTGGTCTCGGAGACA 1020
QY 1115 GCACCATCTCTGACTGCATCGACATCTTTGTGGACCGGGGTGTCTGCACTGCCGTG 1174
Db 1021 GCACCATCTCTGACTGCATCGACATCTTTGTGGACCGGGGTGTCTGCACTGCCGTG 1080
QY 1175 GTCACCAAGTGTGGTCTGAGTCTGGGCTCTATTCCCGCTTTGATGATGATCACTGGCT 1234
Db 1081 GTCACCAAGTGTGGTCTGAGTCTGGGCTCTATTCCCGCTTTGATGATGATCACTGGCT 1140
QY 1235 GCCCAGCAAACTACAAACCTGGACATGATGTGGAGAAAGCCCTGAGCGAGGACA 1294
Db 1141 GCCCAGCAAACTACAAACCTGGACATGATGTGGAGAAAGCCCTGAGCGAGGACA 1200
QY 1295 CTATGTCTGGAGGAGTCTTTCTGCGCAGCCCGCAGAGAGCTTGGGGAAGTATCGAC 1354
Db 1201 CTATGTCTGGAGGAGTCTTTCTGCGCAGCCCGCAGAGAGCTTGGGGAAGTATCGAC 1260
QY 1355 AGGATTGCTGGGAGCAGGTACACAGGCTGTGTAGTGGACGAGACCCAGCATCTCTG 1414
Db 1261 AGGATTGCTGGGAGCAGGTACACAGGCTGTGTAGTGGACGAGACCCAGCATCTCTG 1320
QY 1415 GCGGTGTCTCCCTCTCCGACATCTTTCAGGCACTGTGTCTCAGCCCTGCTGGCATCGAT 1474
Db 1321 GCGGTGTCTCCCTCTCCGACATCTTTCAGGCACTGTGTCTCAGCCCTGCTGGCATCGAT 1380
QY 1475 GCGCTCGGGGCTGAGAAGATCTGAGTCTCAATCCCAAGCCACCTGCACACCTGGAAGC 1534
Db 1381 GCGCTCGGGGCTGAGAAGATCTGAGTCTCAATCCCAAGCCACCTGCACACCTGGAAGC 1439
QY 1535 CAATGAAGGGAAGTGGAGAACTCAGCCTTCATCTTCCCCACCCCTTTCCTGCTGTCAG 1594
Db 1440 CAATGAAGGAATTGAGA-----ACAGCTTCATTTCCCAACCCCAATTTGCTGTTTCAG 1493
QY 1595 CTATGATCAGTAGGCTCTGCCCTGGGCGCATGACACCCAGCCT 1637
Db 1494 CTATGATCAGGCTCTTTCAGCCTTCCAAAATTGCTTTGCTT 1536

RESULT 3

AAD03296

ID AAD03296 standard; DNA; 2109 BP.

XX AC AAD03296;

XX DT 13-JUN-2001 (first entry)

XX DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 CDNA.

XX KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;

KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;

KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;

KW cystathione beta synthase; CBS; cardiac; gene therapy; ss.

XX OS Homo sapiens.

XX FH Key

FT 5'UTR Location/Qualifiers

FT 1..471 /*tag= a

FT 472..1389 /*tag= b

FT CDS /*tag= c

FT 3'UTR /product= "Human Prkag3 protein"

FT 1390..2109 /*tag= c

PN W0200120003-A2.

XX W22-MAR-2001.

PD

XX 11-SEP-2000; 2000WO-EP09896.
PF 10-SEP-1999; 99EP-0402236.
PR 18-MAY-2000; 2000EP-0401388.
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.
PA (LOOF/) LOOFT C.
PA (KALM/) KALM E.
XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX MPI; 2001-244810/25.
DR P-PSDB; AAE00221.
XX New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment of disorders
FT associated with energy metabolism such as diabetes, obesity, and
XX myopathy -
PS Claim 12; Fig 2; 71pp; English.
XX The present sequence is a cDNA encoding human adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC PRKAG3. Mutation in Prkag3 results in an altered regulation of
CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
CC useful as therapeutic for treating carbohydrate metabolism disorders such
CC as diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX
SQ Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;

Query Match 87.9%; Score 1447; DB 22; Length 2109;

Best Local Similarity 97.3%; Pred. No. 0;

Matches 1495; Conservative 0; Mismatches 35; Indels 7; Gaps 2;

QY 101 TTCTCTAGAGCAAGAAACACAGAGCTCATGGCCATCACCAGCTGTCCACAGCTCAGAA 160

Db 1 TTCTCTAGAGCAAGAAACACAGAGCTCATGGCCATCACCAGCTGTCCACAGCTCAGAA 60

QY 161 AGAATCCGTGGGAAACCGAGGCCAAAGCCCTTGAGATGGCAAGGACAGAGTCGGTGGAG 220

Db 61 AGAATCCGTGGGAAACCGAGGCCAAAGCCCTTGAGATGGCAAGGACAGAGTCGGTGGAG 120

QY 221 GAAGGGGNCACACAGGTCAGGGGGAAGTCCCGGTCCAGGCCAGCTGCTGAGTCACCC 280

Db 121 GAAGGGGNCACACAGGTCAGGGGGAAGTCCCGGTCCAGGCCAGCTGCTGAGTCACCC 180

QY 281 GGGCTGGAGGCCACATTCCTCCCAAGACACACCTCTGGCTCAAGCTGATCTTCCTGGGGGTG 340

Db 181 GGGCTGGAGGCCACATTCCTCCCAAGACACACCTCTGGCTCAAGCTGATCTTCCTGGGGGTG 240

QY 341 GGCACCTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCTCAGCTGCAGGC 400

Db 241 GGCACCTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCTCAGCTGCAGGC 300

QY 401 TCCAGCACACATGATGTGGAGCTGGCCAGGAGTTCACAGAGGCTGGGAGTGT 460

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[illegible]

Qy	1541	AGGGAAC	TGGAGAACTCAGCCTTCATCTCCGCCACCCCAATTTGCTGCTCAGCTATGA	1600
Db	1440	AGGAATTGAGA-----ACAGCTTCATTTCCCAACCCCAATTTGCTGCTCAGCTATGA	1493	
Qy	1601	TTCAGGTAGGCTCTGCCTTGGCGCATGACACCAAGCTT	1637	
Db	1494	TTCAGGCTTCTTACGCTTCCAAAATTCCTTTGCTT	1530	
RESULT 4				
AAD03321				
ID	AAD03321	standard; DNA; 2022 BP.		
XX	AAD03321;			
XX	13-JUN-2001	(first entry)		
XX	Sus scrofa	PRKAG3 splice variant DNA.		
XX	Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;			
KW	PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;			
KW	genetic testing; carbohydrate metabolism disorder; skeletal muscle;			
KW	cystathione beta synthase; CBS; cardiac; gene therapy; ds.			
XX	Sus scrofa.			
XX	Location/Qualifiers			
EH	Key	1..1545		
FT	CDS	/*tag= a		
FT	FT	/product= "Sus scrofa Prkag3 splice variant"		
XX	W0200120003-A2.			
XX	22-MAR-2001.			
XX	11-SEP-2000; 2000WO-EP09896.			
XX	10-SEP-1999; 99EP-0402236.			
PR	18-MAY-2000; 2000EP-0401388.			
XX	(INRG) INRA INST NAT RECH AGRONOMIQUE.			
PA	(ANDE/) ANDERSSON L.			
PA	(LOOF/) LOOFT C.			
PA	(KALM/) KALM E.			
XX	Andersson L, Loof C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;			
PI	Iannuccelli N, Gellin J, Le Roy P, Chardon P;			
XX	WT; 2001-244810/25.			
DR	P-PSDB; AAE00224.			
XX	New variants of the gamma subunit of vertebrate adenosine			
PT	monophosphate-activated kinase for diagnosis or treatment of disorders			
PT	associated with energy metabolism such as diabetes, obesity, and			
PT	myopathy -			
XX	Claim 12; Page 69; 71pp; English.			
XX	The present sequence is pig adenosine monophosphate (AMP)-activated			
CC	kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice			
CC	variant DNA. Prkag3 gene is located in the RN locus of chromosome 15.			
CC	Mutation in Prkag3 results in an altered regulation of carbohydrate			
CC	metabolism, particularly in skeletal muscle. PRKAG3 is useful as			
CC	therapeutic for treating carbohydrate metabolism disorders such as			
CC	diabetes, obesity, and disorders associated with muscle metabolism			
CC	such as myopathy and cardiovascular diseases, to modulate AMPK			
CC	activity, and for restoring a normal AMPK function. PRKAG3 sequence			
CC	and its functionally altered mutants are useful for the diagnostic			
CC	evaluation, genetic testing and prognosis of a metabolic disorder,			
CC	preferably a carbohydrate metabolism disorder. Primers that can detect			
CC	a genetic polymorphic marker linked to a sequence encoding PRKAG3, are			
CC	useful for detecting a dysfunction of carbohydrate metabolism resulting			

XX PN W0200220850-A2.
XX PD 14-MAR-2002.
XX PF 10-SEP-2001; 2001WO-US28283.
XX PR 08-SEP-2000; 2000US-231045P.
XX PR 08-JAN-2001; 2001US-260239P.
XX PR 18-JUN-2001; 2001US-299111P.
XX PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX PI Rothschild MF, Ciohanu DC, Malek M, Plastow G;
XX DR WPI; 2002-393850/42.
XX DR P-PSDB; AA522985.
XX PT Screening animals to determine those likely to produce larger litters
XX PT and improved meat quality traits involves assaying for the presence of
XX PT polymorphisms in the AMP activated protein kinase regulatory gamma
XX PT subunit gene -
XX PS Disclosure; Page 89-91; 109pp; English.
XX CC The invention relates to a method for screening animals to determine
XX CC those more likely to produce large litters and improved meat quality
XX CC traits. The method involves assaying for the presence of a genotype
XX CC in the sample of genetic material obtained from animal. The genotype
XX CC is characterised by polymorphism(s) in the AMP activated protein
XX CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
XX CC for screening animals e.g., pigs to determine those most likely to
XX CC exhibit improved meat quality traits and to produce larger litters.
XX CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 69.3%; Score 1142; DB 24; Length 1873;
Best Local Similarity 85.8%; Pred No. 5.6e-288;
Matches 1316; Conservative 0; Mismatches 210; Indels 8; Gaps 4;

QY 95 ATGAGCTTCTAGAGCAAGAAACACAGCTCATGGCCATCAGCTGTGACAGCAGC 154
DB 1 ATGAGCTTCTAGAGCAAGAGAGAGCGCTTCATGGCCATCCCGAGCTGTACCCAGC 60
QY 155 TCAGAAAGATCCGTGGGAAACGAGGGCCAAAGCCTTGACATGGACAGGCAAGATCG 214
DB 61 TCAGAAAGAGCCATGGGGACCAAGGGCCCTTAGATGGACAGGAGGAGAT 120
QY 215 GTGGAGGAGGGAGGCCACAGGCTCAGGGGGAAGGTCCCGGTCCAGGGCCAGCTGTGAG 274
DB 121 GTAGAGGAGGGGGCCCTCCGGGCCGAGGGAAGGTCCCCAGTCCAGGCCAGTTGCTGAG 180
QY 275 TCACCGGGCTGGAGGCCACATTCGCCAAGACCAACACCCCTTGGGTCAAGGTATGC - --T 331
DB 181 TCACCGGGCAGGAGGCCACATTCGCCAAGGCCACACCCCTTGGGCCAAGCGGCTCCCTTG 240
QY 332 GCGGGGTGGGCACTTCACCAACAGAGGTGGGACTGCCCTCCCTCTGACTGTACAGCTCA 391
DB 241 GCGAGGTGGACACACCCCAACAGAGCGGGACATCTCCCTCTGACTGTGAGCTCA 300
QY 392 GCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGCCAGCGAGTTCGCCAGCCACAGAGGCC 451
DB 301 GCTCCGACTCCACACAGACCATCTGGATCTGGGCAATAGAGTTCTCAGCCTCGGGGCCG 360
QY 452 TGGGAGTGTAGCTAGAGGCTGCTGGGAGAGAGGCTGCCCTGTGCTGTCCCGGACG 511
DB 361 TCGGGGGATGAGCT---TGGGCTGGTGGGAGAGAGGCCAGCCCGTGCCTCCCTCCAGAG 417
QY 512 GCCCAATTTCCCAAGCTGGGCTGGGATGAGCAACTTCGGGAAACCCCGCGCCCAAGATCTAC 571
DB 418 GTGCTGTATCCCAAGGCTGGGATGATGAGCTGCAGAAAGCCGGGGGCCCAAGGTCTAC 477

QY 572 ATCGCTTCATCGAGGACACACCTGCTAGCATGCCATGGCAACTAGCTCCACAGCTAGTC 631
DB 478 ATGCACCTTCANGCAGGAGCACACCTGCTAGTACGATGGCGACCGCTCCAACTGGTTC 537
QY 632 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTCTTTTGTCTGTGTGGCAACGCTGTG 691
DB 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTCTTTTGGCCCTGGTGGCCAAAGCGCTC 597
QY 692 CGGGCAGCCCTCTATGGGACAGCAAGAGAGCTTTGTGGGGATGCTGACCAATCACT 751
DB 598 CGAGCGGCACCTTTGTGGGACAGCAAGAGAGCTTCGTGGGATGCTGACCAATCACA 657
QY 752 GACTTCATCTGCTGCTGCTACTACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
DB 658 GACTTCATCTTGTGCTGCTGCTGCTATACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCT 717
QY 812 GAACAAATAGATTGACACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGGCTCTG 871
DB 718 GAAGAAATAGATTGACACCTGGAGGAGATCTACCTTCAAGGCTGCTTCAAGGCTCTG 777
QY 872 GTCTCATCTCTCTTAATGATGAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCGG 931
DB 778 GTCTCATCTCTCTCAATGACAGCTGTTTGAAGCTGTCTACGCTCTCATCAAGAACCGG 837
QY 932 ATCCATCGCTGCTGCTGCTTGTGACCCGGGTGCAGCAAGCTACTCCACATCTCTCACAC 991
DB 838 ATCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
QY 992 AAACGGCTGCTCAAGTTCTCTGACATCTTTTGGTTCCTGCTGCTGCTGCTGCTGCTGCT 1051
DB 898 AAGCGGCTTCTCAAGTTCTCTGACATCTTTGGCACCCCTGCTGCTGCTGCTGCTGCTGCT 957
QY 1052 TACCGCACTATCCAAATTTGGGATGCGGACATTCGCGAGCTTGGCTGTGCTGTGAG 1111
DB 958 TACCGCACTATCCAAATTTGGGATGCGGACATTCGCGAGCTTGGCTGTGCTGTGAG 1017
QY 1112 ACAGCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
DB 1018 ACAGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077
QY 1172 GTGCTCAAGAAATGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
DB 1078 GTGCTCAAGAAATGTGGGAGTGTGGGCTCTACTCTGCTTGTGATGTGATACACCTG 1137
QY 1232 GCTGCGCCACCAACCTACACACCTGACATGATGTGGGAGAGCCCTGAGGCGAGAG 1291
DB 1138 GCTGCGCCCAACCAATACACACCTGACATGATGTGGGAGAGCCCTGAGGCGAGAG 1197
QY 1292 ACATATGTCTGGAGGAGTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1351
DB 1198 ACATGTGCTGGAAGGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257
QY 1352 GACAGGATGTCTGGGAGCAGGTACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1411
DB 1258 GACCGGATGTCTGGGAGCAGGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
QY 1412 TTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1471
DB 1318 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1377
QY 1472 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
DB 1378 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1437
QY 1531 AAGCAATGAAGGAGCTGGAGACCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1590
DB 1438 AAGCAATGAAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1496
QY 1591 TCAGCTATGATTCAGGTAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1624
DB 1497 CTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530

QY 1112 ACAGCACCATCTGACTGACATCTTTTGGACGGGTGTGTGCTGCTGCT 1171
DB 1018 ACAGCACCATCTGACTGACATCTTTTGGACGGGTGTGTGCTGCTGCT 1077
QY 1172 GTGTCACAGAAATGTCAGAGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1231
DB 1078 GTGTCACAGAAATGTCAGAGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1137
QY 1232 GTGTCACAGAAATGTCAGAGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1291
DB 1138 GTGTCACAGAAATGTCAGAGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1197
QY 1292 ACATATGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1351
DB 1198 ACATATGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1257
QY 1352 GACAGAAATGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1411
DB 1258 GACAGAAATGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1317
QY 1412 TTGGGCTGTGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1471
DB 1318 CTGGGCTGTGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1377
QY 1472 GATGCTGTGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1530
DB 1378 GATGCTGTGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1437
QY 1531 AAGCCAAATGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1590
DB 1438 AAGCCAAATGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1496
QY 1591 TCAGCTATGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1624
DB 1497 CTGGCTGTGTCGTGGGCTCTATTCCTCCGCTTTGATGATCACTG 1530

RESULT 7
ID AAD36456
XX AAD36456 standard; DNA; 1873 BP.
AC AAD36456;
DT 09-AUG-2002 (first entry)
XX Pig wild-type PRKAG3 gene.
DE AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; ds.
XX Sus scrofa.
XX
PH Key
FT CDS
FT 1..1395
FT /tag= a
FT /product= "pig PRKAG3 wild-type protein"
FT replace (89, C)
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (154, A)
FT /tag= c
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (595, A)
FT /tag= d
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (599, A)
FT /tag= e
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX W0200220850-A2.
PN 14-MAR-2002.
PD

XX 10-SEP-2001; 2001WO-US28283.
PF 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
PA
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
PI WPI: 2002-393850/42.
DR P-PSDB; AAE22984.
XX
PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene -
XX
PS Claim 17; Fig 1; 109pp; English.
XX
CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig wild-type PRKAG3 gene.
XX
SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
Query Match 69.2%; Score 1140.4; DB 24; Length 1873;
Best Local Similarity 85.7%; Pred. No. 1.5e-287;
Matches 1315; Conservative 0; Mismatches 211; Indels 8; Gaps 4;
QY 95 ATGAGCTTCTAGACAGAAACACAGCTCATGSCCATCCAGCTGTGACCAAGC 154
DB 1 ATGAGCTTCTAGACAGAAACACAGCTCATGSCCATCCAGCTGTGACCAAGC 60
QY 155 TCAGAAAGAAATCCGTGGGAACCGAGGCGCCAAAGGCTTGAGATGACAGAGAAATCG 214
DB 61 TCAGAAAGAAATCCGTGGGAACCGAGGCGCCAAAGGCTTGAGATGACAGAGAAATCG 120
QY 215 GTGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 274
DB 121 GTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 275 TCCACCGGGCTGGAGGCGCACATTCCTCCAGACACACACCTTGGCTCAAGCTGATCC--T 331
DB 181 TCCACCGGGCTGGAGGCGCACATTCCTCCAGACACACCTTGGCTCAAGCTGATCC--T 240
QY 332 GCCGGGTGGGCACTTCCACCAACAGGCTGGGAGCTGCTCCCTCTGACTGTACAGCTCA 391
DB 241 GCCGGGTGGGCACTTCCACCAACAGGCTGGGAGCTGCTCCCTCTGACTGTACAGCTCA 300
QY 392 GCTGACAGGCTCCAGACAGATGATGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAG 451
DB 301 GCTTCCGAGCTCCACACAGACCATCTGGATCTGGGAGTATGAGTCTCAGCTCGGGCGG 360
QY 452 TGGGAGTGTGAGCTAGAAGGCTGCTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 511
DB 361 TCGGGGATGAGCT--TGGGCTGGTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
QY 512 GCCCCTATTTCCAGCTGGGCTGGGAGTACAGAACTGCGGAACCCCGGCGCCAGATCTAC 571
DB 418 GTGCTGTATCCAGGCTGGGCTGGGAGTATGAGCTGACAGAGCGGGGGCGGCGGCTAC 477
QY 572 ATGCGCTTCATCAGGAGCAGACCTGCTACGATGCCATGGCAACTAGCTCCAGCTAGTC 631
DB 478 ATGCGCTTCATCAGGAGCAGACCTGCTACGATGCCATGGCGGAGGAGGAGGAGGAGG 537

Qy	632	ATCTTCGACACCATCGCTGGAGATCAAGAAGGCTTCCTTGTCTGTGTGGCCCAAGCGTGTG	631
Db	538	ATCTTCGACACCATCGCTGGAGATCAAGAAGGCTTCCTTGTCCCTGTGTGGCCCAAGCGGTTC	597
Qy	692	CGGCGACGCCCTCTATATGGACAGCAAGAAGACAGAGACTTTGTGGGGATGCTGACCATCACT	751
Db	598	CGAGCGGCACTTTCTGGGACACAAAGACAGAGACTTCCTGGGGATGCTGACCATCACA	657
Qy	752	GACTTCATCTGGTGCTGCATCGCTACTACAGGTCCGCCCTGTGCAGATCTATGAGATT	811
Db	658	GACTTCATCTGGTGCTGCACCGCTATTACAGTCCGCCCTGTGCAGATCTACGAGATT	717
Qy	812	GAACACATAAAGATTGACACTGGAGGAGATCTACCTTCGAAGGCTGTTCGAAGCCTCTG	871
Db	718	GAAGACATAAAGTTGAGACTCGAGGGAGATCTACCTTCAAGGCTGCTTCAAGCCTCTG	777
Qy	872	GTCTCCATCTCTTAATGATGAGCTGTTTGAAGCTGTCTACACCTCATCAAGAAGCGG	931
Db	778	GTCTCCATCTCTCCCAATTGACAGCGCTTTGCGAAGCTGTCTACGCCCTCATCAAGAAGCGG	837
Qy	932	ATCCATCGGCTGCCTGTTCCTTGACCCGGGTGTGAGCAACGTTACTCCACATCTCATCACAC	991
Db	838	ATCCACCGCTCGCGGTCTGGACCTGTCTCCGGGCTGTCTCCACATCTCATCACAT	897
Qy	992	AAAGCGCTGCTCAAGTTCCTGTCACATCTTTGGTTCCTGTGCGCCCGGCCCTCTCTTC	1051
Db	898	AAGCGGCTCTCAAGTTCCTGTCACATCTTTGGCACCTGTCTGCCCGGCCCTCTCTTC	957
Qy	1052	TACCGCATATCCAAAGATTTGGGCATCGGCACATTCGAGACTTGGCTGTGGTGGTGAG	1111
Db	958	TACCGCACCATCCAAAGATTTGGGCATCGGCACATTCGAGACTTGGGCCGTGGTGGTGA	1017
Qy	1112	ACAGCACCATCTGACTGCTAGCTGGACATCTTTGTGGACGGCGTGTGTCCACTGGCT	1171
Db	1018	ACGGCGCCCATCTGACCGCACTGGACATCTTCGTGGACGGCGTGTGTCCGCTGGCT	1077
Qy	1172	GTGTCAACGAATGTGGTCAGGTCGTGGGCTCTATTCCCGCTTTGATGTGATCACCTG	1231
Db	1078	GTGTCAACGAATGTGGACAGTAGTGGGCCCTTACTCTCGCTTGTGTGATCCACTG	1137
Qy	1232	GCTGCCAGCAACCTACACACCCTGGACATGAGTGTGGGAGAGCCCTGAGGCAGAGG	1291
Db	1138	GCTGCCCAACAACATACCAACCTTGGACATGAATGTGGGAAGCCCTGAGGCAGCGG	1197
Qy	1292	ACATATGTCTGAGGGAGTCCCTTCTCGTCCAGCCCCACGAGACTTTGGGGCAAGTGATC	1351
Db	1198	ACATGTGTCTGAGGGCTCCCTTCTCGAGCCCCACGAGACTTTGGGGGAAGTCAAT	1257
Qy	1352	GACAGGATGCTCGGGACGAGTACACAGGCTGTGTGCTAGTGAGAGACCCAGCATGTC	1411
Db	1258	GACCGGATGTCGGGGAACAGGTGCACCGCTGTGTCTGTGGATGAGACCCAGCACCTT	1317
Qy	1412	TTGGGCTGTGTCTCCCTCTCCGACATCTTTCAGGCACATGGTGTCTAGCCCTCTGGCATC	1471
Db	1318	CTGGGCTGTGTCCCTCTCTGACATCTTTCAGGCTGTGTGTCTACGCCCTGCTGGAAAT	1377
Qy	1472	GATGCCCTCGGGGCTCGAGAATCTGAGTTCCTCAATCCCAGGCCACTT-GCACACCTGG	1530
Db	1378	GATGCCCTCGGGGCTCGAGAACCCTTGAACCTTTGCTCTCAGGCCACTTGGCACACCTGG	1437
Qy	1531	AAGCCAATGAAGGAACTTGAAGAATCTCAGCTTTCATCTTCCCCACCCCACTTTCCTGGT	1590
Db	1438	AAGCCAATGAAGGAGC-CTGTGGACTCAGCTCTCACTTCCCTCTCAGCCCACTTCTGGT	1496
Qy	1591	TCAGCTATGATTCAGGTAGGCTCTGCCCTGGGCC	1624
Db	1497	CTGGCTCTCTTTCAGGTAGGCTCCGCCCGGGGGC	1530

RESULT 8
AAD36458
ID AAD
XX

AC	AAD36458;
XX	
DT	09-AUG-2002 (first entry)
DE	Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
DE	
KW	AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW	screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW	gene; variant; ds.
XX	
OS	Sus scrofa.
PH	
FT	Key Location/Qualifiers
CDS	1..1395
FT	/*tag= a
FT	/product= "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
FT	/replace (154, A)
FT	variation
FT	/*tag= b
FT	/standard_name= "Single nucleotide polymorphism (SNP)"
XX	
PN	WC0200220850-A2.
XX	
XX	14-MAR-2002.
PD	
XX	
PF	10-SEP-2001; 2001WO-US28283.
XX	
PR	08-SEP-2000; 2000US-231045P.
PR	08-JAN-2001; 2001US-260239P.
PR	18-JUN-2001; 2001US-299111P.
XX	
PA	(IOWA) UNIV IOWA STATE RES FOUND INC.
PI	
XX	Rothschild MF, Clohanu DC, Malek M, Plastow G;
DR	
DR	WPI; 2002-393850/42.
DR	P-PSDB; AAE22986.
XX	
XX	Screening animals to determine those likely to produce larger litters
PT	and improved meat quality traits involves assaying for the presence of
PT	polymorphisms in the AMP activated protein kinase regulatory gamma
PT	subunit gene
XX	
PS	Claim 34; Page 93-95; 109pp; English.
XX	
CC	The invention relates to a method for screening animals to determine
CC	those more likely to produce large litters and improved meat quality
CC	traits. The method involves assaying for the presence of a genotype
CC	in the sample of genetic material obtained from animal. The genotype
CC	is characterised by polymorphism(s) in the AMP activated protein
CC	kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC	for screening animals e.g., pigs to determine those most likely to
CC	exhibit improved meat quality traits and to produce larger litters..
CC	The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-52)
XX	
SQ	Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match	69.1%	Score 1138.8	DB 24	Length 1873
Best Local Similarity	85.7%	Prod. No. 3.8e+287		
Matches 1314	Conservative	0	Mismatches 212	Indels 8
Gaps	4			
Qy	95	ATGAGCTTCCTACAGCAAGAAACAGAGCGTCATGGCCATCACAGCTGTGACACAGC	154	
Db	1	ATGAGCTTCCTAGGCAAGAGAGCGGTTGATGCCATCCGAGCTGTAAACCACAGC	60	
Qy	155	TGAGAAAGATTCGTGGGAAACGGAGGGCCAAAGCCCTTGAGATGGACAAGCAGAGTGG	214	
Db	61	TCAGAAAGAACCATGGGACCCAGGGGAACAAGGCCCTCTGATGGACAAGCAGGAGGAT	120	
Qy	215	GTGGAGGAAGGGAGCCACAGGCTCAGGGGGAGGTCCCGGTCAGCCAGCTGCTGTAG	274	
Db	121	GTGAGGAAGGGGGGGCTCCGGGGCCAGGGGAAGTCCCCAGTCGAGGCCAGTTGCTGTAG	180	
Qy	275	TCACCGGGGTGGAGGCCACATCCCAAGACACACACACCCTTGGGTCAAGCTGATCC	331	

Db 181 TCCACCGGCGAGGCGCACATTCGCCAAGGCCACACCTTGGCCCAAGCGGCTCCCTTG 240
QY 332 GCGGGGCTGGGACTCCACCAACAGAGGCTGGGACTGCCCTCCCTCTGACTGTACAGCCTCA 391
Db 241 GCGGAGGTGGACACCCGCCAACAGAGCGGGACATCCCTCCCTCTGACTGTGAGCCTCA 300
QY 392 GCTGCAGGCTCCAGCACAGATGATGTGGAGCTGGGCCCGGAGTTCACAGCCACAGAGCC 451
Db 301 GCCTCCGACTCCAAACAGACCATCTGGATCTGGCATAGAGTTCTCAGGCTCGGCGCG 360
QY 452 TGGGATGTGAGCTAGAGGCTCTGGAGAGAGGCTGCCCTGTGGCTGTCCCGCGAG 511
Db 361 TCGGGGATGAGCT---TGGGCTGGTGGAGAGAGCCAGCCCGCTGCCCATCCCGAGAG 417
QY 512 GCCCCATTTCCCAAGCTGGGCTGGGATGAGCAACTCGGAAACCGCGCGCGAGATCTAC 571
Db 418 GTGCTGTACCCAGGCTGGGCTGGGATGAGCTGAGCAAGCCGGGGCGCCAGCTAC 477
QY 572 ATGGCTTCATCGAGGACACACTGCTACGATGGCATGGCAACTAGCTCCAGCTAGTTC 631
Db 478 ATGCACTTCATCGAGGACACACTGCTACGATGGCATGGGAGCCAGCTCCAACTGGTC 537
QY 632 ATCTTCGACACCATCTCGAGATCAAGAGGCTCTTTGCTCTGTGGGCCAACGGTGTG 691
Db 538 ATCTTCGACACCATCTCGAGATCAAGAGGCTCTTTGCTCTGTGGGCCAACGGGCTTC 597
QY 692 CGGGGACCCCTCTATGGACAGCAAGAGAGGCTTTGTGGGAGTCTGTGACCACTACT 751
Db 598 CGAGCGGACCTTTTGGGACAGCAAGAGAGGCTTGTGGGAGTCTGTGACCACTACA 657
QY 752 GACTTCATCTGGTCTGCATCGCTACTACAGTCCCGCTGGTCCAGATCTATGAGATT 811
Db 658 GACTTCATCTGGTCTGCATCGCTACTACAGTCCCGCTGGTCCAGATCTATGAGATT 717
QY 812 GAACAACATAAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGTCTCAAGCCTCTG 871
Db 718 GAACAACATAAGATTGAGACCTGGAGGAGATCTACTTCAAGGCTGTCTCAAGCCTCTG 777
QY 872 GTCTCATCTCTCCTAATGATGAGCTCTTTGAGAGTGTCTACACCTCATCAAGACCGG 931
Db 778 GTCTCATCTCTCCTAATGAGAGCTCTTGAAGCTGTCTAGCGCCTCATCAAGACCGG 837
QY 932 ATCCATCGCTCGCTGTTCTACCGGCTGTGAGGCAAGCTACTCCACATCTCTCACAC 991
Db 838 ATCCATCGCTCGCTGTTCTACCGGCTGTGAGGCAAGCTACTCCACATCTCTCACAC 897
QY 992 AAAGCGCTGCTCAAGTTCTCTGCACATCTTTGTTGCTCTGCTGCGCGCGCTCTCTTCCTC 1051
Db 898 AAGCGCTTCTCAAGTTCTCTGCACATCTTTGTTGCTCTGCTGCGCGCGCTCTCTTCCTC 957
QY 1052 TAGGGCACTATCCAGATTTGGGATCGGCATCGGCATATCCAGAGCTTGGCTGTGGTGGAG 1111
Db 958 TAGCGCACTATCCAGATTTGGGATCGGCATCGGCATATCCAGAGCTTGGCTGTGGAG 1017
QY 1112 ACAGCACTCATCTGACTGCACTGCACATCTTTGTTGAGCGGCGGTGTCTGCACTGCCT 1171
Db 1018 ACGGCGCCATCTGACCGCACTGGACATCTTCTGGAGCGGCTGTCTGCGCTGCTCT 1077
QY 1172 GTGGTCAAGCAATGTGGTCAAGTCTGGGCTCTATTCGCCCTTTGATGTGATTCACCTG 1231
Db 1078 GTGGTCAAGCAATGTGGTCAAGTCTGGGCTCTATTCGCCCTTTGATGTGATTCACCTG 1137
QY 1232 GCTGCCAGCAACCTTACACACCTGGACATGATGTGGGAGAGGCTTGAGGACAGG 1291
Db 1138 GCTGCCAACAACATACACACCTGGACATGATGTGGGAGAGGCTTGAGGACAGG 1197
QY 1292 ACATATGTCTGAGGAGTCTCTTCTTCCAGCCAGAGAGCTTGGGGAAGTGCATC 1351
Db 1198 ACATGTGTCTGAGGAGTCTCTTCTTCCAGCCAGAGAGCTTGGGGAAGTGCATC 1257
QY 1352 GACAGGATTCCTCGGAGAGAGTACACAGGCTGGTCTAGTGGACAGACCCAGCACTC 1411

Db 1258 GACCGGATTTCCGGGGAACAGGTGCACCCGCTGGTGTCTGTGATGAGACCCAGCACCTT 1317
QY 1412 TTGGGCTGGTCTCCCTCTCCGACATCTTCAGGCACTTGTGTCTCAGCCCTGCTGGCATC 1471
Db 1318 CTGGGCTGGTGTCCCTCTCTGACATCTTCAGGCTCTGTGTCTCAGCCCTGCTGGAATT 1377
QY 1472 GATGCCCTCGGGGCTCTGAGAGATCTGAGTCTCTAATCCCAAGCCACT- GCACACTTGG 1530
Db 1378 GATGCCCTCGGGGCTCTGAGAACCTTGTGAACCTTCTCTCAGGCACTTGGCACACTGG 1437
QY 1531 AAGCCAATGAAGGGAACCTGGGAACTCAGCCTTCTCATCTTCCCCCACCCCATTTGCTGGT 1590
Db 1438 AAGCCAGTAGGAGGAGC- CGTGGACTCAGCTCTCACTTCCCTCAGCCCACTTGTGCT 1496
QY 1591 TCAGCTATGATTTAGGTAGGCTCTGCCCTGGGCC 1624
Db 1497 CTGGCTCTTGTTCAGGTAGGCTCGCGCGGGGCC 1530

RESULT 9
AAD36459
ID AAD36459 standard; DNA; 1873 BP.
XX
AC AAD36459;
XX
DT 09-AUG-2002 (first entry)
XX
DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; variant; ds.
XX
OS Sus scrofa.
XX
FH Key
FT 1..1395
FT CDS
FT /tag= a
FT /product= "pig PRKAG3 polymorphic variant (PRKAG3-199)"
FT variation
FT replace (S95, A)
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200220850-A2.
XX
PD 14-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US28283.
XX
PR 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
DR WPI: 2002-393850/42.
XX P-PSDB: AAE22987.
XX
PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene -
XX
PS Disclosure; Page 98-100; 109pp; English.
XX
CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used

CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters
CC The present sequence is pig PRRAG3 polymorphic variant DNA (PRKAG3

SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match 69.1%; Score 1138.8; DB 24; Length 1873;
Best Local Similarity 85.7%; Pred. NO. 3.8e-287;
Matches 1314; Conservative 0; Mismatches 212; Indels 8; Gaps 4;

Qy	95	ATGAGCTCTCTAGACGAAGAAACACGACGCTCATGCGCCATCACCAGTGTGACCCAGCAGC	154
Db	1	ATGAGCTCTCTAGACGAAGGAGAGCCGTTATGCGCCATCCGAGGTGTAAACACACG	60
Qy	155	TCAGAAGAATCCGTGGCAACAGCAGCGCCAAAGCCTTGAGATGACAAAGGACAGATCG	214
Db	61	TCAGAAGAAGCCATGGGGACACAGGGAACAGAGGCTCTAGATGGACAGGCGAGGAGT	120
Qy	215	GTGGAGGAAGGGAGCCACCAGGTTCAGGGGGAGGTGCCCGGTTCCAGGCCAGTGTGTGAG	274
Db	121	GTAGAGGAAGGGGGCCCTCCGGCCCGAGGGAAGTCCCCAGTCCAGGCCAGTGTGTGAG	180
Qy	275	TCCACCGGCTGGAGGCCACATTTCCCAAGACACACCTTTGGCTCAAGCTGATCC--T	331
Db	181	TCCACCGGCGAGGAGGCCACATTTCCCAAGGCCACACCTTTGGCCAAAGCGCTCTCTTG	240
Qy	332	GCCGGGTGGGACATCTCCACCAACAGGCTGGGAGTGCCTCCGCTCTGACTGTACAGCTCA	391
Db	241	GCCGAGTGGACAACCCCCCAACAGACGGGGACATCTTCCCTCTGACTGTGAGGCTCA	300
Qy	392	GCTCGAGGCTCCACACAGATGATGTGGAGCTGGCCAGGAGTTCCACGCCACAGAGGCC	451
Db	301	GCTTCCGACTCCCAACACAGACCATCTGGATCTGGGCATAGAGTTCTCAGCCTCGCGGG	360
Qy	452	TGGGAGTGTGAGCTAGACAGGCTCTCGAAGAGAGGCTTGCCCTGTGCCTGTCCCGCAG	511
Db	361	TCGGGGATGAGCT--TGGGCTGGTGGAGAGAGCCAGGCCGTCCTCCACAGAG	417
Qy	512	GCCCCATTTCCCAAGCTGGGTGGGATGACGAACATGCGGAACCGCGGCCAGAGTCTAC	571
Db	418	GTGCTGTACCCAGGCTGGCTGGGATGATGAGCTGCAGAGCCGGGGCCAGGCTCTAC	477
Qy	572	ATGGCTTTATGCAGAGAGACACCTGTCAGATGCGCATGGCACTAGTCTCAAGCTAGTC	631
Db	478	ATGCACATTCATGCAGGAGCACACCTGCTAGCATGCCATGGCGAOCAGCTCCAACTGGTC	537
Qy	632	ATCTTCCACACCATCTCGAGATCAAGAGGCGCTTTTGCTCTGGTGGCCACAGGCTGTG	691
Db	538	ATCTTCCACACCATCTCGAGATCAAGAGGCGCTTTTGCCCTTGGTGGCCACAGGCATC	597
Qy	692	CGGCGACCCCTCATGGGACAGCAAGAAGCAGAGCTTTGTGGGGATGCTGACCATCACT	751
Db	598	CGAGCGCACCTTTGTGGGACAGCAAGAAGCAGAGCTTCTGTGGGATGCTGACCATCA	657
Qy	752	GACTTCAATCCTGGTGTGATGCTACTACAGTTCGCCCTGGTGGCCAGATCTATGAGATT	811
Db	658	GACTTCAATCTTGTGTGTGCACCGCTATTAGAGTTCGCCCTGGTGGCCAGATCTACGAGATT	717
Qy	812	GAACAACATAAATTCAGACCTGGAGGGAGATCTACTCGAAGGCTGCTTCAAGCCTCTG	871
Db	718	GAAGAACATTAAGATTGAGACCTGGAGGGAGATCTACTTCAAGGCTGCTTCAAGCCTCTG	777
Qy	872	GTCTCCATCTCTCCTAATGATAGCTGTTTGAAGCTGTACACCTCTATCAAGAACCGG	931
Db	778	GTCTCCATCTCTCCCAATGCACGCTGTTTGAAGCTGTACGCGCTCATCAGAACCGG	837
Qy	932	ATCCATCGCCTGCCTTCTTGAACCGGCTGTCAAGGCAAGTACTCCACATCCTCACACAC	991
Db	838	ATCCACCGCCTGCCGCTCTCGACCTGTCTCCGGGGCTGTCTCCACATCCTCACACAT	897
Qy	992	AAAGCCTGTCAAGTTCCTTCCATCTTGTGGTTCCTGCTGCCCGGGCCCTCTCTCTCC	1051
Db	898	AAAGGGGCTCTCAAGTTCCTTCCATCTTTTGGACCCCTGCTGCCCGGGCTCTCTCTCTC	957

PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX {IOWA } UNIV IOWA STATE RES FOUND INC.
PA Rothschild MF, Ciobanu DC, Malek M, Plastow G;
PI WPI; 2002-393850/42.
DR P-PSDB; AAE22988.
XX
XX Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene -
XX
XX Disclosure; Page 102-104; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
XX
XX
SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match 69.1%; Score 1138.8; DB 24; Length 1873;
Best Local Similarity 85.7%; Pred. No. 3.8e-287;
Matches 1314; Conservative 0; Mismatches 212; Indels 8; Gaps 4;

Qy 95 ATGAGCTTCTCTAGAGCAAGAAACACAGCTCATGGCCATCCAGCTGTGACCAAGCAGC 154
Db 1 ATGAGCTTCTCTAGAGCAAGAGAGAGCGCTTCATGGCCATCCGAGCTGAACCAACAGC 60

Qy 155 TCAGAAAGAAATCCGTGGAAACGGAGGGCCAAAGCCTTGAGATGGACAGGACAGATCG 214
Db 61 TCAGAAAGAAACCCATGGGACCAAGGGAAACAGGCTCTAGATGGACAGGAGGAGAT 120

Qy 215 GTGGAGGAAGGGAGGCCACAGGTCAAGGGGAAGTCCCGGTCCAGGCCAGCTGCTGAG 274
Db 121 GTAGAGGAAGGGGGGCCCTCGCGCCGAGGGAGAGGTCCCAAGTCCAGGCCAGTTGCTGAG 180

Qy 275 TCCACCGGGCTGGAGGCCACATTCGCCAAGACACACCTTTGGCTCAAGCTGATCC---T 331
Db 181 TCCACCGGGCAGGAGGCCACATTCGCCAAGGCCACACCTTTGGGCCAAGCGCTCCCTTG 240

Qy 332 GCGGGGTGGGCACCTCCACACAGGGTGGGACTGGCTCCCTCTGACTGTACAGCCTCA 391
Db 241 GCGGAGGTGGAAACACCCCAACAGAGCGGGACATCTCCCTCTGACTGTGACGCTCA 300

Qy 392 GCTGAGCCTCCAGCAGATGATGTGAGCTGGCCAGGAGTTCACAGCCACAGAGGCC 451
Db 301 GCTCCGACTCCACACAGACACATCTGGATCTGGGCATAGAGTCTCAGCCTCGGGGGG 360

Qy 452 TGGGAGTGTGAGCTAGAGCCCTGCTGGAAAGAGAGGCTGCCCTGTGCTGTCCCGCAG 511
Db 361 TCGGGGATGAGCT---TGGGCTGTGGGAAGAGAGCCAGCCCGTGGCCATCCCAAGAG 417

Qy 512 GCGCCATTTCCAGCTGGGCTGGGATGACGAACTGGGGAACCCCGGGCCCAAGATCTAC 571
Db 418 GTGCTGTTTACCAGGCTGGGCTGGGATGATGAGCTGCAAGAGCGGGGCCAGGCTCTAC 477

Qy 572 ATGGCTTCATGAGGAGCACCTCTGATGATGCGATGGCACTAGCTCCAGCTAGTTC 631
Db 478 ATGCACTTCATGCAAGGAGCACCTCTGATGATGCGATGGCGACAGCTCCAAACTGGTC 537

Qy 632 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGCTCTGTGGTGGCAAGGTGTG 691
Db 538 ATCTTCGACACCATGCTGGAGATCAAGAAGGCTTCTTTGCTCTGTGGTGGCCACAGCGCTC 597

Qy 692 CGGGCAGCCCTCTATGGGACAGCAAGACAGAGACTTTGTGGGATGCTGACCATCACT 751
Db 598 CAAGCGGCACCTTTGTGGGACAGCAAGACAGAGACTTCGTGGGATGCTGACCATCA 657

Qy 752 GACTTCATCTGCTGCTGCTACTACAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 811
Db 658 GACTTCATCTGCTGCTGCTACTACAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717

Qy 812 GAACACATATAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTTCAAGCCTCTG 871
Db 718 GAAGACATATAGATTGAGACCTGGAGGAGATCTACTTCAAGGCTGCTTTCAAGCCTCTG 777

Qy 872 GTCTCCATCTCTCTATATGATAGCTGTTGAGCTGTCTACACCTCTACACCTCTACAGAACCGG 931
Db 778 GTCTCCATCTCTCTCTATATGATAGCTGTTGAGGCTGCTTACGCTCTCTACAGAACCGG 837

Qy 932 ATCCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 991
Db 838 ATCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897

Qy 992 AAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1051
Db 898 AAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957

Qy 1052 TACCGCATATCCAGATTTGGGATCGGCATCTCCGAGACTTGGCTGTGGTGTGGAG 1111
Db 958 TACCGCATATCCAGATTTGGGATCGGCATCTCCGAGACTTGGCTGTGGTGTGGAG 1017

Qy 1112 ACAGCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
Db 1018 ACAGCACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077

Qy 1172 GTGGTCAACGAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231
Db 1078 GTGGTCAACGAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137

Qy 1232 GCTGCCACAGCAATCTACACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1291
Db 1138 GCTGCCACAGCAATCTACACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197

Qy 1292 ACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1351
Db 1198 ACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257

Qy 1352 GACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1411
Db 1258 GACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317

Qy 1412 TTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1471
Db 1318 TTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1377

Qy 1472 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1530
Db 1378 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1437

Qy 1531 AAGCCAAATGAAGGAACTTGGAGAACTCAGCTTCTATCTTCTTCTTCTTCTTCTTCTTCT 1590
Db 1438 AAGCCAAATGAAGGAACTTGGAGAACTCAGCTTCTATCTTCTTCTTCTTCTTCTTCTTCT 1496

Qy 1591 TCAGCTATATTCAGGTAGGCTCTGCGCTGGGCC 1624
Db 1497 CTGGCTTGTGTTTCAGGTAGGCTCTGCGCTGGGCC 1530

RESULT 11
AAD03295
ID AAD03295 standard; cDNA; 1867 BP.
XX
AC AAD03295;
XX
DT 13-JUN-2001 (first entry)
XX

QY 1178 AACGATGTCAGGTCGTGGGCTCTATTCCCGCTTTGATGATTCACCTGGCTGC 1237
DB 1078 AAGAACTGGACAGGTAGTGGGCTCTACTCTCGCTTTGATGATTCACCTGGCTGC 1137
QY 1238 CAGCAACCTACAACCACTGGACATGAGTGTGGGAGAGCCCTGAGGAGAGACATTA 1297
DB 1138 CACAAACATACAACCACTGGACATGATGATGAGGAGAGCCCTGAGGAGAGACATTA 1197
QY 1298 TGTCTGGAGGAGTCTTCTTCTGCGAGCCGACAGAGAGCTTGGGGAGTATGACAGC 1357
DB 1198 TGTCTGGAAGGCTCTTCTTCTGCGAGCCGACAGAGAGCTTGGGGAGTATGACAGC 1257
QY 1358 ATTGCTCGGAGCAGGTACACAGCTGTGTGCTAGTGAGAGAGCCAGCATCTTGGGC 1417
DB 1258 ATTGCTCGGAGCAGGTACACAGCTGTGTGCTAGTGAGAGAGCCAGCATCTTGGGC 1317
QY 1418 GTGCTCTCCCTCCGACATCTTTCAGGACCTGTGTGCTCAGCCCTGCTGCGATGCG 1477
DB 1318 GTGCTCTCCCTCCGACATCTTTCAGGACCTGTGTGCTCAGCCCTGCTGCGATGCG 1377
QY 1478 CTGCGGCTCGAGAGATCTGAGTCTTCAATCCCAAGCCACT-CCACACTGGAAGCCA 1536
DB 1378 CTGCGGCTCGAGAGATCTGAGTCTTCAATCCCAAGCCACTGGAAGCCACTGGAAGCCA 1437
QY 1537 ATGAGGGAACCTGGAGAACTCAGCCTTCACTTCCCGCCACCCCACTTGTGCTCAGCT 1596
DB 1438 GTGAGGGAGC-CGTGGACTAGTCTCACTTCCCTCAGCCCACTTGTGCTCAGCT 1496
QY 1597 ATGATTCAGGTAGGCTCTGCGGCTGGGC 1624
DB 1497 CTTGTTTCAGGTAGGCTCTGCGGCTGGGC 1524

RESULT 12

ABA08485
ID ABA08485 standard; cdNA: 547 BP.

AC ABA08485;

XX 11-JAN-2002 (first entry)

DE Human AMP-activated protein kinase subunit homologue cdNA, SEQ ID NO:261.
DE Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer; ss.

OS Homo sapiens.

XX WC0200157188-A2.

PN 09-AUG-2001.

PD 05-FEB-2001; 2001WO-US03800.

PF 03-FEB-2000; 2000US-0496914.

XX 27-APR-2000; 2000US-0560875.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457740/49.

XX

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XX

XX

DR P-PSDB; ABB11241.
XX Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
XX
XX Claim 1; Page 429; 1963pp; English.

CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.

XX Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;

Query Match 27.2%; Score 448.8; DB 22; Length 547;
Best Local Similarity 99.6%; Pred. No. 3.5e-107;
Matches 450; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 738 TCGTGACCATCAGTCTTCATCCCTGGTGTGCTGCTACTACAGTCCGCCCTGGTCC 797

DB 1 TCGTGACCATCAGTCTTCATCCCTGGTGTGCTGCTACTACAGTCCGCCCTGGTCC 60

QY 798 AGATCTATGAGATTGACACATAGATTGAGACTCGAGGAGATCTACCTGCAAGCT 857

DB 61 AGATCTATGAGATTGACACATAGATTGAGACTCGAGGAGATCTACCTGCAAGCT 120

QY 858 GCTTCAAGCCCTCTGGTCTCCATCTCTCTTAATGATAGCTGTTGAAGCTGTCTACACC 917

DB 121 GCTTCAAGCCCTCTGGTCTCCATCTCTCTTAATGATAGCTGTTGAAGCTGTCTACACC 180

QY 918 TCATCAAGAACCGGATCCATCGGCTGCTGCTTCTTTGACCCGGTGTGAGCAACGATCTCC 977

DB 181 TCATCAAGAACCGGATCCATCGGCTGCTGCTTCTTTGACCCGGTGTGAGCAACGATCTCC 240

QY 978 ACATCTCTCACACACAAAGCCCTGCTCAAGTCTTCGACATCTTGTGCTCCCTGCTGCC 1037

DB 241 ACATCTCTCACACACAAAGCCCTGCTCAAGTCTTCGACATCTTGTGCTCCCTGCTGCC 300

QY 1038 GGCCCTCTCTCTCTACCGCACTATCCAAAGATTGGGGCATCGGCACATCCGAGACTTGG 1097

|||||
301 GGCCCTCCTCTCTACCGCACTATCCAGATTGGGCAATCCGACATTTGG 360
1098 CTGTGGTCTGGAGACAGCACCATCTCTGACTGCACTGGACATCTTTGGACCGCGTGG 1157
361 CTGTGGTCTGGAGACAGCACCATCTCTGACTGCACTGGACATCTTTGGACCGCGTGG 420
1158 TGTCTGCACTGCTGTGGTCAACGAATGTGGT 1189
421 TGTCTGCACTGCTGTGGTCAACGAATGTGGT 452

RESULT 13
AAH43682
ID AAH43682 standard; DNA; 989 BP.
XX
AC AAH43682;
XX
DT 21-JAN-2002 (first entry)
XX
DE PRKAG3 intron 2 - intron 4.
XX
XX Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
KW metabolic disease; diabetes; obesity; substitution; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT intron 1..21
FT /*tag= a
FT /number= "Intron 2"
FT /note= "3' portion of intron 2"
FT 22..177
FT /*tag= b
FT /number= "Exon 3"
FT 178..541
FT /*tag= c
FT /number= "Intron 3"
FT 542..945
FT /*tag= d
FT /number= "Exon 4"
FT 946..989
FT /*tag= e
FT /number= "Intron 4"
FT /note= "5' portion of intron 4"
XX
PN WO200177305-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-SE00765.
XX
PR 07-APR-2000; 2000US-195663P.
XX
PA (AREX-) AREXIS AB.
XX
PI Andersson L, Luthman H, Marklund S;
XX
DR WPI; 2001-657170/75.
XX
PT New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
PS Example 1; Fig 2; 25pp; English.
XX
CC The sequences given in AAH43681-84 represents genomic fragments
CC encoding the human AMP-activated protein kinase gamma 3 subunit
CC (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
CC is useful in determining a risk estimate of a metabolic disease,
CC such as diabetes or obesity, in a subject. The variation may occur
CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of

a G for a C at nucleotide 320, resulting in the amino acid
CC substitution P71A; in exon 4 variation may be a substitution of a
CC T for a C at nucleotide 550; and in exon 10 variation may be a
CC substitution of a T for a C at nucleotide 1037, resulting in the
CC amino acid substitution R340W. There may also be nucleotide variation
CC in intron 6.
XX
SQ Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
Query Match 24.7%; Score 407.2; DB 22; Length 989;
Best Local Similarity 99.3%; Pred. No. 3.2e-96;
Matches 409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 247 AGGTCCCGGTCCAGGCAAGCTGATCCTCCGCGGGTGGGCACTCCACCAACAGGTGGGACTG 306
DB |||||||
540 AGGTCCCGGTCCAGGCAAGCTGATCCTCCGCGGGTGGGCACTCCACCAACAGGTGGGACTG 599
QY 307 CACACCCCTTGGCTCAAGCTGATCCTCCGCGGGTGGGCACTCCACCAACAGGTGGGACTG 366
DB |||||||
600 CACACCCCTTGGCTCAAGCTGATCCTCCGCGGGTGGGCACTCCACCAACAGGTGGGACTG 659
QY 367 CCTCCCTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGTGGC 426
DB |||||||
660 CCTCCCTCTGACTGTACAGCCTCAGCTGCAGGCTCCAGCACAGATGATGTGGAGTGGC 719
QY 427 CACGGAGTTCCAGCCACAGAGGCTGGGAGTGTGAGCTAGAAGGCTCTCTGGAAGAGAG 486
DB |||||||
720 CACGGAGTTCCAGCCACAGAGGCTGGGAGTGTGAGCTAGAAGGCTCTCTGGAAGAGAG 779
QY 487 GCCTGCCCTGTGCTGTCCCGCAGGCGCCCATTTCCCAAGCTGGGCTGGGATCACCACCT 546
DB |||||||
780 GCCTGCCCTGTGCTGTCCCGCAGGCGCCCATTTCCCAAGCTGGGCTGGGATCACCACCT 839
QY 547 GCGGAAACCCGCGGCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGC 606
DB |||||||
840 GCGGAAACCCGCGGCCAGATCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGC 899
QY 607 CATGGCAACTAGCTCCAAAGCTAGTCACTTCGACACCATGCTGGAGATCAAG 658
DB |||||||
900 CATGGCAACTAGCTCCAAAGCTAGTCACTTCGACACCATGCTGGAGATGAGG 951

RESULT 14
ABK84324
ID ABK84324 standard; cDNA; 1578 BP.
XX
AC ABK84324;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #895.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
PR 03-OCT-2000; 2000US-237189P.
XX
PA (GENE-) GENE LOGIC INC.

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:37:44 ; Search time 4099.65 Seconds
(without alignments)
6506.409 Million cell updates/sec

Title: US-09-826-581-5
Perfect score: 1647
Sequence: 1 ttgctgtggcgtggccaca.....acaccagccttagttcttc 1647

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_esti.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pin.*
21: em_gss_vit.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query %		DB ID	Description
	Score	Match Length		
1	456.4	27.7	572 13	BI344527 373008 MA
2	384	23.3	970 9	AL533446
3	380	23.1	758 9	AJ396118
4	374.6	22.7	685 10	BB630381
5	366.8	22.3	921 9	AL548987
6	363.2	22.1	905 9	AL555228

SUMMARIES

7	361	21.9	940	9	AL554278
8	360.6	21.6	1085	13	BM548053
9	355	21.9	937	14	BQ947745
10	354	21.5	548	13	BI775360
11	353	21.4	944	14	BQ954908
12	352.6	21.4	728	13	BQ504184
13	350.4	21.3	1070	14	BQ224866
14	350	21.3	908	9	AL552459
15	346.8	21.1	864	13	BI858240
16	343	20.8	826	9	AL519198
17	342.8	20.8	951	9	AL513784
18	340.4	20.7	1015	14	BM907915
19	339.4	20.6	854	14	BQ434582
20	336.6	20.4	1134	14	BM922418
21	336.6	20.4	1013	13	BM462694
22	336	20.4	864	14	BQ216466
23	335	20.3	1004	13	BM470188
24	333.2	20.2	852	14	BQ441941
25	333	20.2	1104	13	BM561956
26	330	20.0	848	14	BQ424978
27	329.2	20.0	595	13	BM487789
28	328.8	20.0	967	9	AL524822
29	328.6	20.0	1006	13	BM469833
30	326.8	19.8	868	14	BQ435355
31	322.4	19.6	954	14	BQ963077
32	319.6	19.4	905	14	BQ920095
33	317.6	19.3	827	14	BQ572978
34	316.4	19.2	870	13	BI910928
35	312.8	19.0	647	13	BM440762
36	310.2	18.8	784	9	AU080009
37	308.4	18.7	841	13	BI546514
38	303.4	18.4	633	13	BJ072114
39	303.4	18.4	808	13	BI771184
40	301	18.3	636	12	BG713637
41	299.6	18.2	591	13	BQ495978
42	298	18.1	782	13	BI819312
43	295.6	17.9	444	12	BF890374
44	293.4	17.8	761	9	AL632024
45	291	17.7	907	14	BQ439463

ALIGNMENTS

RESULT 1
BI344527
LOCUS 373008 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence. EST 30-JUL-2001
DEFINITION BI344527
ACCESSION BI344527.1 GI:15037807
VERSION BI344527.1
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 572)
AUTHORS Pahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT


```
QY 1167 TGCCTGTGGTCAACGAATGTGGTCAGGTCTGGGGCTCTATTCCCGCTTTGATGTGATTC 1226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 690 TGCAGTGTGGTGAAGAAGGGGTGTGGTGACATCTACTCCAAAGTTTGATGTTATCA 749
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1227 ACCTGGCTGCCAGCAACCTTACAAACCTGGACATGAGTGTGGGAAGCCCTGAGGC 1286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 750 ATCTGGCAGCAGAAGACCTTACAAACCTAGATTAATCTGTAAGACCTTGCAC 809
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1287 AGAGGACATGATGTGGAGGAGTCTCTTCCTGCGACCCCAAGAGAGCTTGGGGAAG 1346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 810 ATCGATCACTACTTGGGGGTCTCTCAAGTGTCTACCTGCATGAGACTCTGGAGACCA 869
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1347 TGAACGACAGGATCTCGGAGCAGGTACACAGGCTGGTGTAGTGTGACAGACCCAGC 1406
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 870 TCATCAACAGGCTAGTGAAGCAGAGGTTCCCGACTTGTAGTGTGGATGAAATGATG 929
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1407 ATCTCTTGGCGGTGCTCCCTCTCCGACATCTCTCAGGC 1446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 930 TGGTCAAGGAATGTATCACTGTCTGACATCTCTGCAGC 969
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
AJ396118 758 bp mRNA linear EST 25-JAN-2001
LOCUS AJ396118 dkfz426 Gallus gallus cDNA clone 25f16r1, mRNA sequence.
ACCESSION AJ396118
VERSION AJ396118.1 GI:7127728
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
AUTHORS Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy
,J., Korn,B. and Buerstedde,J.M.
TITLE A large database of chicken bursal ESTs as a resource for the
analysis of vertebrate gene function
JOURNAL Genome Res. 10 (12), 2062-2069 (2000)
MEDLINE 20568495
COMMENT Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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Db 1 ACCAGCTCAAACTCGCTCTCTTCGACACTTCCCTTCAGTGAAGAAGGCTTCTTGCA 60
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QY 674 CTGTGTCACACGGTGTGGGACGCCCTCTATGGACAGCAGACGACAGCTTTGTG 733
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RESULT 4
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DEFINITION musculus cDNA clone A030014A04 5', mRNA sequence.
ACCESSION BB630381
VERSION BB630381.1 GI:16467364
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 685)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
,Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
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,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
UNPUBLISHED (2001)
JOURNAL Contact: Yoshihide Hayashizaki
COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.			
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	/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 5 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Li Center Drive a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://fulllength.invitrogen.com"			
BASE COUNT	237 a 218 c 199 g 250 t 1 others			
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QY	627 TAGTAFATTTGGACAC	CAATGCTGGAGATCA	AGAAGCCCTCTTTG	CTCTGTGGCCCAAG 686
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QY	687 GTGTGGGGCAGCCCT	CTATGGCAGCAGCA	GAAGAAGCAGAGCT	TTTGTGGGATGTGACCA 746
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QY	867 CTCTGTCTCCATCT	CTCTCTAATGATAG	CCCTGTTTGAAGCT	GTGTACACCTCATCAAGA 926
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QY	927 ACCGGATCATCGCT	CGCTCTTTCGAC	CGGTGTACAGCAAG	CTACTCCACATCTCTCA 986
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QY	987 CACACAAAGCCCTG	CTCAAGTTCCCTG	CACATCTTTTGGT	TCCCTCTGCTCCCGGCTCTCT 1046
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age 27. Library is oligo-dT primed and directionally
cloned (EcorV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."
BASE COUNT      285 a 259 c 251 g 286 t      4 others
ORIGIN
Query Match      21.9%; Score 360.6; DB 13; Length 1085;
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RESULT 9
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AGENCOURT 8863556 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6423989
5', mRNA sequence.
ACCESSION      BQ947745
VERSION        BQ947745.1 GI:22363223
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 937)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: DCTD/DPG/Gazdar
              cDNA Library Preparation: Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
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                  GCCACGAG(G). Library constructed by Ling Hong in the
                  laboratory of Gerald M. Rubin (University of California,
                  Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                  Superscript II RT (Life Technologies). Note: this is a
                  NIH_MGC Library."
BASE COUNT      240 a 212 c 235 g 247 t      3 others
ORIGIN
Query Match      21.6%; Score 355; DB 14; Length 937;
Best Local Similarity 65.6%; Pred. No. 5.8e-78;
Matches 531; Conservative 0; Mismatches 277; Indels 1; Gaps 1;
QY 649 GGAGATCAAGAGAGCCCTTCTTCTGCTGTCGTCGCAACGGTGTGCGGAGCCCTCTATG 708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GCAGGTGAAGAAAGCTTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 709 GCACAGCAGAGCAGCAGCTTTGTGGGATGCTGACCATCATCTGCTGCTGCTGCTGCT 768
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GGATAGTAGAAGCAAGAGTTTGTGGGATGCTGACCATCATCTGCTGCTGCTGCTGCT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 769 GCATCGCTACTACAGGTCCCTGTCAGATCTATGAGATTGAACACATGAAGATTGA 828
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GCACCGCTACTATTAATCAGCCTTGTACAGATCTATGAGCTAGAGAACACAGATTGA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 829 GACCTGGAGGAGATCTTACCTGCAAGGCTGCTTCAAGCCTCTGCTGCTGCTGCTGCT 888
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AACTTGGAGAGAGGTGTATCTCCAGGACTCTTTAAACCGCTTGTGCTGCTGCTGCT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	1 (bases 1 to 944)	NIH-MGC http://mgc.nci.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov	Tissue Procurement: DCTD/DTF/Gazdar	cdNA Library Preparation: Rubin Laboratory
			cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Agencourt Bioscience Corporation
			Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	http://image.llnl.gov
			Plate: LLCM2596	row: i column: 24
			High quality sequence start:	693.

FEATURES	source
1. .944	Location/Qualifiers
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:6421343"	
/clone_lib="NIH_MGC.18"	
/tissue_type="large cell carcinoma"	
/lab_host="DH10B (phage-resistant)"	
/note="Organ: lung; Vector: pORF7; Site.1: XhoI; Site.2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACAGAC(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
253 a	224 c 208 g 257 t 2 others
BASE COUNT	
ORIGIN	

Query Match	21.4%	Score 353;	DB 14;	Length 944;
Best Local Similarity	63.7%;	Prod. No. 1.9e-77;		
Matches 550;	Conservative	0;	Mismatches 312;	Indels 1;
Gaps	1;			
QY	567	TCTACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGCAACTAGCTCCCAAGC	626	
Db	80	TGTAATATCCCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCGCACAGCTCCCAAT	139	
QY	627	TAGTCATCTTTGCACACCACATGCTGGAGATCAAGAAGSCCTCTTTTGCTCTGGTGGCCACAG	686	
Db	140	TGGTTGTAATTTGATAGCTGCCCTGCAGGTGAAGAAAGCTTTTTTGGCTTTGGTGACTAACG	199	
QY	687	GTGTGGGGGAGGCCCTCTATGGCAGACAGCAGAGAGAGCTTTGTGGGGATGCTGACCA	746	
Db	200	GTGTACGAGTGCCTCTTATGGGATAGTAAGAAGCAAAAGTTTTTGTGGCATGCTGACCA	259	
QY	747	TCACGTACTTCATCCTGGTGGTGCATCGCTACTACAGGTGCCCTCGTCCAGACTCATG	806	
Db	260	TCACGTATTTTCATCAATATVCTGCACCGCTACTATAATACAGCCTTGGTACAGACTCATG	319	
QY	807	AGATTGAACACATCAAGATTTGAGACCTTGGAGGAGAGATCTACTCTCAAGGCTGCTTCAAGC	866	
Db	320	AGCTAGAAGAACACAGATAGAACTTGGAGAGAGTGTATCTCCAGSACTCTTTAAAC	379	
QY	867	CTCTGGTCCCATCTCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCCCTCATCAAGA	926	
Db	380	CGCTGTCTGCATTTCTCCTAATGCCAGCTTGTTTGATGCTGTCTCTTCATTAAATTCGGA	439	
QY	927	ACCGGATCCATCGCCTGCTGTCTTGACCCGGTGTCAAGGCAAGCTACTCCACATCCCTCA	986	
Db	440	ACAAGATCCACAGGCTGCCAGTTATTGACCCGAATTCAGGCAATTACTTTGTATACCTCTCA	499	
QY	987	CACACAAACCGCTGCTCAAGTTCCTGCACATCTTTGGTTCCCTGCTGCCCGGCCCTCCT	1046	
Db	500	CCCAAGCGCATCTCGAAGTTCCTCAAAATGTTGTTTATCACTGAGTTCCCAAGCCAGAGT	559	
QY	1047	TCCTCTACCGCACTATCCAAAGATTTGGGCAATCGGCACATTCGGAGACTTGGCTGTGGTGC	1106	

Db	560	TCATGTCCAAAGTCTCTGAAGAGGCTACAGATTGGCACCTATGCCAATATTGCTATGGTTC	619		
QY	1107	TGGAGACGACGCCATCTGACTGCATCGAGCATCTTTTGTGGACCGCGTGTCTGTGCAC	1166		
Db	620	GCACTACCACCCCGCTCTATGTGGCTCTGGGATTTTGTACAGCATCGAGTCTCAGCCC	679		
QY	1167	TGCGTGTGTCAACGAATGTGGTCAGGTCGTGGGCTCTATTCGCCGTTTGTATGTGATTC	1226		
Db	680	TGCCAGTGGTGGATGAGAAGGCGGTGTGGTGACATCTACTCCAAGTTTGTATGTTATCA	739		
QY	1227	ACCTGGCTGCCCAGCAACCTTACAACCA-CCTGGACATGACTGTGGGAAGCCCTGAGG	1285		
Db	740	ATCTGGCAGCAAAAGACCTTACAACAACCCCTAGATGTATCTGTGACTAAAGCCTTGGCAA	799		
QY	1286	CAGAGGACACTATGTCTGGAGGGAGTCCCTTCCTGCCAGCCGCCACGAGAGCTTGGGGAA	1345		
Db	800	CATCGATCACATTACTTTGAGGGTGNTCTCAAGTCTACCTGCATGAGACTCTGGAGAC	859		
QY	1346	GTATCGACACAGGATTCCTCGGGACAGGTACACAGAGCTGGTGTAGTGGACGACGACCG	1405		
Db	860	ATCATCCACAGGCTAGTGGAAAGCAGAAAGTTTCAACCGACTGTAAAGGTTGAATGAAATGAT	919		
QY	1406	CATCTCTTTGGGCGTGGTCTCCCT	1428		
Db	920	GTGCCCAAGGGAATTGTATCACT	942		
RESULT 12					
BJ504184/c					
LOCUS	BJ504184	MF01PSA cdna Oryzias latipes cdna clone MF01PSA006A14	3', linear EST 08-AUG-2002		
DEFINITION	mRNA sequence.				
ACCESSION	BJ504184				
VERSION	BJ504184.1	GI:22156146			
KEYWORDS	EST.				
SOURCE	Japanese medaka.				
ORGANISM	Oryzias latipes				
REFERENCE	Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H. (bases 1 to 728)				
AUTHORS	Medaka EST Project in Takeda's lab				
TITLE	Unpublished (2001)				
JOURNAL	Contact: Tadasu Shin-i				
COMMENT	Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.				
FEATURES	Location/Qualifiers				
	1..728				
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	/strain="d-rR"				
BASE COUNT	/db_xref="taxon:8090"				
	/clone="MF01PSA006A14"				
	/clone_lib="MF01PSA cdna"				
	/sex="mixture of female and male"				
	/tissue_type="whole embryo"				
	/dev_stage="fry stage 40"				
ORIGIN	182 a	161 c	174 g 210 t 1 others		
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Best Local Similarity 68.1%; Pred. No. 2e-77;					
Matches 490; Conservative 0; Mismatches 230; Indels 0; Gaps 0;					
Qy	524	AGCTGGGCTGGGATGACGAATGCGGAACCGGGCCGACATCTACATCGCTTCATG	583		
Db	725	AAACTTGAATACATGATGACCTGCTGGAACGACAGATGATATTNACATCGCGCTTATG	666		

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db_xref	"/db_xref="taxon:9606"
clone	"/clone="IMAGE:6058577"
clone_lib	"/clone_lib="NIH_MGC_68"
tissue_type	"/tissue_type="large cell carcinoma"
lab_host	"/lab_host="DH10B (phage-resistant)"
note	"/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."
Technology	"/Technology="Life Technologies"
BASE COUNT	275 a 247 c 263 g 284 t 1 others
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Best Local Similarity	64.4%; Pred. No. 8.9e-77;
Matches	556; Conservative 0; Mismatches 306; Indels 2; Gaps 2;
QY	620 TCCAACTAGTCTATCCGACACATCTGGAGATCAAGAAAGCGCTCTTTCTGCTCGTGG 679
Db	1 TCCAAATTTGGTTGATATGATAGCTCCCTGCAGGTGAAGAAAGCTTTTTCGTTGGTG 60
QY	680 GCGAAGGTGTGCGGGAGCCCTCTATGGAGACAGAAAGAGAGAGCTTTTGTGGGATG 739
Db	61 ACTAAGCGGTGACGAGCTGCCCCCTTATGGGATAGTAAGAAAGCAAGTTTGTGGCATG 120
QY	740 CTGACCATCACTGACTCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 799
Db	121 CTGACCATCACTGATTTTATCAATATCTGACCGCTACTATAATCAGGCTTTGGTACAG 180
QY	800 ATCTATGAGATTGAACAATTAAGATTGAGCTGGAGGAGATCTACCTGCAAGGCTGC 859
Db	181 ATCTATGAGTGAAGAACACAGATAGAACTTGGAGAGAGGTATCTCCAGGACTCC 240
QY	860 TTCAGGCTCTGGTCTCATCTCTCTTAATGATAGCTTTTGAAGCTGTCTACACCTTC 919
Db	241 TTTAAACCGCTTGTCTGATTTCTCTTAATGCGACGCTTTTGTGATGCTGTCTCTCATTA 300
QY	920 ATCAAGAAACGGATCCATCGCTGCTGTTTGTGACCGGGTGTGAGCAACGCTACTCCAC 979
Db	301 ATTGGGAACAAGATCCACAGGCTGCCAGTTATTGACCCAGATCAGGCAATACTTTGTAC 360
QY	980 ATCTCATACACAAACGGCTGCTCAAGTTCCTGCAATCTTTTGGTTCCTGTCGCCCGG 1039
Db	361 ATCTCATCCACACAGCGATTTCTGAAGTTCCTCAAAATGTTTATCACTGAGTTCCCAAG 420
QY	1040 CCTCTCTCTCTACCGCAGTATCCAGATTTGGGCATCGGCACATTCGAGAGCTGGCT 1099
Db	421 CCAGAGTTTATGTCCAAGTCTCTGGAAGAGCTACAGATTGGGACCTATATGCAATATGCT 480
QY	1100 GTGGTGTGGAGACAGCACCCTCTGACTGCACTGGACATCTTTTGTGGACCGGCTGTG 1159
Db	481 ATGGTTCGCACTACCAACCCCGTCTATGTGGCTCTGGGGATTTTTGTACAGCATCGAGTC 540
QY	1160 TCTGCACTGCCTGTGGTCAAGAAATTTGGTTCAGGTCCTGGGCTCTATATCCCGCTTTGAT 1219
Db	541 TCAGCCCTGCGAGTGTGGATGAGAGGGCGGTGTGGGACATCTACTCCAAAGTTTGT 600
QY	1220 GTGATTCACCTGCGCTCCCGCAGCAACCTACACACCGCTGGAGCATGAGTGTGGGAAGCC 1279
Db	601 GTTATCACTTGGCAGCAGAAAGACACCTACCACACCTAGATGATCTGTGACTAAAGCC 660
QY	1280 CTGAGGAGAGGACACTATGCTGGAGGAGTCCCTTCCCTGCCAGCCCCACGAGAGCTTG 1339
Db	661 TTGCAACATCGATCACTTACTTTGAGGGTGTCTCAAGTGTCTACCTGCTGAGACTGTG 720
QY	1340 GGGGAAGTGTATCGACAGATTG-CTCGGGAGAGGTTACACAGGCTGGTGTGTAGTGGAGCA 1398
Db	721 GAGACCATCATCAACAGGCTAGTGAAGCAGAGGTTCCACCGACTTGTAGTGGTGTGATGA 780
QY	1399 GACCCAGCATCTCTTGGG-CGTGGTCTCCCTCTCCGACATCTTTTCAGGCACTGTGCTCA 1457

Db 781 AATGATGTGGTCCAGGAAATGCTATCACTGTCTGCATCCTCGACGCCCTGGTGTCC 840

QY 1458 GCCCTGCTGCATCGATGCCCTCG 1481

Db 841 CCGGTGGAGAAAAAACCCCTTG 864

RESULT 14

AL552459 908 bp mRNA linear EST 16-FEB-2001

LOCUS AL552459 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1070YC03 5

DEFINITION prime, mRNA sequence.

ACCESSION AL552459

VERSION AL552459.1 GI:12891378

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. 908

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0D1070YC03"

/clone_lib="LTI_NFL006.PL2"

/tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 239 a 222 c 199 g 247 t 1 others

ORIGIN

Query Match 21.3%; Score 350; DB 9; Length 908;

Best Local Similarity 65.6%; Pred. No. 1e-76;

Matches 509; Conservative 1; Mismatches 266; Indels 0; Gaps 0;

QY 567 TCTACATGCGCTTATGACGAGACACACTGCTACGATGCCATGCGCACTAGCTCCAAAGC 626

Db 131 TGTATATCTCTTCATGAAGTCTCATCGCTGCTATGACCTGATCCCAAGCTCCAAAT 190

QY 627 TACTCATCTTCGACACCATCTGGAGATCAAGAGCCCTCTTGTCTGTGGTGGCCACG 686

Db 191 TGGTGTATTGTATGATCCCTGTCAGGTGAAGAAAGCTTTTGTGTGGTGTACTAAGC 250

QY 687 GTGTGCGGGACGCCCTCTATGGGACAGCAAGACGAGCTTTGTGGGATGCTGACCA 746

Db 251 GTGTACGAGCTGCGCCCTTTATGGATAGTAAGAAAGCAAGTTTGTGGGATGCTGACCA 310

QY 747 TCACTGATCTATCTGCTGCTGATCGCTACTACAGTCCGCCCTGTGTCAGATCTATG 805

Db 311 TCATGTATTTTCATATATCTGCGCCGCTACTATATATCAGCTTGGTGTACAGATCTATG 370

QY 807 AGATTGAACACATATGATGATGAGCTGAGGGAGATCTACTGACGAGCTGCTTCAAGC 866

Db 371 AGCTAGAAGACACAGATAGAACTTGGAGAGAGGTGTATCTCCAGGACTCCTTTAAAC 430

QY 867 CTCGTGCTCCATCTCTCTTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGA 926

Db 431 CGCTTGTCTGATTTCTCTTAATGCCAGCTTTGTTGTATGCTGTCTCTTAATTAATCGGA 490

QY 927 ACCGATCCATCGCTGCTGCTTCTTGACCGGTGTGACGACGCTACTCCACATCTCA 986

Db 491 ACAAGATCCACAGGCTGCCAGTTATTGACCCAGAAATCAGGCAATCTTTGTACATCTCA 550

QY 987 CACAAAACGCTGCTCAAGTTCTCGACATCTTTGTTGCTCCCTGCTGCCCGGCCCTCT 1046

Db 551 CCCACAGCGCATCTGAGTTCTCAATTTGTTATCACTGASTTCCCACAGCAGAT 610

QY 1047 TCTCTACCGCACTATCCAAAGATTGGGCATCGGCACATTCGAGAGCTTGGCTGTGTC 1106

Db 611 TCATGTCCAAGTCTCTGGAAGAGCTACAGATGGCACTATGCCAATATTTGCTATGTTTC 670

QY 1107 TGGAGACAGACCATCTCTGACTGCTGACATCTTTGTTGGACCGGCTGTGTCGCAC 1166

Db 671 GCATCTACACCCCGCTCTATGTGGCTCTGGGATTTTGTACAGCATCGAGTCTCAGCC 730

QY 1167 TGCTGTGGTCAACGAATGTGTCAGGTCTGTTGGGCTCTATTCGCCCTTTGATGTGATTC 1226

Db 731 TGCCAGTGGTGGATGAGAGGGGCGTGTGGACATCTACICCAAGTTTGTATGATCA 790

QY 1227 ACCTGGCTGCCAGCAAACTACAACTGACATGAGTGTGGGAGAGCCCTGAGGC 1286

Db 791 ATCTGGCAGCAGAAAGACCTACAACTAGATGTATCTGTGACTAAAGCTTGTCAAC 850

QY 1287 AGAGACACTATGCTGGAGGAGTCTCTTCTGCCAGCCCCACGAGAGCTTGGGG 1342

Db 851 ATCGATCACATTAATTGAGGGTGTCTCAAGTGTCTACCTGTCATGAGACTCTGGRG 906

RESULT 15

BI858240 864 bp mRNA linear EST 10-OCT-2001

LOCUS 603384001F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5392777 5,

DEFINITION mRNA sequence.

ACCESSION BI858240

VERSION BI858240.1 GI:15998987

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 864)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAM12001 row: a column: 02

High quality sequence stop: 830.

Location/Qualifiers

1. 864

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5392777"

/clone_lib="NIH_MGC_87"

/tissue_type="mammary adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: breast, vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 223 a 202 c 203 g 236 t

ORIGIN

Query Match		21.1%; Score 346.8; DB 13; Length 864;
Best Local Similarity		65.3%; Pred. No. 6.3e-76;
Matches 555; Conservative 0; Mismatches 292; Indels 3; Gaps 3;		
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Db	2	ATCCCAAGCTCCAAATTTGGTTGATTTGATACCTCCCTGCAGGTGAAGAAAGCTTTT 61
QY	668	TTTGCTCTGGTGCCAAAGGGTGTGGGCGAGCCCTCTATGGGACAGCAAGAAGCAGAGC 727
Db	62	TTTGCTTTGGTGACTAACGGTGTAGGAGCTGCCCTTTATGGGATAGTAAGAACAAAGT 121
QY	728	TTTGTGGGATGCTGACCATCACTGACTTCATCCTGGTGTGCTGATCGTACTACAGTCC 787
Db	122	TTTGTGGGATGCTGACCATCACTGACTTCATCAATATCCTGCACCGCTACTATAATCA 181
QY	788	CCCTGTGTCAGATCTATGAGATTGAACAACATAAGATTGAGACCTGGAGGGAGATCTAC 847
Db	182	GCCTTGGTACAGATCTATGAGTGAAGAACAACAGATAGAATCTGGAGAGAGGTGTAT 241
QY	848	CTGCAAGGCTGTCTCAAGCCTCTGCTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCT 907
Db	242	CTCCAGGACTCCTTTAAACCCCTGTCTGCATTTCTCCTAATGCCAGCTTCTTTGATGCT 301
QY	908	GTCTACACCTCATCAAGAAGCGGATCCATCGCCTGCCTGTTCTTGGACCCGGTGTACGC 967
Db	302	GTCTCTTTCAATTATCGGAACAAGATCCACAGGCTGCCAGTTATTGACCCAGAATCAGC 361
QY	968	AACGTACTCTCCACATCTCACACACAAAGCGCTGCTCAAGTTCCTGCACATCTTTGGTTCC 1027
Db	362	AATACTTTGTACATCTCTACCCACAGGCAATCTGAGTTCTCAAAATTTGTTATCACT 421
QY	1028	CTGCTGCCCGGCCCTTCCTCTACCGCACTATCCAAAGATTGGGCATCGGCACATTC 1087
Db	422	GAGTTCCCAAGCCAGAGTTTCATGTCCAAGTCTCTGGAAGACTACAGATTGGCACCTAT 481
QY	1088	CGAGACTTGGCTGTGGTGTGGAGACAGCACGCCATCTGACTGCACTGGACATCTTTGTG 1147
Db	482	SCCAATATTTGCTATGTCTGCGACTACCAACCCCGTCTATGTGGCTCTGGGAATTTTGT 541
QY	1148	GACCGGGCTGTGCTCACTGCTGTGTCAACGAATGTGTGTCAGTCTGTGGGCTCTAT 1207
Db	542	CAGCATCGATCTCACCCCTGCCAGTGTGGATGAGAGGGGGTGTGGTGGACATCTAC 601
QY	1208	TCCCGCTTTGATGTGATTCACCTGGCTGCCCGAGCAACCTTACAACCACTGGACATGAGT 1267
Db	602	TCCAAGTTTGATGTATCAATCTGCGACGAGAAAAGACCTTACAACAACCTAGATGATCT 661
QY	1268	GTGGGAGAACCCCTGAGGCGAGGACACTATGCTGGAGGGAGTCTTTCTGCGAGCCC 1327
Db	662	GTGACTAAAGCCTTGCACATCGATCACTACTTTGAGGGTGT-CTCAAGTGTACTCTG 720
QY	1328	CACGAGAGCTTGGGGAAGTGATCGACAGGATTG-CTCGGGAGCAGGTACACAGGCTGT 1386
Db	721	CATGAGACTCTGGAGACCATCATCAACAGGCTAGTGGAGCCGAGGGTTTCAACGACTGT 780
QY	1387	GCTAGTGGAGAGACCCAGCATCTCTTGGGGTGGTCCCTCCCTCCGACATCCTTCAGGC 1446
Db	781	AGTGTGTGATGAAATGATGTGTCAGGGACATGT-TCACTGTCTTGACATCCTGCAGGC 839
QY	1447	ACTGGTGTCT 1456
Db	840	CCTGGTGTCT 849

Search completed: June 13, 2003, 05:58:20
Job time : 4104.65 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:37:44 ; Search time 4099.65 Seconds

(without alignments)
6506.409 Million cell updates/sec

Title:

US-09-826-581-5

Perfect score: 1647

Sequence: 1 ttggtctgggtggccaca.....acaccagcctcttagcttc 1647

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vit:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_oth:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456.4	27.7	572	13	B1344527 373008 MA
2	384	23.3	970	9	AL533446
3	380	23.1	758	9	AJ396118
4	374.6	22.7	685	10	B8630381
5	366.8	22.3	921	9	AL548987
6	363.2	22.1	905	9	AL555228

7	361	21.9	940	9	AL554278
8	360.6	21.9	1085	13	BM548053
9	355	21.6	937	14	BQ947745
10	354	21.5	548	13	B1775360
11	353	21.4	944	14	BQ954908
12	352.6	21.4	728	13	BJ504184
13	350.4	21.3	1070	14	BQ224866
14	350	21.3	908	9	AL552459
15	346.8	21.1	864	13	B1858240
16	343	20.8	826	9	AL519198
17	342.8	20.8	951	9	AL513784
18	342	20.8	1015	14	BM907915
19	340.4	20.7	854	14	BQ434582
20	339.4	20.6	1134	14	BM922418
21	336.6	20.4	1013	13	BM462694
22	336	20.4	864	14	BQ216466
23	335	20.3	1004	13	BM470188
24	333.2	20.2	852	14	BQ441941
25	333	20.2	1104	13	BM561956
26	330	20.0	848	14	BQ424978
27	329.2	20.0	595	13	BM487789
28	328.8	20.0	967	9	AL524822
29	328.6	20.0	1006	13	BM469833
30	326.8	19.8	868	14	BQ435355
31	322.4	19.6	954	14	BQ963077
32	319.6	19.4	905	14	BQ920095
33	317.6	19.3	827	14	BQ572978
34	316.4	19.2	870	13	B1910928
35	312.8	19.0	647	13	BM440762
36	310.2	18.8	784	9	AU080009
37	308.4	18.7	841	13	B1546514
38	303.4	18.4	633	13	BJ072114
39	303.4	18.4	808	13	B1771184
40	301	18.3	636	12	BG713637
41	299.6	18.2	591	13	B17495978
42	298	18.1	782	13	B1819312
43	295.6	17.9	444	12	BF890374
44	293.4	17.8	761	9	AL632024
45	291	17.7	907	14	BQ439463

ALIGNMENTS

RESULT 1
B1344527
LOCUS
DEFINITION 373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION B1344527
VERSION B1344527.1 GI:15037807
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 572)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCACAGTCACGAG
Plate: 119 row: 1 column: 11
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1. .572
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

FEATURES

source

BASE COUNT 106 a 190 c 151 g 124 t
ORIGIN
Query Match 27.7%; Score 456.4; DB 13; Length 572;
Best Local Similarity 89.8%; Pred. No. 1.8e-103;
Matches 501; Conservative 0; Mismatches 56; Indels 1; Gaps 1;
QY 853 AGGCTGCTCAAGCCTTGGTCTCCATCTCTCTTAATGATGAGCTGTGTAAGCTGCTA 912
Db 15 AGGCTGCTCAAGCCTTGGTCTCCATCTCTCCCAATGACAGCCTCTTGAAGCTGCTA 74
QY 913 CACCTCATCAAGAACCGATCATCGCTCGCTGTTCTTGACCGGCTCTCAGCAAGCT 972
Db 75 CGCCTCATCAAGAACCGATCACCGCTCGCGGCTCTGAGCCCTGTCTCCGGGGCTGT 134
QY 973 ACTCCACATCTCACACAAAGCCTGCTCAAGTCTCTGCACATCTTTGGTTCCTGCT 1032
Db 135 GCTCCACATCTCACACATAAGCGCTCTCAAGTCTCTGCACATCTTTGGCACCTGCT 194
QY 1033 GCGCGGCGCTTCTCTCTACCGCACTATCCAGATTTGGGATCGGCAATCCGAGA 1092
Db 195 GCGCGGCGCTTCTCTCTACCGCACTATCCAGATTTGGGATCGGCAATCCGAGA 254
QY 1093 CTTGGCTGTGCTGTGAGACAGACCCATCTGACCTGACCTGGACATCTTTGGACCG 1152
Db 255 CTTGGCTGTGCTGTGAAACGGCGCCATCTGACCGCACTGGACATCTTTGGACCG 314
QY 1153 GGGTGTGCTGCACTGCCCTGTGCTCAAGAAATGTGTGAGGTGCTGGGCTCTATTCCG 1212
Db 315 GCGTGTGCTGCGCTGCTGCTGCTCAAGAAATGTGTGAGGTGCTGGGCTCTATTCCG 374
QY 1213 CTTGATGTGATTCACCTGGCTGCGGAGCAAACTTACACCACTGGATGAGTGTGG 1272
Db 375 CTTGATGTGATTCACCTGGCTGCGGAGCAAACTTACACCACTGGATGAGTGTGG 434
QY 1273 AGAAGCCTGAGGAGGACACTATGTCTGAGGAGTCTTTCTGCGACGCCACGA 1332
Db 435 AGAAGCCTGAGGAGGAGACTGTGTGGAAGGCTCTTTCTGCGACGCCACGA 494
QY 1333 GAGCTTGG-GGAAGTGTGACAGAGTGTCTCGGAGCAGGTACACAGCTGGTGTAG 1391
Db 495 GACCTTGGGGAAGTCAATGACCGGATTTCCGGGAACAGGTGCACCGCTGGTGTG 554
QY 1392 TGGAGGAGCCAGCATC 1409
Db 555 TGGATGAGACCGACCC 572

RESULT 2
AL533446 970 bp mRNA linear EST 13-FEB-2001
LOCUS AL533446 LTI_FL015_Brn1 Homo sapiens cDNA clone CS0DN004YN03 5
DEFINITION prime, mRNA sequence.
ACCESSION AL533446
VERSION AL533446.1 GI:12796939
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 970)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .970
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DN004YN03"
/clone_lib="LTI_FL015_Brn1"
/sex="male"
/tissue_type="Adult brain"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was constructed by Life Technologies.
Contact : Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 255 a 230 c 217 g 268 t
ORIGIN
Query Match 23.3%; Score 384; DB 9; Length 970;
Best Local Similarity 64.8%; Pred. No. 3.3e-85;
Matches 570; Conservative 0; Mismatches 310; Indels 0; Gaps 0;
QY 567 TCTACATCGCTTCATCGAGGACACCTGCTAGATGCCATGCGCACTAGCTCAAGC 626
Db 90 TGTATATCTTCCTTCATGAAGTCTCATGCTGCTGACCTGATTCGCCAAGCTCAAT 149
QY 627 TAGTATCTTCGACACCATCTCGAGATCAGAGGCCCTTCTTGCTCTGGTGGCAAGC 686
Db 150 TGGTGTATTTGATACCTCCCTCGAGGTGAAGAAAGCTTTTGGTGGTGAATACG 209
QY 687 GTGTGGGGAGCCCTCTATGGGACAGCAAGAACAGAGCTTTGTGGGATGCTGACCA 746
Db 210 GTGTAGGAGCTGCCCTTTATGGATAGTAAGAACAAAGTTTGTGGCATGCTGACCA 269
QY 747 TCATGACTTCTCCTGCTGCTACTGATCAGGTCCCTGCTGGTGGTGGTGGTGGTGG 806
Db 270 TCATGATTTTCATCAATATCTCGACCGCTACTATAAATCAGCCTTGGTACAGATCT 329
QY 807 AGATTGAACACATCAAGATTGAGACCTGGAGGAGATCTACCTGCAAGCTGCTCAAGC 866
Db 330 AGCTAGAAGAACAAAGATAGAAGTTGGAGAGAGGTGATCTCCAGGACTCCTTTAAGC 389
QY 867 CTCTGCTTCCATCTCTCTTAATGATAGCTTTTGAAGCTGTCTACACCTCATCAAGA 926
Db 390 CGCTTGTCTGATTTCTCTTAATGCCAGCTTGTGTGATGCTGTCTCTTCAATTAATCG 449
QY 927 ACGGATCCATCGCTGCTGCTTCTTGACCCCGGTGTCAAGCAAGGTACTCCACATCTCA 986
Db 450 ACAAGATCCACAGGCTGCCAGTTATTGACCCAGAAATCAGGCAATCTTTGTACATCTCA 509
QY 987 CACACAAAGCCTGCTCAAGTCTCGACATCTTTGGTTCCTGCTGCCCGGCCCTCT 1046
Db 510 CCCAAGCAGGACTCTTGAAGTCTCTCAAAATTTTATCTAGTGTCTCCCAAGCAGAGT 569
QY 1047 TCTCTACCGCACTATCCAAAGATTTGGGATCGGCACATTCGAGACTTGGTGTGGTGC 1106
Db 570 TCAATGCCAAGTCTCTGGAAGACCTACAGATTGGCACTATGCCAATATTTGCTATGGTTC 629
QY 1107 TGGAGACAGCACCCATCTCTGACTGGACATCTTTGTGGACCGCGCTGTCTGTGAC 1166
Db 630 GCACCTACCAACCCCGTCTATGTGCTCTGGGATTTTGTGACAGCATCGAGTCTCAGCCC 689

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QY 1167 TGCTGTGTCACGAATGTGGTCAGGTGCTGGGCGCTCTATTCCCGCTTTGATGTGATTC 1226
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Db 690 TGCCAGTGGTGGATGAGAGGGCGGTGTGGTGACATCTACTCCAAGTTTGTATGTTATCA 749
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QY 1227 ACCTGGTGCCGACGAAACCTACAAACCACTGGACATGAGTGTGGGAGAAGCCCTGAGGC 1286
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Db 750 ATCTGGCAGCAGAAGACCTACAAACCACTAGATGATCTGTGACTAAAGCCCTTGAAC 809
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QY 1287 AGAGGACATATGCTGTGAGGAGTGCCTTTCTGCGAGCCCAACGAGAGCTTGGGGGAAG 1346
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QY 1347 TGATCGACAGATTGCTCGGAGGAGGTACACAGGCTGGTGTAGTGGACGAGACCCAGC 1406
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Db 870 TCATCAGAGCTAGTGGAGAGAGGTTCACGACTTGTAGTGGTGGATGAATGATG 929
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QY 1407 ATCTCTTGGCGTGTCTCCCTCTCCGACATCTTCAGGC 1446
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Db 930 TGGTCAAGGGAATTGATCACTGTCTGACATCTCGCAGGC 969
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RESULT 3
AJ396118 758 bp mRNA linear EST 25-JAN-2001
LOCUS AJ396118 dkfz426 Gallus gallus cDNA clone 25f16r1, mRNA sequence.
ACCESSION AJ396118
VERSION AJ396118.1 GI:7127728
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 758)
AUTHORS J., Korn, B. and Buerstedde, J.M.
TITLE A large database of chicken bursal ESTs as a resource for the
analysis of vertebrate gene function
JOURNAL Genome Res. 10 (12), 2062-2069 (2000)
MEDLINE 20568495
COMMENT Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
1. .758
/organism="Gallus gallus"
/strain="CB"
/db_xref="taxon:9031"
/clone="25f16r1"
/tissue_type="Bursa of Fabricius"
/cell_type="Bursal lymphocyte"
/dev_stage="2-3 weeks old"
BASE COUNT 168 a 238 c 186 g 166 t
ORIGIN

Query Match 23.1%; Score 380; DB 9; Length 758;
Best Local Similarity 69.3%; Pred. No. 2.9e-84;
Matches 518; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 614 ACTAGTCCAAAGTATGATCTCTCGACACCAATGCTGAGATCAAGAAGCCCTCTTTGCT 673
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Db 1 ACCAGTCCAAACTGCTGCTCTTCGACACTTCCCTTCAGGTGAAGAAGCCTTCTTGCA 60
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QY 674 CTGGTGCCCAACGGTGTGGGCGACGCCCTCTATGGGACAGCAGCAAGCAGCTTTGTG 733
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Db 61 CTGGTCAACAATGGCTGGGCGACGCCCGCTGTGGGACAGCAAAAACAGAGCTTTGTG 120
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QY 734 GGGATGTGACCATCACTGACTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 793
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Db 121 GGCAATGCTGACCATCACTGACTTTCATCAACATCTGCGCGCTACTACAAAGTGGCCCATG 180
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QY 794 GTCCAGATCTATGAGATTGAACAACATAGATTGAGACCTGGAGAGGAGATCTACTCGAA 833
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Db 181 GTGCAGATCTATGAGTGGAGGAGCACAATAATCGAGACGTGGAGAGAGGTGTACTCGAC 240
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QY 854 GGCTGCTTCAAGCCTCTGGTCTCCATCTCTCTAATGATAGCCTGTTTGAAGCTGCTTAC 913
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Db 241 GACTCTTTAAGCGTGTGGTCTGCAATCTCCCAATGCCAGCCTTTTGTGATGCCGTCTCC 300
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QY 914 ACCCTATCAAGAACCGGATCCATCGCTGCTGTTTGTGACCCGGTGTGACGAAAGTA 973
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Db 301 TCCCTGATCGCAATAAGATCCACCGCTCCCGCTCATCGACCCGCACTCGGCGCAACACT 360
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QY 974 CTCACATCTCTCACACAAAGCGCTGCTCAAGTCTCTGACATCTTGGTTCCTGCTG 1033
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Db 361 CTCTACATCTCAACCCCAAGCGCATCTCAAGTCTCTCAACTCTTTATTGAGAGGTC 420
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QY 1034 CCGCGCGCTCTTCTTCTACCGCACTATCCAAGATTGGGCATTCGGCAGATTCGGAGAC 1093
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Db 421 CCAAGCCTGAGTTTATGGCCCGGACTTTGGAGAGCTGCAGATCGTACTACAGCAAC 480
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Db 481 ATCGCGGTGTGAGCACCAGCACTCCCATCTATGTGCTCTGGGCATCTTCTGCGAGCAC 540
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QY 1154 CGTGTGCTGCACTGCTGTGGTCAACGAATGTGTCAGTTCGTGGCCCTCTATTCCCGC 1213
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Db 541 CGCGTCTCCGCTCTGCGCGGTGGTTCGATGATTCGGGGGGGGTGGTATATCTACTCCAAG 600
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QY 1214 TTGTATGTGATTACCTTGGCTGCCAGCAACCTACAAACCTGGACATGAGTGTGGGA 1273
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Db 601 TTCGAGCTTATCAATTGGCAGCTGAGAGACCTTACAAACCTGGACGTGAGGTGAGC 660
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QY 1274 GAAGCCCTGAGGAGGACATATGTCTGGAGGAGTCTTCTTCGCGACCCCGACGAG 1333
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Db 661 CGGCGCTGCGACGACCGCTCCCATTTAGTGGCGGTCTCAAAATGCTACAAACAGAA 720
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QY 1334 ACCTTGGGGAGTGTATCGACAGGATTG 1361
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Db 721 ACCTTGAAGCCATCATCAACCGCCTGG 748
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RESULT 4
BB630381 685 bp mRNA linear EST 26-OCT-2001
LOCUS BB630381 RIKEN full-length enriched, 6 days neonate skin Mus
DEFINITION musculus cDNA clone A030014A04 5', mRNA sequence.
ACCESSION BB630381
VERSION BB630381.1 GI:16467364
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 685)
REFERENCE Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
```


QY 889 TGATAGCCTGTTGAGCTGTCTACACCTCCTCATCAAGACCGGATCCATCGCTGCCTGT 948
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QY 949 TCTTGACCCGGTGTGAGGACCTTACTCCACATCTCTCACACAAAGCGCTGTCAAGTT 1008
Db 301 TATTGACCCAGCATCAGGCAATCTTGTATCATCTCTCACCAAGCGCATCTGAGTT 360
QY 1009 CTGTCACATCTTTGGTTCCTGTGCTGCCCGGCCCTCTTCCTCTACCGCATATCAAGA 1068
Db 361 CCTCAAAATGTTTATCATCTGAGTTCCCAAGCAGAGTTTATGTCACAGTCTCTGGAAGA 420
QY 1069 TTTGGGCATCGGCACATCCGACCTTGGCTGTGCTGTGCTGTGAGACACACCCATCTGNC 1128
Db 421 GCTACAGATTTGGCACCCTATGCGCAATATGCTATGTTTGGCTGTGCTGTGAGTCTATGT 480
QY 1129 TGCACTTGACATCTTTTGTGACCGGGGTGTGTCTGCTGCTGTGTGCTCAACGAATGTGG 1188
Db 481 GGCTCTGGGGATTTTGTACAGCATCGAGTCTCAGCCCTGCCAGTGTGTGATGAGAGG 540
QY 1189 TCAGGTGCTGGGCTCTATTCCTGCTTTGATGTGATTCACCTGGCTGCCAGCAAACTTA 1248
Db 541 GCGTGTGTGGACATCTACTTCAAGTTTGTATGTTTATCAATCTGGCAGCAGAAAGACTTA 600
QY 1249 CAACCACTTGACATGAGTGTGGAGAAGCCCTGAGGAGAGACACTATGCTGTGGAGG 1308
Db 601 CACAACCTAGATGTATCTGTGACTAAGCCTTGAACATCGATCACAATTACTTTGAGG 660
QY 1309 AGTCCTTTCTGCCAGCCCAACAGAGAGCTTGGGGGAAGTGTATCGACAGGATTCCTCGGA 1368
Db 661 TGTCTCAAGTCTACCTGTCATGAGA-CTCTGSAGACATCATNCACAGGCTAGTGGAGC 719
QY 1369 GCAGGTACACAGCTGTGCTAGTGGACAGACCCAGCATCTTTGGGCTGTGCTCCCT 1428
Db 720 AGAGGCTACCCAGCTTGTAGTGTGGATGAAATGATGTGTCAGGGAATGTATCACT 779
QY 1429 CTCGACATCTCTCAGGCACTGTGTCTCA 1457
Db 780 GTCTGACATCTTGACGGCCCTGTGTCTCA 808

RESULT 10
BI775360
LOCUS 548 bp mRNA linear EST 25-SEP-2001
DEFINITION 467815 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BI775360
VERSION BI775360.1 GI:15776346
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 548)
Smith,T.P.L., Grosse,W.M., Preking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chikco-McKown,C.G.,
Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers

FORWARD: AGGAAACAGCTATGACCAI
BACKWARD: GTTTCCTCAGTCACGAG
Plate: 90 row: I column: 16
Seq primer: ATTAGTGACACTATAG.
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Location/Qualifiers
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/db_xref="taxon:9913"
/clone_lib="MARC 2B0V"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semilendonsus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 119 a 173 c 163 g 93 t
ORIGIN
Query Match 21.5% Score 354; DB 13; Length 548;
Best Local Similarity 81.5%: Fred. No. 7.8e-78;
Matches 448; Conservative 0; Mismatches 95; Indels 7; Gaps 3;
QY 166 CCGTGGGAAACGAGGCGCAAGCCTTTGAG-ATGGACAAGGACAGAAGTCGCTGGAGAG 224
Db 2 CCTTGGGGAACAGAGGACCAAGGTCTCAAGTATGGAAGCCAGGAGATGTAAGGAA 61
QY 225 GGAGGCCACAGGTTCAGGGGGAAGTCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGC 284
Db 62 GGGAGCTGGCAGGCTTGGAGGAGGTCCCAATTCGAAGCAGCTGCTGAGTCCACCGGC 121
QY 285 TGAGGCCACATTCCTCCAGACACACCTTGGCTCAAGCTGATCC--TGCCGGGTGG 341
Db 122 TGGAGGCCACATTCCTCCAGGCCACACCTTGGCCCAAGCCACTCCCTTGTCCGGGTGG 181
QY 342 GCACCTCCACCAACAGGCTGGGAGTGCCTCCCTCTGACTGTACAGCCTCAGCTCCAGGCT 401
Db 182 GCACCCCAACACAGACAGACAGAGCTCCCTCTGACTGTACAGCCTCCGCTCCAGCT 241
QY 402 CCAGCACAGATGATGTGGAGCTGGCCAGAGTTCACAGCCACAGAGCCTTGGGAGTGTG 461
Db 242 CCAGCACAGCATCTGGATCAGGGCATATAGTTCATCAGCCCAAGCAGCGTGGGGGATG 301
QY 462 AGCTAGAGGCTGTCTGGAAGAGAGGCTGCCTGTGCTGTGCTGCCGACGCGCCCATTTTC 521
Db 302 AGCT---CGGCTGTGGAAGAGAGGCGCCCATTTGCCGTCGCCGAGTCCCGGTGC 358
QY 522 CCAAGCTGGGCTGGATGACGAATCGCGAAACCCGGGCGCCAGATCTACATCGCTTCA 581
Db 359 TCATGCTCGCTGGAGCATGAGCTGGGAAACCATGGGCTCAGGTCTACATGCACTTCA 418
QY 582 TGCAGGACACACCTGTCTACGATGCCATGGCAACTAGTTCACAGCTAGTCAATCTTCACA 641
Db 419 TGCAGGACACACCTGTCTACGATGCCATGGCAACCAGCTTCCAAAGCTGTCTATCTCGACA 478
QY 642 CCATGCTGGAGATCAAGAGCGCTTTCTGCTGCTGGTGGCCACGCTGTGGGGACGCC 701
Db 479 CCATGCTAGACATCAAGAAGCGCTTTCTTTGCTGCTGGTGGCCAAATGGTCTCCGCGCCAC 538
QY 702 CTCTATGGGA 711
Db 539 CTCTATGGGA 548

RESULT 11
BI7754908
LOCUS 944 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_8826665 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:5421343
5', mRNA sequence.
ACCESSION BI7754908
VERSION BI7754908.1 GI:22370386
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 944)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

Tissue Procurement: DCDP/DP/Gazdar

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LCM2596 row: i column: 24

High quality sequence stop: 693.

Location/Qualifiers

FEATURES

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1..944

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6421343"

/clone_lib="NIH_MGC_18"

/tissue_type="large cell carcinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGCGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC library."

BASE COUNT 253 a 224 c 208 g 257 t 2 others

ORIGIN

Query Match

Best Local Similarity 21.4%; Score 353; DB 14; Length 944;

Matches 550; Conservative 0; Mismatches 312; Indels 1; Gaps 1;

Qy 567 TCTACATCGCTTCATCGAGGACACACCTGCTACGATGCGCACTAGCTCCAAAGC 626

Db 80 TGTATATTCCTTCATGAAGTCTCATCGCTGCTATGACCTGATCCCAAGCTCCAAAT 139

Qy 627 TAGTCATCTTCGACACATGCTGGAGATCAAGAGGCTCTTTTGTCTGCTGGGCCAAGC 686

Db 140 TGGTTGTATTGTAGTACCTCCCTGCAGGTGAAGAAAGCTTTTGTGCTTGGTGACTAAGC 199

Qy 687 GTGTGGGGGAGCGCCCTCTATGGGACAGCAAGACGAGCTTTGTGGGATGCTGACCA 746

Db 200 GTGTACGAGCTGCGCCCTTTATGGATAGTAGAAGCAAGTTTGTGGGATGCTGACCA 259

Qy 747 TCATCTGACTTCACTCGTGGTGCATCGCTACTACAGTCCCGCCCTGGTCCAGATCTATG 806

Db 260 TCATCTGATTTTCATCAATATCTGCACCGCTACTATAATCAGCCTTGGTACAGATCTATG 319

Qy 807 AGATTGAACACATAGATTGAGACCTGAGGGAGATCTACCTGCAAGGCTGCTTCAAGC 866

Db 320 AGCTAGAGACACAGATAGAACTTGGAGAGGTTATCTCCAGGACTCCTTTAAAC 379

Qy 867 CTTCTGGTCTCACTCTCCTTAATGATAGCTGTTTGAAGCTGCTACACCTCTCAAGA 926

Db 380 CGCTTGTCTGATTTCTCTTAATGCGAGCTTTTGTGATGCTGCTCTTCAATTAATCGGA 439

Qy 927 ACCGATCCATCTGCTCTGTTTGTACCGGGTGTGAGGCAAGTACTCCACATCTTCA 986

Db 440 ACAAGATCCACAGCTGCCAGTTATTGACCCAGAAATCAGGCAATACTTTGTACATCTTCA 499

Qy 987 CACACAAAGCGCTCTCAAGTCTCTGCATCTTTTGGTTTCCCTGCTGCCCGGCCCTCCT 1046

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Qy 1047 TCTCTACCGCATCTCCAAAGATTGGGCACTGGGCACATTCGAGACTTGGCTGTGGTGC 1106

Db 560 TCATGTCCAAGTCTCTGGAAGACTACAGATTGGCACTATGCCAATATTGCTATGGTTC 619

Qy 1107 TGGAGACAGCACCACCTCCTGACTGCACATCTTTTGGAGCCGCGCTGTCTGTCAC 1166

Db 620 GCACATACCAACCCCGCTCTATGTGGCTCTGGGATTTTGTACAGCATCGAGTCTCAGCCC 679

Qy 1167 TGCTTGTGGTCAACGAATGTGGTCAGGTCGTGGGCTCTATTCCCGCTTTGATGTATTC 1226

Db 680 TGCCAGTGGTGGATGAGAAGGCGGTGTGGTGACATCTACTCCAAGTTTGTATGTATCA 739

Qy 1227 ACCTGCTGCCCAACCAACCTACAACA-CCTGGACATGAGTGGGAGAGCCCTGAGG 1285

Db 740 ATCTGGCAGAGAAAGACCTCAACAACCCPAGATGATCTGTGACTAAAGCCTTTGCAA 799

Qy 1286 CAGAGGACACTGTCTGAGGAGGATCCCTTCTCCAGCCCAAGAGAGCTTTGGGGAA 1345

Db 800 CATCGATCACAATTACTTTGAGGGTGTCTCAAGTCTTACCTGCGATGAGACTCTGGAGAAC 859

Qy 1346 GTGATCGACAGATTTGCTCGGAGCAGGTACACAGCGCTGTGTAGTGGACGAGCCCG 1405

Db 860 ATCATCCACAGGCTAGTGGAGCAGAAAGTTCAAGTCTTACCTGCGATGAGACTCTGGAGAAC 919

Qy 1406 CATCTCTTGGGGCTGGTCTCCCT 1428

Db 920 GTGGCCAAAGGAATTGTATCACT 942

RESULT 12

BJ504184/c

LOCUS BJ504184 MF01FSA cDNA Oryzias latipes cdna clone MF01FSA006A14 3',

DEFINITION mRNA sequence.

ACCESSION BJ504184

VERSION BJ504184.1 GI:22156146

KEYWORDS EST.

SOURCE Japanese medaka.

ORGANISM Oryzias latipes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

1 (bases 1 to 728)

Kohara,F., Shin-I., Kimura,T., Narita,T., Jindo,T. and Takeda,H.

Medaka EST Project in Takeda's lab

Unpublished (2001)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1..728

/organism="Oryzias latipes"

/strain="d-rR"

/db_xref="taxon:8090"

/clone="MF01FSA006A14"

/clone_lib="MF01FSA cDNA"

/sex="mixture of female and male"

/tissue_type="whole embryo"

/dev_stage="fry stage 40"

BASE COUNT 182 a 161 c 174 g 210 t 1 others

ORIGIN

Query Match 21.4%; Score 352.6; DB 13; Length 728;

Best Local Similarity 68.1%; Pred. No. 2e-77;

Matches 490; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

Qy 524 AAGCTGGGCTGGGATGAGGAGTGGGAAACCGCGCCGAGATCTACATGCGCTTATG 583

Db 725 AAACCTGAACATAGATGATGCGCTGCTGGAACCAAGAGTATATTTNACATGCGCTTATG 666


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QY 584 CAGGAGCACACCTGCTACGATGCCATGCAACTAGCTCCCAAGCTAGTCATCTTCGACACC 643
Db 665 AAATCCCAACAAGTGCATGACATCTGCCAGAGCTCCCAAGTGTGTTTGGACACA 606
QY 644 ATGCTGAGATCAAGAAGCCCTTTCTGCTGCTGCTGCCAACGGTGTGGGGGACAGCCCT 703
Db 605 GCGCTACAAGTAAGAAGCCCTTTTGCATTGGTGGCCAAACGGTGTGGAGCTGCACCG 546
QY 704 CTATGGGACAGCAAGAAGCAGAGCTTTTGTGGGATGCTGACCATCTAGCTATCATCTG 763
Db 545 CTGTGGGACAGCAAGAAGCAGAGCTTTTGTGGTATGCTGACTATCACAGACTTCATCATC 486
QY 764 GTGCTGCATCGCTACTACAGTGCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 823
Db 485 ATACTGCACAGATATATAGTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
QY 824 ATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAAGCTGCTGCTGCTGCTGCTGCT 883
Db 425 CTTGAGACCTGGAGAGAGGCTTACCTTCAAGCAACCTTCAAGCCGTTGGTTAAACATATCA 366
QY 884 CTTATGATAGCTGTTTGAAGCTGTCTACACCTCTATCAAGCCTATCAAGACCGGATCATCGCTG 943
Db 365 CCAGATGCAAGCCCTTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
QY 944 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1003
Db 305 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246
QY 1004 AAGTTCCTGACATCTTTGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063
Db 245 AAGTTCCTGCACTTTTATGATGAATGCCAAGCCAGCTTTCATGAAGCAGACTCTA 186
QY 1064 CAGATTTGGCATCGGCACATCTCGAGACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
Db 185 AGTAGCTGGGAATGGCAGCTACCGACATCGCTTACATTCACCCAGACACCCCATC 126
QY 1124 CTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183
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QY 1184 TGTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
Db 65 TCAGGCACAGTGTGGACATTTACTCAAAAGTTGATGATTAACCTGCTGCTGCTGCTGCTGCT 6

RESULT 13
BQ224866
LOCUS
DEFINITION BQ224866 1070 bp mRNA linear EST 02-MAY-2002
5' mRNA sequence.
ACCESSION BQ224866
VERSION BQ224866.1 GI:20406266
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DP/GenD
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13323 row: n column: 18
High quality sequence stop: 636.
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6058577"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 275 a 247 c 263 g 284 t 1 others
ORIGIN
Query Match 21.3%; Score 350.4; DB 14; Length 1070;
Best Local Similarity 64.4%; Pred. No. 8.9e-77;
Matches 556; Conservative 0; Mismatches 306; Indels 2; Gaps 2;
QY 620 TCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAGGCTTCTTCTGCTGCTG 679
Db 1 TCCTAATTTGGTGTATTTGATAGCTCCCTGCGAGGTGAAGAAGCTTTTTCGTTGGTG 60
QY 680 GCGAAGCTGTGCGGGGAGCCCTCTATGGACACAGCAAGAGCAGAGCTTTTGTGGGATG 739
Db 61 ACTAAGCGTGTACGAGCTGCCCTTTATGGGATAGTAAGAGCAAGTTTGTGGGCGATG 120
QY 740 CTGACCATCATGACTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
Db 121 CTGACCATCATGACTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 800 ATCTATGAGATTGAACAACATTAAGATTGAGACTGCGAGGAGATCTACCTGCAAGCTGC 859
Db 181 ATCTATGAGCTTAGAAGCAACAGATAGAACTTGGAGAGAGGTGATCTCCAGGCTCC 240
QY 860 TTCAAGCTCTGCTCTCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCC 919
Db 241 TTTAAACCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 920 ATCAGAACCGGATCCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 979
Db 301 ATTGGAACAAGATCCACAGCTGCCAGTTATGACCCAGAATCAGGCAATCTTTGTGAC 360
QY 980 ATCTCTACACAAACCGCTGCTCAAGTTCCTGCAATCTTTGCTGCTGCTGCTGCTGCTG 1039
Db 361 ATCTCTACCAAGCGCATTCGAAGTTCCTCAAAATGTTTATCATGAGTTTCCCAAG 420
QY 1040 CCTCTCTCTCTACCGCATATCCAAAGATTTGGGATCGGCACATTCGAGACTTGGCT 1099
Db 421 CCAGAGTTCATGCTCAAGTCTCTGGAAGAGCTACAGATTGGCACCCTATGCCAATATGCT 480
QY 1100 GTGGTGTGGAGACAGCACCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1159
Db 481 ATGTTTCGCACTACGACCCCGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 1160 TCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1219
Db 541 TCAGCCCTGCGCAGTGGTGGATGAGAAGGGGCGTGTGGGACATCTACTCCAAAGTTTGA 600
QY 1220 GTGATTTCACCTGCGCCAGCAACCTACAAACACCTTGGACATGAGTGTGGGAGAGCC 1279
Db 601 GTTATCAATCTGGCAGCAGAAAGACCTACCAACACCTAGATGTATCTGTGACTAAAGCC 660
QY 1280 CTGAGGAGAGGACACTATCTGCTGAGGAGTCTCTTCTGCTGCTGCTGCTGCTGCTGCT 1339
Db 661 TTGCAACATCGATCACATTTACTTTGAGGCTGCTCTCAAGTCTACCTGCTGCTGCTGCT 720
QY 1340 GGGAGAGTGTGACAGGATTTGCTGGGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1398
Db 721 GAGACCATCATCAACAGGCTAGTGGAGCAGAGGTTCCACGACTTGTAGTGTGGATGA 780
QY 1399 GACCCAGCATCTCTTGGG-CGTGCTCTCTCTCGGACATCTTTCAGGACCTGCTGCTCA 1457
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Db      781 AAATGATGGTCCAGGGAATGGTATCACTGTCTGACATCCCTGCAGCCCTGGTGTCC 840
QY      1458 GCCCTGCTGGCATCGATGCCCTCG 1481
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RESULT 14
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LOCUS   AL552459 LRI_NFL006_PL2 908 bp mRNA linear EST 16-FEB-2001
DEFINITION AL552459 LRI_NFL006_PL2 Homo sapiens cDNA clone CS0D1070YC03 5
prime, mRNA sequence.
ACCESSION AL552459
VERSION   AL552459.1 GI:12891378
KEYWORDS  ESR.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
           Genoscope - Centre National de Sequencage
           BP 191 91006 EVRY cedex - France
           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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                     /db_xref="taxon:9606"
                     /clone="CS0D1070YC03"
                     /clone_lib="LRI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"

BASE COUNT   239 a 222 c 199 g 247 t
ORIGIN
Query Match      21.3%; Score 350; DB 9; Length 908;
Best Local Similarity 65.6%; Pred. No. 1e-76;
Matches 509; Conservative 1; Mismatches 266; Indels 0; Gaps 0;

QY      567 TCTACATGCGCTTCATGACGAGGACACACCTGCTACGATGCCATGCCAAGTACTGCTCCAAAGC 626
Db      131 TGTATACTCTTCATGAAGTCTCATCGCTGCTATGACCTGATATCCCAAGAGTCCCAAT 190
QY      627 TAGTCATCTTCGACACCATGCTGAGATCAAGAGGCCCTTCCTTCTCTGGTGGCCAAAG 686
Db      191 TGGTTGATTGATACGCTCCCTGCAGGTGGAAGAAGCTTTTTCCTTGGTACTAACG 250
QY      687 GTGTGGGGGAGCCCTCTATGGGACAGCAAGAGAGCTTGTGGGGATGCTGACCA 746
Db      251 GTGTACAGTGGCCCTTTATGGGATAGTAGAAGCAAAAGTTTGTGGGCATGCTGACCA 310
QY      747 TCACGTACTTCATCTCTGGTGTGCTGATCGCTACTACAGGTCGCCCTCGGTCCAGATCTATG 806
Db      311 TCACGTATTTCACTAATCTCTGCACCCCTACTATAATCAGCCTTGTACAGATCTATG 370
QY      807 AGATTGAACAACATAAGATTGAGACCTGGAGGGAGATCTACCTGCAAGGCTGCTTCAAGC 866
Db      371 AGCTAGAAGAACAACAAGATAGAAAAGTTGGAGAGAGGTGATCTCCAGGACTCCCTTAAAC 430
QY      867 CTCCTGGTCTCCACATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCCCTCATCAAGA 926

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Db      431 CGCTTGTCTGCATTTCTCTAATGCCAGCTTGTGTTGATGCTGTCTCTTCATTAATTCGA 490
QY      927 ACCGGATCCATCGCCTGCTGCTTCTTGACCGGTGTGTCAGCAAGCTACTCCACATCTCTCA 986
Db      491 ACAAGATCCACAGGCTGCCAGTTATTGACCCAGAAATCAGGCAATACTTTGTACATCTCTCA 550
QY      987 CACACAAACGCTGCTCAAGTTCCTGTCACATCTTTTGGTTCCCTGCTGGCCGCGCCCTCT 1046
Db      551 CCCAAGCCGCAATCTGAAGTTCTCTCAAAATGTTTATCTAGTTCAGTTCGCCAAGCCAGAGT 610
QY      1047 TCCTCTACCCGCACTATCCAAAGATTTGGGCATCGGCACATTCGAGACCTTGGCTGTGGTGC 1106
Db      611 TCATGTCCCAAGTCTCTGGAAGAGCTACAGATTGCACTATGCAATATTTGCTATGCTTC 670
QY      1107 TGGAGACAGACCCATCTGACTGCTGACTGCTGACATCTTTTGGACCGGCTGTGCTGCTGAC 1166
Db      671 GCATCTACACCCCGCTCTATGTGGCTCTGGGGATTTTGTACAGCATGCGACTCTCAGCCC 730
QY      1167 TGCCTGTGGTCAACGAATCTGTCAGGTCGTCGCTCTTANTCCCGCTTTTGTATCTGATTC 1226
Db      731 TCCAGTGTGGTGAAGAGAGGCGCTGTGGTGGACATCTCTCCAAAGTTTGTATGATCA 790
QY      1227 ACCTGGCTGCCAGCAAACTACAAACCTTGGACATGAGTGTGGAGAGCCCTTGAGGC 1286
Db      791 ATCTGGCAGCAGAAAAGACCTACAACAACCTAGATGATCTGTGACTAAAGCCTTGAAC 850
QY      1287 AGAGACACTATGCTGGAGGAGTCTCTTCTCCAGCCCAACAGAGAGCTTGGGG 1342
Db      851 ATCGATCACATTACTTTGAGGGTGTCTCAAGTGTCTACCTGCTGATGAGACTCTGGRG 906

RESULT 15
BI58240
LOCUS   BI58240 864 bp mRNA linear EST 10-OCT-2001
DEFINITION 603384001F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5392777 5',
mRNA sequence.
ACCESSION BI58240
VERSION   BI58240.1 GI:15998987
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 864)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: DCTD/DIP
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM12001 row: a column: 02
           High quality sequence stop: 830.

FEATURES             source
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5392777"
                     /clone_lib="NIH_MGC_87"
                     /tissue_type="mammary adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 Kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."

BASE COUNT   223 a 202 c 203 g 236 t
ORIGIN

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Result No.	Query			ID	Description	
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2	366.6	22.3	1435	2	US-08-878-989-14	Sequence 14, Appl
3	366.6	22.3	1435	4	US-09-272-736-14	Sequence 14, Appl
4	49	3.0	7218	1	US-08-232-463-14	Sequence 8, Appl
5	41.2	2.5	1022	4	US-09-056-105-8	Sequence 14, Appl
6	40.2	2.4	7218	1	US-08-232-463-14	Sequence 14, Appl
7	39.6	2.4	1022	4	US-09-056-105-18	Sequence 18, Appl
8	39.6	2.4	2531	1	US-08-299-849B-14	Sequence 14, Appl
9	39.6	2.4	2531	2	US-08-142-368A-14	Sequence 14, Appl
10	39.6	2.4	2531	3	US-08-967-727-14	Sequence 14, Appl
11	39.6	2.4	2531	4	US-08-037-230D-14	Sequence 10, Appl
12	39.6	2.4	4895	4	US-09-056-105-10	Sequence 10, Appl
13	38.8	2.4	289	4	US-09-007-005-17	Sequence 17, Appl
14	38.8	2.4	289	4	US-09-244-796-17	Sequence 17, Appl
15	38.8	2.4	6816	4	US-09-404-650-1	Sequence 1, Appl
16	38.8	2.4	6855	4	US-09-404-650-3	Sequence 3, Appl
17	38.4	2.3	1458	4	US-09-500-569-15	Sequence 15, Appl
18	38.2	2.3	3489	2	US-08-728-323A-1	Sequence 1, Appl
19	38.2	2.3	3489	4	US-09-298-568-1	Sequence 1, Appl
20	38.2	2.3	32207	2	US-08-770-379-20	Sequence 20, Appl
21	38.2	2.3	32207	4	US-08-757-669A-20	Sequence 20, Appl
22	38.2	2.3	32207	4	US-09-230-371A-20	Sequence 20, Appl
23	38	2.3	961	4	US-09-165-863-45	Sequence 45, Appl
24	38	2.3	1926	4	US-09-249-585A-4	Sequence 4, Appl
25	38	2.3	1931	2	US-09-130-114-2	Sequence 2, Appl
26	38	2.3	2531	1	US-08-299-849B-13	Sequence 13, Appl
27	38	2.3	2531	2	US-08-142-368A-13	Sequence 13, Appl

Db 176 TGTATACCTTCCTTATGAAGTCTCATGCTGCTATGAAGTCTGATTCGCCACAAGCTCCAAAT 235
QY 627 TAGTCATCTCGACACCATCTGGAGATCAAGAAGCCCTCTTTCCTCTGCTGGTGGCAAG 686
Db 236 TGGTTGATTTGATACATCCCTCGAGTGAAGAAAGCTTTTTCCTGCTGGTGGTAAAG 295
QY 687 GTGTGGGGAGCCCTCTATGGGACAGCAAGAGAGCTTTTGTGGGATGCTGACCA 746
Db 296 GTGTAGAGCTGCCCTTTATGGGATTAAGAACAAAGTTTGTGGGATGCTGACCA 355
QY 747 TCATGACATCAVCTTGGTGGTGCATCGCTACTACAGGTCCCCCTGGTCCAGCATATG 806
Db 356 TCATGATTCATCAATCTCGCCGCTACTATAATCAGCTTGTGGTACAGATCTATG 415
QY 807 AGATTGACACATAAGATTGACACCTGGAGGAGATCACTGCTGCAAGGCTGCTCAAGC 866
Db 416 AGTAGAAGACAAAGATGAAGCTTTGGAGAGAGGTATCTCCAGGACTCTTTAAAC 475
QY 867 CTGTGCTGCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAG 926
Db 476 CGTTGTCGCAATTCCTTAATGCCAGCTTGTGTGATGCTGTCTTTCATTAATTCGA 535
QY 927 ACCGGATCATCGCTGCTGCTGCTGACCCGGTGTCCAGCAAGTACTCCACATCTCA 986
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QY 987 CACAAAGCCGCTGCTCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1046
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QY 1047 TCCTCTACCGCAGCTATCAAGATTTGGGATCGGACATTCGAGACTTGGCTGTGGTGC 1106
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Db 716 GCATACCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 775
QY 1167 TGCTGTGCTCAAGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1226
Db 776 TGGCAGTGGTGAAGAGAGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 835
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RESULT 2

US-08-878-989-14
: Sequence 14, Application US/08878989
: Patent No. 5885803
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Corley, Neil C.
: APPLICANT: Guebler, Karl G.
: APPLICANT: Lal, Preeti
: APPLICANT: Goli, Surya K.
: APPLICANT: Shah, Purvi
: TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
: TITLE OF INVENTION: KINASES

NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PENITUT01
CLONE: 1452972
US-08-878-989-14

Query Match 22.3%; Score 366.6; DB 2; Length 1435;
Best Local Similarity 62.9%; Pred. No. 3.3e-87;
Matches 567; Conservative 0; Mismatches 334; Indels 0; Gaps 0;

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Db 183 TTTACATGGATTCATGAGGTGCACCAAGTGTATGCAATGCTTCCACACAGTTCAAAGC 242
QY 627 TAGTCATCTTCGACACCATCTGTCGAGATCAAGAAGCCCTTCTTGTCTGCTGCTGCTGCTGCT 686
Db 243 TTGTTGCTTTGATACATACATTAAGTTAAAAAGGCCCTTCTTGTGTTGTTGTTGTTGTTGTTGTT 302
QY 687 GTGTGGGGGAGCCCTCTATGGGACAGCAAGAGCAGAGCTTGTGGGATGCTGACCA 746
Db 303 GTGTGGGAGCAGCCCTGTTGGGAGAGTAAAAAAGTTTGTAGGAATGCTAACAA 362
QY 747 TCATGACTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806
Db 363 TTACAGATTTCATTAATATACATAGATACATTAATACCTATGTTGTTGTTGTTGTTGTTGTTGTT 422
QY 807 AGATTGACAAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCCAAGC 866
Db 423 AATTAGAGGAACATAAAATTGAACATGGAGGAGCTTTTATTACAGAACATTTAAGC 482
QY 867 CTCTGGTCTCCATCT 926
Db 483 CTTTGTGTAATATATCTCCAGATGCAAGCCTCTTCTGATCTGTATCTCTCTCTCTCTCTCTCTCTCT 542
QY 927 ACCGGATCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 986
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Db 783 TGCTGTGTGGATGAGTCAAGAAAGTTGTAGATATTTATCCAAATTTGATGTAAITA 842
Qy 1227 ACCTGGCTGCCAGCAAACTCAACACCTGGACATGATGTGGGAGAACCCCTGAGGC 1286
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Db 903 ACCGTCACAGTATTTTGAAGTGTGTGAAGTGCATATAGCTGGAAATACTGGAGACCA 962
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Qy 1407 ATCTCTGGGGGTGCTCCCTCTCCGACATCCCTTCAGGACATGCTGCTCAGCCCTGTG 1466
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Qy 1467 G 1467
Db 1083 G 1083

RESULT 3

US-09-272-796-14
; Sequence 14, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF INVENTIONS: 21
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PENITUT01
; CLONE: 1452972
US-09-272-796-14

Query Match 22.3%; Score 366.6; DB 4; Length 1435;
Best Local Similarity 62.9%; Pred. No. 3.3e-87;
Matches 567; Conservative 0; Mismatches 334; Indels 0; Gaps 0;

Qy 567 TCTACATCGCTTTCATCGACGACACACCTGCTACGATGCCATGGCAACTAGTCTCAAGC 626
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Qy 627 TAGTCATCTTCGACACCATGCTGGAGATCAAGAAGCGCTCTTTGCTCTGTGGGCCAAGC 686
Db 243 TTGTTGCTCTTGATACATACATTAAGTTAAAAGGCCCTCTTTGCTTTGGTAGCCACG 302
Qy 687 GTGTGGGCGACCCCTCTATGGGACAGCAAGAAGCAGAGCTTTTGGGATGCTGACCA 746
Db 303 GTCTCCGACGCGCACTGTGGGAGAGTAAAAACAAGTTTGTAGGAATGCTAAACA 362
Qy 747 TCACTGACTTTCATCTCGTGTGCTGCTACTACGATCGCTACAGTCCCGCTGGTCCAGATCTATG 806
Db 363 TTAAGATTTTCAATAATATATACATAGATACATATAATACCTATGTTAGTACAGATTATG 422
Qy 807 AGATTGAACACATAAGATTGAGACCTGGAGGAGATCTACTGCAAGGCTGCTTCAAGC 866
Db 423 AATTAGAGACATATAAATTGAACATGGAGGAGCTTTATTTACAAGAAACATTTAAGC 482
Qy 867 CTCTGCTGCCATCTCTTAATGATAGCTGTGTTGAAGCTGTCTACACCTCATCAAGA 926
Db 483 CTTTAGTGAATATATCTCCAGATGCAAGCTCTTCGATGCTGTATCTCTCTTGTATCAAAA 542
Qy 927 ACCGATCCATCGCTGCTGCTTTGACCCGCTGTACAGCAAGCTACTCCACATCTCA 986
Db 543 ATAAATCCACAGATTTGCCCTTATTGACCTATCAGTGGGAATGCACATTATATATCTTA 602
Qy 987 CACACAAACGCTGCTCAAGTTCTGACATCTTTGTTTCCCTGCTGCCCGCGCTCTCT 1046
Db 603 CCACAAAGATCTCAAGTCTCCAGCTTTTATGCTGTATATGCCAAAGCGCTGCCT 662
Qy 1047 TCCTCTACCGCACTATCCAGATTTGGGATCGGCACATTCGACAGACTTGGCTGTGGTGC 1106
Db 663 TCATGAACGACAACTCGGATGAGCTTGAATAGGAACGCTACCAACAATTTGCCCTCATAC 722
Qy 1107 TGGAGACACCCATCTGACTGCACTGCACTCTTTGTGGACCGCGGTGTGCTGCAC 1166
Db 723 ATCCAGACACTCCCATCATCAAGCGCTTGAACATATTTTGGAAAGACCAATATCAGCTC 782
Qy 1167 TGCTGTGGTCAACGAATGTGGTCAAGTGTGGGCGCTCTATTCCCGCTTTGATGTGATTC 1226
Db 783 TGCTGTGTGGATGAGTCAAGAAAGTTGTAGATATTTATTTCCAAATTTGATGTAAITA 842
Qy 1227 ACCTGGCTGCCAGCAAACTCAACACCTGGACATGATGTGGGAGAACCCCTGAGGC 1286
Db 843 ATCTTGTCTCTGAGAAACATACATAAOCCTAGATATCACGCTGACCCAGGCCCTTCAGC 902
Qy 1287 AGAGGACACTATGCTGGAGGAGTCCCTTCTTCCAGCCCAAGAGAGCTTGGGGGAG 1346
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Db	963	TCCTGCACAGATAGTAAAGACTGAGGTCCTCCATCGCGCTGGTGGTGAATATGAAGCAGATA	1022
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QY	1457	G 1467	
Db	1083	G 1083	

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1  RESULT 4
2  US-08-232-463-14
3  ; Sequence 14, Application US/08232463
4  ; Patent No. 5670367
5  ; GENERAL INFORMATION:
6  ; APPLICANT: DORNER, F.
7  ; APPLICANT: SCHEIFLINGER, F.
8  ; APPLICANT: FALKNER, F. G.
9  ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
10 ; NUMBER OF SEQUENCES: 52
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Foley & Lardner
13 ; STREET: 1800 Diagonal Road, Suite 500
14 ; CITY: Alexandria
15 ; STATE: VA
16 ; COUNTRY: USA
17 ; ZIP: 22313-0299
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/08/232.463

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Dd	1037	AGCTTGCAGATTT	T	1116		
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QY	924	AGAACGGATFCCATCGCTGCTTCTTGACCGGTGTACGAACGACTCCA	CATCCC	983		
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Dd	1117	YYY	Y	1176		
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? Sequence 8, Application US/09056105
? Patent No. 6287569
? GENERAL INFORMATION:
? APPLICANT: KIPPS, THOMAS J.
? APPLICANT: WU, YUNQI
? TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
? TITLE OF INVENTION: PROCESSING
? FILE REFERENCE: 233/221
? CURRENT APPLICATION NUMBER: US/09/056,105
? CURRENT FILING DATE: 1998-04-06
? EARLIER APPLICATION NUMBER: 60/043,467
? EARLIER FILING DATE: 1997-04-10
? NUMBER OF SEQ ID NOS: 35
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 8
? LENGTH: 1022
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-056-105-8

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Qy	433	GTTCGCCACACAGAGCGCTGGGAGTGTGAGCTAGAAAGCCCTGCTGGAAGAGAGCGCTGC	492	
Db	359	CTCGCTGAGCAGAGTCTCTTCCAGAGAAGCATCAGTAAAGGTGGATGATCTGGC	418	
Qy	493	CCTGTGCTCTGCCCGCAGGCCCCATTTCCAAAGCTGGGCTGGGATGAGAACTGGGAA	552	
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Qy	553	ACCCGGCGCCAGATCATACATGCGCTTCATGCAGGAGCACACCTGCTACGATGCCATGGC	612	
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Qy	613	AACCTAGCTCCAAGCTAGTCATCTTCGACACCATGCTGGAGATCAAGAAGGCTCTTTTGC	672	
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RESULT 6
US-08-232-463-14/C

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RESULT 8
US-08-299-849B-14
: Sequence 14, Application US/08299849B
: Patent No. 5612201
: GENERAL INFORMATION:
: APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
: APPLICANT: Leth , Bernard; Szaikora, Jean-Pierre; De Smet, Charles;
: APPLICANT: Chomez, Patrick
: TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
: TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
: NUMBER OF SEQUENCES: 48
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pelfe & Lynch
: STREET: 805 Third Avenue
: CITY: New York City
: STATE: New York
: ZIP: 10022
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
: COMPUTER: IBM
: OPERATING SYSTEM: PC-DOS
: SOFTWARE: Wordperfect
: CURRENT APPLICATION DATA:

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CURRENT APPLICATION DATA:

RESULT. T 11

US-08-037-230D-14
Sequence 14, Application US/08037230D
Patent No. 6235525
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses The
NUMBER OF SEQUENCES: 30
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26-MARCH-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6235525man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LTD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884

Query Match 2.4%; Score 39.6; DB 3; Length 2531;
Best Local Similarity 44.4%; Pred. No. 0.54;
Matches 159; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

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US-09-244-796-17/c
: Sequence 17, Application US/09244796

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GenCore version 5.1.6
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Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	278.8	16.9	1014	10	US-09-826-581-4
5	168.2	10.2	1722	10	US-09-826-581-3
6	127.2	7.7	11527	9	US-10-108-605-70
7	123.6	7.5	1446	9	US-09-826-846-559
8	85	5.2	378	10	US-09-864-761-3373
9	63.2	3.8	427	10	US-09-783-590-11098
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13	52	3.2	821	10	US-09-826-581-1
14	46	2.8	396	9	US-09-918-995-16257
15	43.4	2.6	458	10	US-09-864-761-693
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19	39.6	2.4	594	9	US-10-123-155-10

20	39.6	2.4	1716	9	US-10-093-766-38	Sequence 38, Appl
21	39.4	2.4	273	10	US-09-864-761-17480	Sequence 17480, A
22	38.8	2.4	5562	10	US-09-030-482B-18	Sequence 18, Appl
23	38.8	2.4	6816	10	US-09-935-541-1	Sequence 1, Appl
24	38.8	2.4	6855	10	US-09-935-541-3	Sequence 3, Appl
25	38	2.3	659158	9	US-09-771-208-20	Sequence 20, Appl
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27	37.8	2.3	1230	9	US-09-894-844-114	Sequence 114, App
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c	37	2.2	1964	9	US-10-245-103-41	Sequence 41, Appl
c	37	2.2	1964	9	US-10-245-107-41	Sequence 41, Appl
c	37	2.2	1964	9	US-10-245-143-41	Sequence 41, Appl
c	40	2.2	1964	9	US-10-245-771-41	Sequence 41, Appl
c	41	2.2	1964	9	US-10-245-851-41	Sequence 41, Appl
c	42	2.2	1964	9	US-10-245-883-41	Sequence 41, Appl
c	43	2.2	1964	9	US-10-237-535-41	Sequence 41, Appl
c	44	2.2	1964	9	US-10-238-183-41	Sequence 41, Appl
c	45	2.2	1964	9	US-10-238-283-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-826-581-5
; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SI
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5

Query Match	100.0%;	Score 1647;	DB 10;	Length 1647;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1647;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	TTGGTCTTGGGCTGGCCACATGGAGCCCGGGCTGGAGCAGCAGCTGCGCAGGACCCCTTC	60	
Db	1	TTGGTCTTGGGCTGGCCACATGGAGCCCGGGCTGGAGCAGCAGCTGCGCAGGACCCCTTC	60	
QY	61	CTGGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCTTAGACGACGAAACAG	120	
Db	61	CTGGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCTTAGACGACGAAACAG	120	
QY	121	CAGCTATGGCCATCACCAGCTGTGACACAGCAGCTCAGAAAGAAATCCGTGGGAAACGGAG	180	
Db	121	CAGCTATGGCCATCACCAGCTGTGACACAGCAGCTCAGAAAGAAATCCGTGGGAAACGGAG	180	
QY	181	GGCCAAAGCCTTGAGATGGACAGGCAAGAGTCGGTGGAGGAGGAGGCCACAGGTCA	240	

Db 181 GGCACAAAGCCTTGATGAGCAAGCAGAGTGGTGGAGAGGGGAGCCACCAAGTCA 240
QY 241 GGGGGAAGTCCCGGTCAGGCCAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTTCCC 300
Db 241 GGGGGAAGTCCCGGTCAGGCCAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTTCCC 300
QY 301 CAAGACACACCCCTTGGCTCAAGCTGATGCTTGC CGGGGGTGGGCACTCCACCAAGGGTG 360
Db 301 CAAGACACACCCCTTGGCTCAAGCTGATGCTTGC CGGGGGTGGGCACTCCACCAAGGGTG 360
QY 361 GGACTGCTCCCTCTGACTGTACAGCCTCAGCTGCAAGCTCCAGACAGATGATGTGA 420
Db 361 GGACTGCTCCCTCTGACTGTACAGCCTCAGCTGCAAGCTCCAGACAGATGATGTGA 420
QY 421 GCTGGCCACGAGTTCACAGCCACAGAGGCGCTGGAGTGTGAGCTAGAGGCGCTGTGGA 480
Db 421 GCTGGCCACGAGTTCACAGCCACAGAGGCGCTGGAGTGTGAGCTAGAGGCGCTGTGGA 480
QY 481 AGAGAGGCGCTGCTGCTGTGCTGCTCCCGCAGGCCCCATTTCCCAAGCTGGGTGGATGA 540
Db 481 AGAGAGGCGCTGCTGCTGTGCTGCTCCCGCAGGCCCCATTTCCCAAGCTGGGTGGATGA 540
QY 541 CGAAGTGGGAAACCGGCGCCGAGATCTACATGCGCTTCATGCAAGGACACACCTGCTA 600
Db 541 CGAAGTGGGAAACCGGCGCCGAGATCTACATGCGCTTCATGCAAGGACACACCTGCTA 600
QY 601 CGATGCCATGGCAACTAGCTTCAAGCTAGTCACTTCGACACCACTGCTGGAGTCAAGAA 660
Db 601 CGATGCCATGGCAACTAGCTTCAAGCTAGTCACTTCGACACCACTGCTGGAGTCAAGAA 660
QY 661 GGCCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 GGCCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 GCAGAGCTTTGGGATGCTGACCACTGACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 GCAGAGCTTTGGGATGCTGACCACTGACTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CAGGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 781 CAGGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 GATCTACCTGCAAGGCTGCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 GATCTACCTGCAAGGCTGCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 TGAAGCTGCTACACCTCATCAAGAACCGGATCCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 TGAAGCTGCTACACCTCATCAAGAACCGGATCCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GTCAGGCAAGCTACTCCACATCTCTACACACAAAGCGCTGCTCAAGTTCTGCACTCTT 1020
Db 961 GTCAGGCAAGCTACTCCACATCTCTACACACAAAGCGCTGCTCAAGTTCTGCACTCTT 1020
QY 1021 TGGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1021 TGGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 CACATTCGAGACTTGGCTGTGGTGGAGACAGCACCCATCCTGACTGCACTGGACAT 1140
Db 1081 CACATTCGAGACTTGGCTGTGGTGGAGACAGCACCCATCCTGACTGCACTGGACAT 1140
QY 1141 CTTTGTGGACCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 1141 CTTTGTGGACCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 CTTCTATTCGGCTTTGATGTGATTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1201 CTTCTATTCGGCTTTGATGTGATTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 CATGAGTGTGGGAGAACCTGAGGAGGAGACATATGCTGAGGGGAGTCTCTTCTCTG 1320

Db 1261 CATGAGTGTGGGAGAACCTGAGGAGGAGACATATGCTGAGGGAGTCTCTTCTCTG 1320
QY 1321 CCAGCCCCACAGAGAGCTTTGGGGAGTATGACAGAGATTGCTCGGGAGCAGGTACAG 1380
Db 1321 CCAGCCCCACAGAGAGCTTTGGGGAGTATGACAGAGATTGCTCGGGAGCAGGTACAG 1380
QY 1381 GCTGTGCTAGTGTGACGAGACCCAGCATCTCTTGGGCTGTGCTCCTCTCCGACATCCT 1440
Db 1381 GCTGTGCTAGTGTGACGAGACCCAGCATCTCTTGGGCTGTGCTCCTCTCCGACATCCT 1440
QY 1441 TCAGGCACTGCTGCTCAGCCCTGCTGGCATGATGCCCTCGGGGCGCTGAGAAGATCTGAG 1500
Db 1441 TCAGGCACTGCTGCTCAGCCCTGCTGGCATGATGCCCTCGGGGCGCTGAGAAGATCTGAG 1500
QY 1501 TCTCAATCCCAAGCCACTTGCACACTTGAAGCCCAATGAAGGAACTGGAGAACTCAGC 1560
Db 1501 TCTCAATCCCAAGCCACTTGCACACTTGAAGCCCAATGAAGGAACTGGAGAACTCAGC 1560
QY 1561 CTTTCATCTTCCCGCACCCCATTTGCTGCTTTCAGTATGATTGAGGTAGGCTTGCCTTG 1620
Db 1561 CTTTCATCTTCCCGCACCCCATTTGCTGCTTTCAGTATGATTGAGGTAGGCTTGCCTTG 1620
QY 1621 GGCCATGACACAGCCTCTTAGTCTTC 1647
Db 1621 GGCCATGACACAGCCTCTTAGTCTTC 1647

RESULT 2
US-09-826-581-2
; Sequence 2, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SU
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-2

Query Match 24.7%; Score 407.2; DB 10; Length 989;
Best Local Similarity 99.3%; Pred. No. 8e-111;
Matches 409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 247 AGTCCCGGTCAGGCGCAGCTGCTGAGTCCACCGGGTGGAGCCACATTTCCCAAGAC 306
Db 540 AGTCCCGGTCAGGCGCAGCTGCTGAGTCCACCGGGTGGAGCCACATTTCCCAAGAC 599
QY 307 CACACCCCTTGGCTCAAGCTGATCCTGCCGGGTGGGCACTCCACCAAGGTTGGAGTG 366
Db 600 CACACCCCTTGGCTCAAGCTGATCCTGCCGGGTGGGCACTCCACCAAGGTTGGAGTG 659
QY 367 CTTCCCTCTGACTGTACAGCCTCAGCTCAGGCTCCAGCAGACATGATGTTGGAGTGGC 426
Db 660 CTTCCCTCTGACTGTACAGCCTCAGCTCAGGCTCCAGCAGACATGATGTTGGAGTGGC 719
QY 427 CAGGAGTTTCCCGACGACAGGCGCTGGAGTGTGAGTAGAAGGCGCTGCTGGAAGAG 486
Db 720 CAGGAGTTTCCCGACGACAGGCGCTGGAGTGTGAGTAGAAGGCGCTGCTGGAAGAG 779
QY 487 GCTGCGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
Db 780 GCTGCGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839

QY 547 GCGGAAACCCGCGCCAGATCTACATGCGCTTCATGCGAGGAGCACACCTGCTAGCATGC 606
|||||
Db 840 GCGGAAACCCGCGCCAGATCTACATGCGCTTCATGCGAGGAGCACACCTGCTAGCATGC 899
QY 607 CATGCGAACTAGCTCCCAAGTAGTATCATCTTCGACACCAATGCTGGAGATCAAG 658
|||||
Db 900 CATGCGAACTAGCTCCCAAGTAGTATCATCTTCGACACCAATGCTGGAGGTGAGG 951

RESULT 3
US-09-925-297-2
; Sequence 2, Application US/09923297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1691
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1093)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-2

Query Match 23.9%; Score 393.4; DB 10; Length 1691;
Best Local Similarity 65.1%; Pred. No. 1.2e-106;
Matches 580; Conservative 0; Mismatches 311; Indels 0; Gaps 0;

QY 567 TCATCATCTTCGACACCATCTGAGATCAAGAAGCCCTCTTTGCTCTGGTGGCCACG 686
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Db 123 TGTATACITCTTCATGAAGTCTCATCGCTGCTATGAGCTGATGCCAGATATCCCAAGTCCAAAT 182
QY 627 TAGTCATCTTCGACACCATCTGAGATCAAGAAGCCCTCTTTGCTCTGGTGGCCACG 686
|||||
Db 183 TGTGTTGATTTGATACCTTCGAGTCAAGAAAGCTTTTTCCTTTGGTGGTAAAG 242
QY 687 GTGTGGGCGAGCCCTCTATGGACAGCAAGAGAGCTTTGTGGGATGCTGACCA 746
|||||
Db 243 GTGTAGAGCTGCCCCCTTATGGGATAGTAAAGCAAGTTTGTGGGATGCTGACCA 302
QY 747 TCATGACTTCATCTCGTCTGCATCGCTACTACAGTCCCTCCCTGGTCCAGATCTATG 806
|||||
Db 303 TCATGATTTCAATATCTCGCCGCTACTATAAATCAGCCTTGGTACAGATCTATG 362
QY 807 AGATTGACACATTAAGATTGAGACCTGGAGGAGATCTACTCCAGAGCTGCTTCAAG 866
|||||
Db 363 AGCTAGAGCAACAGATGAAGTTCGAGAGAGGTGATCTCCAGAGCTCTCTTAAAC 422
QY 867 CTGTGCTTCCTCTCTCTAAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGA 926
|||||
Db 423 CGTTGTCTGATTTCTCTTANTGCCAGCTTGTTGATGCTCTCTCTCAATTAATTCGA 482
QY 927 ACCGGATCAGCGCTGCTGTTTTCACCCGCTGTACAGCAAGCTACTCCACATCTCA 986
|||||
Db 483 ACAAGATCCACAGGCTGCCAGTTATTGACCCAGATCAGCAATATTGTTACATCTCA 542
QY 987 CACAAAGGCTCTGCTCAAGTCTGTCATATCTTTGGTTCCTGCTCCCGGCCCTCT 1046
|||||
Db 543 CCACAAAGGCTCTGCTCAAGTCTGTCATATCTTCAAAATGTTTATCACTGAGTTCCCAAGCCAGAGT 602
QY 1047 TCCCTCTACCGCACTATCCAGATTTGGGATCGGCACATTCGAGAGCTTGGTCTGC 1106
|||||

Db 603 TCATGTCCAAGTCTCTGGAAGAGCTACAGATTGGCACCTATATGCCAATATTGCTATGTTTC 662
QY 1107 TGAGAGACACACCCATCTGACTCCACTGACATCTTTGTGGACGGGTGTGTGTGCAC 1166
|||||
Db 663 GCATCTACACCCCTCTATGTGCTCTGGGATTTTGTACAGCATCGAGTCTCAGCCC 722
QY 1167 TGCTGTGTGCTCAACGAATGTGGTCAGGTCTGGGCTCTATTCCCGCTTTGTGATGTGATTC 1226
|||||
Db 723 TGGCAGTGGTGTGAGAGGGGCTGTGTGGACATCTACTCCAAAGTTTGTATGTTATCA 782
QY 1227 ACCTGCTCCCGACGAAACCTTACAAACACCTGGACATGAGTGTGGGAGAACCCCTTGAGC 1286
|||||
Db 783 ATCTGCGACGAGAAAGACCTTACAAACACCTAGATGATCTGTGACTAAAGCCTTGCAAC 842
QY 1287 AGAGGACACTATGCTGTGGAGGAGTCTTCTTCCTGCGACGCCCCACGAGAGCTTGGGGAAG 1346
|||||
Db 843 ATCGATCACATTAATTTGAGGGTGTCTCAAGTGCTTACCTGCATCAGACTCTGGAGACCA 902
QY 1347 TGATCGACAGGATTCCTCGGAGCAGCTACACAGGCTGTGTAGTGGTGGATGAAATGATG 1406
|||||
Db 903 TCATCAACAGGCTAGTGAAGCAGAGGTTCCACGACTTGTAGTGGTGGATGAAATGATG 962
QY 1407 ATCTTGTGGGCTGTCTCCCTTCGACATCTTCAGGCACTCTGCTGCTCA 1457
|||||
Db 963 TGGTCAAGGAATTTGATCACTGCTGACATCTCTCAGGCCCTTGTGCTCA 1013

RESULT 4
US-09-826-581-4
; Sequence 4, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SI
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-4

Query Match 16.9%; Score 278.8; DB 10; Length 1014;
Best Local Similarity 97.6%; Pred. No. 1.1e-72;
Matches 283; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1358 ATTGCTCGGAGCAGGTACAGAGCTGTGTAGTGGAGAGACCCAGCATCTCTTGGGC 1417
|||||
Db 725 ATTGCGGACCCACAGGTACAGAGCTGTGTAGTGGAGAGACCCAGCATCTCTTGGGC 784
QY 1418 GTGCTCTCCCTCTCCGACATCTTCAGGCACTGGTCTCAGCCCTGTGTGATGATGCC 1477
|||||
Db 785 GTGCTCTCCCTCTCCGACATCTTCAGGCACTGGTCTCAGCCCTGTGTGATGATGCC 844
QY 1478 CTGGGGCTTGAGAGATCTGAGTCTCAATCCAGCCACCTGCACACCTTGAAGCCAA 1537
|||||
Db 845 CTGGGGCTTGAGAGATCTGAGTCTCAATCCAGCCACCTGCACACCTTGAAGCCAA 904
QY 1538 TGAAGGGAATCGAGAATCTGAGCTTCCATCTCCGCCACCCCATTTGCTGTTTCAAGTA 1597
|||||
Db 905 TGAAGGGAATCGAGAATCTGAGCTTCCATCTCCGCCACCCCATTTGCTGTTTCAAGTA 964
QY 1598 TGATTCAGGTAGGCTCTGCCCTGGGCAATGACACAGCCTCTTAGTCTTC 1647
|||||
Db 965 TGATTCAGGTAGGCTCTGCCCTGGGCAATGACACAGCCTCTTAGTCTTC 1014


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; NAME/KEY: misc feature
; LOCATION: (73)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (120)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (132)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (245)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (259)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (275)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (281)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (316)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (341)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (350)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (360)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (363)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (409)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (411)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (425)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-11098

Query Match      3.8%; Score 63.2; DB 10; Length 427;
Best Local Similarity 59.0%; Pred. No. 9, 4e-09;
Matches 124; Conservative 0; Mismatches 82; Indels 4; Gaps 1;

Qy      832 CTGGAGGAGATCTACCTGCAAGGCTGTTCAGCCCTCTGGTCTCCATCTCTCCTAATGA 891
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      3 CAGAGGAGAGTGATCTCCAGGACTCTCTTAAACCGCTGTGTGATCTTTCCTAATGC 62

Qy      892 TAGCCTGTTTGAAGCTCTACACCTCATCAAGAACGGATCCATCGCTCCCTGTTCT 951
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      63 CAGCTGTTTATGCTGTCTCTTCAATTAATCGGAAGAAGATCCACAGCTGCCAGTNA 122

Qy      952 TCACCC-----GGTCTCAGGCAAGCTACTCCATCTCCACACAAACCGCTGCTCAAGT 1007
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      123 TCACCCAGNAATCAGGGCAATACCTTTGTGACATCTCCACCAAGGCCCATTTCTGA 182

Qy      1008 TCTGCACATCTTTGGTTCCTCTGCCGCC 1037
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      183 TTCCTCAAAATGTTTATGCACCTGAGTCCC 212

RESULT 10
US-09-864-761-20146/c
; Sequence 20146, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20146
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009974.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
; OTHER INFORMATION: NT HIT: g11430152, EVALUE 2.00e-22
; OTHER INFORMATION: EST_HUMAN HIT: BE327467.1, EVALUE 3.00e-06
; OTHER INFORMATION: SWISSPROT HIT: P54619, EVALUE 3.00e-03
US-09-864-761-20146

Query Match      3.3%; Score 54; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 3, 1e-06;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      651 AGATCAAGAGCCCTTCTTCTCTGGTGGCCCAACGGTGTGCGGGGAGCCCTC 704
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Db 54 AGATCAGAAGGCTCTCTTGGTGGCCACAGGTGTGGCGGAGGCCCTC 1
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RESULT 11
US-10-198-846-2282/c
; Sequence 2282, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2282
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2, 3, 4, 5
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-2282
Query Match 3.2%; Score 53.4; DB 9; Length 457;
Best Local Similarity 53.6%; Pred. No. 7.8e-06;
Matches 111; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 978 ACATCCTCACACAAAGCCCTCTCAAGTTCCTCGCACATCTTTGGTTCCTCGTGCCTCC 1037
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Db 234 ACATCCTCACACAAAGCGATTCTGAAGTTCCTCAAAATTGTTATCATCGAGTTCCTCCA 175
|||||
QY 1038 GGCCTCTCTCTACCGCACTATCCAAAGATTGGGATCGGCACATCCGAGACTTGG 1097
|||||
Db 174 ACCGAGATTATCTCAACTCTCTCGAAGACTACAGATTGGCACTATGCCAATATTG 115
|||||
QY 1098 CTGTGGTGTGGAGACAGCCATCTCTGACTGCATGACATCTTTGTGGACCGGTG 1157
|||||
Db 114 CTATGTTTGGCACTACCAACCCCGTCTATGTGGCTCTGGGATTTTGTACCTGCCGGG 55
|||||
QY 1158 TGTCTGCACTGCCTGTGGTCAACGAAT 1184
|||||
Db 54 CGCCGGCCACCGCGGGGAGCTCCAAT 28
|||||
RESULT 12
US-10-198-846-2472/c
; Sequence 2472, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2472
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2, 16, 22, 23, 27, 28, 30, 36, 39, 73, 462, 481, 540, 559,
; LOCATION: 590, 604, 634, 636, 676, 680, 772, 774, 809, 849, 870, 873,
; LOCATION: 876, 886, 893, 895, 896, 897
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-2472
Query Match 3.2%; Score 52.2; DB 9; Length 897;
Best Local Similarity 56.8%; Pred. No. 2.2e-05;
Matches 96; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 978 ACATCCTCACACAAAGCCCTCTCAAGTTCCTCGCACATCTTTGGTTCCTCGTGCCTCC 1037
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Db 252 ACATCCTCACACAAAGCGATTCTGAAGTTCCTCAAAATTGTTATCATCGAGTTCCTCCA 193
|||||
QY 1038 GGCCTCTCTCTACCGCACTATCCAAAGATTGGGATCGGCACATCCGAGACTTGG 1097
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Db 192 AGCCAGAGTTATGTCCAAAGTCTCTGGAAGAGTACAGATTGGCACTATGCCAATATTG 133
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QY 1098 CTGTGGTGTGGAGACAGCCATCTCTGACTGCATGACATCTTTGT 1146
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Db 132 CTATGTTTGGCACTACCAACCCCGTCTATGTGGCTCTGGGATTTTGT 84
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RESULT 13
US-09-826-581-1
; Sequence 1, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-1
Query Match 3.2%; Score 52; DB 10; Length 821;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGGTCTGGGCTGGCCACATGGAGCCCGGCTGGAGCAGCAGCTGGCGAGG 52
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Db 313 TTGGTCTGGGCTGGCCACATGGAGCCCGGCTGGAGCAGCAGCTGGCGAGG 364
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RESULT 14
US-09-918-995-16257
; Sequence 16257, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
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RESULT 11
US-10-198-846-2282/c
; Sequence 2282, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2282
; LENGTH: 457
; TYPE: DNA
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; NAME/KEY: misc_feature
; LOCATION: 2, 16, 22, 23, 27, 28, 30, 36, 39, 73, 462, 481, 540, 559,
; LOCATION: 590, 604, 634, 636, 676, 680, 772, 774, 809, 849, 870, 873,
; LOCATION: 876, 886, 893, 895, 896, 897
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-2472
Query Match 3.2%; Score 52.2; DB 9; Length 897;
Best Local Similarity 56.8%; Pred. No. 2.2e-05;
Matches 96; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 978 ACATCCTCACACAAAGCCCTCTCAAGTTCCTCGCACATCTTTGGTTCCTCGTGCCTCC 1037
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Db 252 ACATCCTCACACAAAGCGATTCTGAAGTTCCTCAAAATTGTTATCATCGAGTTCCTCCA 193
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QY 1038 GGCCTCTCTCTACCGCACTATCCAAAGATTGGGATCGGCACATCCGAGACTTGG 1097
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QY 1098 CTGTGGTGTGGAGACAGCCATCTCTGACTGCATGACATCTTTGT 1146
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Db 132 CTATGTTTGGCACTACCAACCCCGTCTATGTGGCTCTGGGATTTTGT 84
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RESULT 13
US-09-826-581-1
; Sequence 1, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-1
Query Match 3.2%; Score 52; DB 10; Length 821;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGGTCTGGGCTGGCCACATGGAGCCCGGCTGGAGCAGCAGCTGGCGAGG 52
|||||
Db 313 TTGGTCTGGGCTGGCCACATGGAGCCCGGCTGGAGCAGCAGCTGGCGAGG 364
|||||
RESULT 14
US-09-918-995-16257
; Sequence 16257, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
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NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16257
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-995-16257

Query Match 2.8%; Score 45; DB 9; Length 396;
Best Local Similarity 47.8%; Pred. No. 0.0012;
Matches 133; Conservative 0; Mismatches 145; Indels 0; Gaps 0;
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QY 478 GGAAGAGAGCGCTCCCTGTGCTGCCCGCAGCCGCCATTTCCCAAGCTGGGCTGGGA 537
DB 116 CGCGAGGAGCAGGCCACAGCTGTCCACCCCTGTCCTCTGTGAGAGAGCGCGC 175
QY 538 TGAGAACTCGGAAACCGCGGCCAGATCTACATCGCTTCATGCGAGGAGCAGCCTG 597
DB 176 ACAAAGAACCGGAGGAGGAGGAGAGAGATCCGCTGGTCAGCCACCGCGAGGAGCCCGT 235
QY 598 CTAGCATGCCATGCACTAGCTCCAACTAGTCACTTGGACACCATGCTGGAGATCAA 657
DB 236 GCCTGGTGACACAGCAGCGCCAGCTCTTCATGGTGGCGGTGAAGCAGGAGTGAG 295
QY 658 GAAGCGCTTCTTTGCTCTGCTGGTGGCCACAGCGTGTGCGGG 695
DB 296 CCAAGCCAATTGCGCACCTTCACCCAGCGCCCTGCAGG 333

RESULT 15
US-09-864-761-693
Sequence 693, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 693
LENGTH: 458
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006966.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.6
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.5
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.9
US-09-864-761-693
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Best Local Similarity 64.4%; Pred. No. 0.0073;
Matches 65; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
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DB 202 GCAGGTCCATCGCTGGTGGTAAATGAAGCAGATAGTATTGTGGGTATTATTCCCT 261
QY 1429 CTCCGACATCTTCAGGCACCTGGTCTCAGCCCTGCTGGCA 1469
DB 262 GTCCGACATCTTCAAGCCCTGATCTCCACACGACGAGTA 302

Search completed: June 13, 2003, 09:00:38
Job time : 521.839 secs

GenCore version 5.1.6
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(without alignments)
9216.782 Million cell updates/sec

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Perfect score: 61
Sequence: 1 acaaggcagaagtcgctgga.....gggggaaggtcccggtcca 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1	61	100.0	1647	6	AX281582 Sequence
2	61	100.0	2109	6	AX099776 Sequence
3	61	100.0	2115	6	AX099802 Sequence
4	61	100.0	2115	9	AF214519 Homo sapi
5	61	100.0	2290	9	HS249977 Homo sapi
6	51	83.6	989	6	AX281579 Sequence
c 7	51	83.6	152129	2	AC027416 Homo sapi
c 8	51	83.6	206854	9	AC009974 Homo sapi
9	41.8	68.5	1867	6	AX099774 Sequence
10	41.8	68.5	1873	4	AF214520 Sus scrofa
11	41.8	68.5	1873	6	AX099800 Sequence
12	41.8	68.5	1873	6	AX398331 Sequence
13	41.8	68.5	1873	6	AX398333 Sequence
14	41.8	68.5	1873	6	AX398337 Sequence
15	41.8	68.5	1873	6	AX398339 Sequence
16	41.8	68.5	2022	6	AX099804 Sequence
17	40.2	65.9	1873	6	AX398335 Sequence
18	33.4	54.8	5888	4	AF214521 Sus scrofa
19	33.4	54.8	146577	2	AC128070 Rattus no
20	33.4	54.8	190183	2	AC129703 Rattus no
21	33.4	54.8	192968	2	AC127107 Rattus no
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24	31.4	51.5	808	6	AX398342 Sequence
25	29.6	48.5	31549	9	AC096857 Homo sapi
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27	29.6	48.5	123551	2	AC005809 Homo sapi
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c 29	28.6	46.9	123288	9	AL354712 Human DNA
c 30	28.6	46.9	159802	2	AC019262 Homo sapi
c 31	28.6	46.9	166258	2	AL451066 Homo sapi
c 32	28.2	46.2	155012	8	AF003257 Oryza sat
c 33	28.2	46.2	170931	2	AC129656 Rattus no
c 34	28	45.9	170586	2	AL356126 Homo sapi
c 35	28	45.9	171999	2	AC121225 Rattus no
c 36	28	45.9	172510	9	AL512424 Human DNA
c 37	28	45.9	184056	2	AC024551 Homo sapi
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c 39	27.8	45.6	78782	2	AC095594 Rattus no
c 40	27.8	45.6	206531	2	AC055858 Homo sapi
c 41	27.6	45.2	166018	9	AC022868 Homo sapi
c 42	27.6	45.2	168839	9	AC022826 Homo sapi
c 43	27.6	45.2	180464	2	AC116351 Homo sapi
c 44	27.4	44.9	49721	2	AC104991 Homo sapi
c 45	27.4	44.9	58640	2	AC111698 Rattus no

ALIGNMENTS

RESULT 1
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LOCUS AX281582 1647 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 5 from Patent WO0177305.
ACCESSION AX281582
VERSION AX281582.1 GI:16608833
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Andersson, L., Luthman, H. and Marklund, S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 5 18-OCT-2001;

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BASE COUNT    346 a    502 c    462 g    337 t
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Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 200 ACAAGGCAGAGTCGGTGAGGAGGGAGCCACCGAGTCAGGGGGAAGTCCCGGTCC 259
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QY 61 A 61
Db 260 A 260

RESULT 2
AX099776
LOCUS      2109 bp      DNA      linear      PAT 02-APR-2001
DEFINITION Sequence 3 from Patent WO0120003.
ACCESSION AX099776
VERSION   AX099776.1 GI:13538810
KEYWORDS human.
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 2109)
AUTHORS   Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
TITLE     Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL   INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
FEATURES  Location/Qualifiers
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Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 A 61
Db 166 A 166

RESULT 4
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LOCUS      2115 bp      mRNA      linear      PRI 03-JUN-2000
DEFINITION Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
mRNA, complete cds.
ACCESSION AF214519
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Query Match    100.0%; Score 61; DB 6; Length 2109;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 A 61
Db 160 A 160

RESULT 3
AX099802
LOCUS      2115 bp      DNA      linear      PAT 02-APR-2001
DEFINITION Sequence 29 from Patent WO0120003.
ACCESSION AX099802
VERSION   AX099802.1 GI:13538836
KEYWORDS human.
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 2115)
AUTHORS   Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
TITLE     Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL   INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
FEATURES  Location/Qualifiers
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BASE COUNT    460 a    622 c    562 g    471 t
ORIGIN
Query Match    100.0%; Score 61; DB 6; Length 2115;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 106 ACAAGGCAGAGTCGGTGAGGAGGGAGCCACCGAGTCAGGGGGAAGTCCCGGTCC 165
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QY 61 A 61
Db 166 A 166

RESULT 4
AF214519
LOCUS      2115 bp      mRNA      linear      PRI 03-JUN-2000
DEFINITION Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
mRNA, complete cds.
ACCESSION AF214519
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VERSION      AF214519.1  GI:8215681
KEYWORDS     Homo sapiens
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 2115)
AUTHORS      Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
              Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
              Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
              and Andersson,L.
TITLE        A mutation in PRKAG3 associated with excess glycogen content in pig
              skeletal muscle
JOURNAL      Science 288 (5469), 1248-1251 (2000)
MEDLINE      20280150
PUBMED       10818001
REFERENCE    2 (bases 1 to 2115)
AUTHORS      Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
              Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
              Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
TITLE        Direct Submission
JOURNAL      Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
              University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
              Sweden
FEATURES     Location/Qualifiers
              source      1..2115
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                        /gene="PRKAG3"
              CDS          1..1395
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                        /note="AMPK3"
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                        TDFILVHRYRSLPVQIYEIQHKTWREIYLQGCPLVSLSPNDSLFEAVITLI
                        KNRHRLVDPVSGNVLHILTHKRLKEHIFGSLPSPFYRTIQDLGIGTFDL
                        AVVLEATILALDIFVDRRVSAIPVNECGQVGLYSRFDVIHLAAQQTYNHLDMSV
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BASE COUNT   460 a 522 c 562 g 471 t
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Query Match      100.0%; Score 61; DB 9; Length 2115;
Best Local Similarity 100.0%; Pred. No. 5.4e-08;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGGCGAGAAGTCGGTGAGAGAGGGGAGCCACCAGGTCCAGGGGAGAGTCCCGGTCC 60
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Db 106 ACAGGCGAGAAGTCGGTGAGAGAGGGGAGCCACCAGGTCCAGGGGAGAGTCCCGGTCC 165
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QY 61 A 61
Db 166 A 166

RESULT 5
HSA249977      2290 bp mRNA linear PRI 07-APR-2000
LOCUS          Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
DEFINITION     (AMPK gamma 3 gene).
ACCESSION      AJ249977
VERSION        AJ249977.1 GI:6688200
KEYWORDS       AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.

SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Andersson,L., Luthman,H. and Marklund,S.
TITLE        Variants of the human amp-activated protein kinase gamma 3 subunit
              Patent: WO 0177305-A 2 18-OCT-2001;
              Arexis AB (SE)

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SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 2290)
AUTHORS      Cheung,P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D.
TITLE        Characterization of AMP-activated protein kinase gamma-subunit
              isoforms and their role in AMP binding
JOURNAL      Biochem. J. 346 Pt 3, 659-669 (2000)
MEDLINE      20164049
PUBMED       10698692
REFERENCE    2 (bases 1 to 2290)
AUTHORS      Carling,D.
TITLE        Direct Submission
JOURNAL      Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC
              Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
              London, W12 0NN, UNITED KINGDOM
FEATURES     Location/Qualifiers
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BASE COUNT     501 a 674 c 617 g 498 t
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Query Match      100.0%; Score 61; DB 9; Length 2290;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGGCGAGAAGTCGGTGAGAGAGGGGAGCCACCAGGTCCAGGGGAGAGTCCCGGTCC 60
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Db 202 ACAGGCGAGAAGTCGGTGAGAGAGGGGAGCCACCAGGTCCAGGGGAGAGTCCCGGTCC 261
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QY 61 A 61
Db 262 A 262

RESULT 6
AX281579      989 bp DNA linear PAT 02-NOV-2001
LOCUS          Sequence 2 from Patent WO0177305.
DEFINITION     AX281579
ACCESSION      AX281579
VERSION        AX281579.1 GI:16608830
KEYWORDS       human.
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Andersson,L., Luthman,H. and Marklund,S.
TITLE        Variants of the human amp-activated protein kinase gamma 3 subunit
              Patent: WO 0177305-A 2 18-OCT-2001;
              Arexis AB (SE)

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Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGCAGACTCGTGGAGGAGGGAGCCACAGCTCAGCGGGAAGCT 51
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RESULT 7
AC027416/c
LOCUS              152129 bp      DNA      linear      HTG 07-JUN-2000
DEFINITION Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
unordered pieces.
ACCESSION          AC027416
VERSION            AC027416.2 GI:8317289
KEYWORDS            HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE              Homo sapiens.
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 152129)
  Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-504G11
Unpublished
2 (bases 1 to 152129)
  Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
  Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,F.,
  Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G.,
  Campiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
  Collymore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
  Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
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  Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
  Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
  Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,
  Levine,K., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
  McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
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  Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
  O'Neil,D., Olivier,T.M., Oliver,J., Peterson,K., Pierre,N.,
  Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
  Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
  Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
  Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
  Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye.W.J.,
  Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
TITLE
JOURNAL
COMMENT
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7458
Center clone name: 504_G.11
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

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Consensus quality: 135376 bases at least Q40
Consensus quality: 143264 bases at least Q30
Consensus quality: 146503 bases at least Q20
Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1005: contig of 1005 bp in length
* 1006 1105: gap of 100 bp
* 1106 2402: contig of 1297 bp in length
* 2403 2502: gap of 100 bp
* 2503 3823: contig of 1321 bp in length
* 3824 3923: gap of 100 bp
* 3924 5020: contig of 1097 bp in length
* 5021 5120: gap of 100 bp
* 5121 6161: contig of 1041 bp in length
* 6162 6261: gap of 100 bp
* 6262 7547: contig of 1286 bp in length
* 7548 7647: gap of 100 bp
* 7648 9983: contig of 2336 bp in length
* 9984 10083: gap of 100 bp
* 10084 12556: contig of 2473 bp in length
* 12557 12656: gap of 100 bp
* 12657 15043: contig of 2387 bp in length
* 15044 15143: gap of 100 bp
* 15144 17123: contig of 1980 bp in length
* 17124 17223: gap of 100 bp
* 17224 19466: contig of 2243 bp in length
* 19467 19566: gap of 100 bp
* 19567 21928: contig of 2362 bp in length
* 21929 22028: gap of 100 bp
* 22029 24319: contig of 2291 bp in length
* 24320 24419: gap of 100 bp
* 24420 27059: contig of 2640 bp in length
* 27060 27159: gap of 100 bp
* 27160 30170: contig of 3011 bp in length
* 30171 30270: gap of 100 bp
* 30271 33968: contig of 3698 bp in length
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* 34069 38179: contig of 4111 bp in length
* 38180 38279: gap of 100 bp
* 38280 42366: contig of 4087 bp in length
* 42367 42466: gap of 100 bp
* 42467 46365: contig of 3899 bp in length
* 46366 46465: gap of 100 bp
* 46466 51285: contig of 4820 bp in length
* 51286 51385: gap of 100 bp
* 51386 55871: contig of 4486 bp in length
* 55872 55971: gap of 100 bp
* 55972 60595: contig of 4624 bp in length
* 60596 60695: gap of 100 bp
* 60696 66595: contig of 5900 bp in length
* 66596 66695: gap of 100 bp
* 66696 73218: contig of 6523 bp in length
* 73219 73318: gap of 100 bp
* 73319 77115: contig of 3797 bp in length
* 77116 77215: gap of 100 bp
* 77216 85022: contig of 7807 bp in length
* 85023 85122: gap of 100 bp
* 85123 93314: contig of 8192 bp in length
* 93315 93414: gap of 100 bp
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* 101194 101293: gap of 100 bp
* 101294 113090: contig of 11797 bp in length

* 113091 113190: gap of 100 bp
* 113191 123496: contig of 10306 bp in length
* 123497 123596: gap of 100 bp
* 123597 137837: contig of 14241 bp in length
* 137838 137937: gap of 100 bp
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Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2925 ACAAGGCAGAAAGTCGGTGGAGGAAGGGAGCCACCAGGTCAGGGGAAGGT 2875
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RESULT 8

AC009974/c

LOCUS

DEFINITION

AC009974

AC009974

VERSION

AC009974.9

KEYWORDS

HTG.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 206854)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)

99063792

8447074

2 (bases 1 to 206854)

Harris, A. and Cotton, M.

The sequence of Homo sapiens BAC clone RP11-459119

Unpublished (2001)

3 (bases 1 to 206854)

Waterston, R.H.

Direct Submission

Submitted (08-SEP-1999) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

4 (bases 1 to 206854)

Waterston, R.H.

Direct Submission

Submitted (08-NOV-2001) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

5 (bases 1 to 206854)

Waterston, R.H.

Direct Submission

Submitted (03-JAN-2002) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

6 (bases 1 to 206854)

Waterston, R.

Direct Submission

Submitted (09-JAN-2002) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On Nov 8, 2001 this sequence version replaced gi:13431203.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu/gsc

Contact: saplens@watson.wustl.edu

----- Summary Statistics

Center project name: H_NH0459119

NOTICE: This sequence may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping

clone sections once, or longer because we provide a small overlap

between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate

chemistry, or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459I19; actual end is at base position 206854 of RP11-459I19.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

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VERSION
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS
1 (bases 1 to 1867)
Rogel-Gallard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
TITLE
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS
1 (bases 1 to 1873)
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M.,
Rogel-Gallard, C., Paul, S., Iannuccelli, N., Rask, L., Ronne, H.,
Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
and Andersson, L.
TITLE
A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle
JOURNAL
Science 288 (5469), 1248-1251 (2000)

MEDLINE 20280150
PUBMED 10818001
REFERENCE 2 (bases 1 to 1873)
AUTHORS Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
Rogel-Gallard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
Kalm, E., le Roy, P., Chardon, P. and Andersson, L.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden
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ACCESSION
VERSION
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS
1 (bases 1 to 1873)
Rogel-Gallard, C., Looft, C., Kalm, E., Milan, D., Robic, A.,
Chardon, P.
TITLE
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL
Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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DEFINITION Sequence 3 from Patent W00220850.
ACCESSION AX398333
VERSION AX398333.1 GI:21261108
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1
REFERENCE
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prka3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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DEFINITION Sequence 7 from Patent W00220850.
ACCESSION AX398337
VERSION AX398337.1 GI:21261112
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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BASE COUNT 382 a 580 c 535 g 376 t
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Query Match 68.5%; Score 41.8; DB 6; Length 1873;
Best Local Similarity 80.3%; Pred. No. 0.021;
Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ACAAGCAGAGTCCGTCGAGGAGGGAGCCACAGCTCAGGGGAGGTCCCCGGTCC 60
Db 106 ACAAGCAGAGGATGTAGAGGAGGGGGCCCTCCGGCCGAGGAGGTCCCCAGTCC 165

Qy 61 A 61
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RESULT 13
AX398333 LOCUS 1873 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 3 from Patent W00220850.
ACCESSION AX398333
VERSION AX398333.1 GI:21261108
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1
REFERENCE
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prka3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
FEATURES
source
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ALVLSFAGIDALGA"
BASE COUNT 381 a 581 c 535 g 376 t
ORIGIN

Query Match 68.5%; Score 41.8; DB 6; Length 1873;
Best Local Similarity 80.3%; Pred. No. 0.021;
Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ACAAGCAGAGTCCGTCGAGGAGGGAGCCACAGCTCAGGGGAGGTCCCCGGTCC 60
Db 106 ACAAGCAGAGGATGTAGAGGAGGGGGCCCTCCGGCCGAGGAGGTCCCCAGTCC 165

Qy 61 A 61
Db 166 A 166

RESULT 14
AX398337 LOCUS 1873 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 7 from Patent W00220850.
ACCESSION AX398337
VERSION AX398337.1 GI:21261112
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1
REFERENCE
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14	31.4	51.5	808	24	AAD36462 Pig PRKAG3 gene 5'
15	26.2	43.0	2541	23	AA84523 DNA encoding novel
16	25.6	42.0	323	22	AAAL21877 Human breast cance
17	25.6	42.0	711	23	AA84420 DNA encoding novel
18	25.4	41.6	2238	20	AAAX24826 Calcium activated
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35	24.6	40.3	1068	23	ABL27039 Drosophila melanog
36	24.6	40.3	2445	21	AAZ95746 Murine bone morpho
37	24.6	40.3	2447	17	AAQ74084 Murine BMP-9 CDNA.
38	24.6	40.3	2448	14	AAQ35243 Encodes murine bon
39	24.6	40.3	2463	22	AAH16987 Human CDNA sequenc
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41	24.6	40.3	3140	23	ABL27038 Drosophila melanog
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ALIGNMENTS

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ID AAH43685 standard; cDNA; 1647 BP.

XX AC AAH43685;
XX DT 21-JAN-2002 (first entry)
XX DE PRKAG3 CDNA.

XX KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
XX KW metabolic disease; diabetes; obesity; substitution; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
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PN WO200177305-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-SE00765.
 XX 07-APR-2000; 2000US-195665P.
 XX (AREX-) AREXIS AB.
 XX Andersson L, Luthman H, Marklund S;
 XX WPI; 2001-657170/75.
 XX P-PSDB; QQB47679.
 XX New variants of human AMP-activated protein kinase gamma3 subunit
 PT associated with a metabolic disease e.g. diabetes or obesity and method
 PT for determining a risk estimate of diseases in subject by detecting the
 PT variant -
 XX Disclosure; Fig 5; 25pp; English.
 XX This sequence represents the full length cDNA encoding the human
 CC AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
 CC the presence of the PRKAG3 DNA, or a variant, is useful in determining
 CC a risk estimate of a metabolic disease, such as diabetes or obesity,
 CC in a subject. The variation may occur in exons 3, 4 or 10. In exon
 CC 3 variation may be a substitution of a G for a C at nucleotide 320,
 CC resulting in the amino acid substitution P71A; in exon 4 variation may
 CC be a substitution of a T for a C at nucleotide 550; and in exon 10
 CC variation may be a substitution of a T for a C at nucleotide 1037,
 CC resulting in the amino acid substitution R340W. There may also be
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 ID AAAD03296 standard; DNA; 2109 BP.
 XX
 AC AAAD03296;
 XX
 DT 13-JUN-2001 (first entry)
 XX
 DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
 XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiac; gene therapy; ss.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 5'UTR 1..471
 FT /*tag= a
 FT 472..1389
 FT /*tag= b

FT 3'UTR /product= "Human Prkag3 protein"
 FT 1390..2109
 FT /*tag= c
 XX WO200120003-A2.
 XX 22-MAR-2001.
 XX 11-SEP-2000; 2000WO-EP09896.
 XX 10-SEP-1999; 99EP-0402236.
 XX 18-MAY-2000; 2000EP-0401388.
 XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
 XX (ANDE/) ANDERSSON L.
 XX (LOOF/) LOOFT C.
 XX (KALM/) KALM E.
 XX Andersson L, Looff C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
 XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;
 XX WPI; 2001-244810/25.
 XX P-PSDB; AAE00221.
 XX New variants of the gamma subunit of vertebrate adenosine
 PT monophosphate-activated kinase for diagnosis or treatment of disorders
 PT associated with energy metabolism such as diabetes, obesity, and
 PT myopathy -
 XX Claim 12; Fig 2; 71pp; English.
 XX The present sequence is a cDNA encoding human adenosine monophosphate
 CC (AMP)-activated kinase (PRKAG3) gamma subunit muscle-specific isoform,
 CC PRKAG3. Mutation in PRKAG3 results in an altered regulation of
 CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
 CC useful as therapeutic for treating carbohydrate metabolism disorders such
 CC as diabetes, obesity, and disorders associated with muscle metabolism
 CC such as myopathy and cardiovascular diseases, to modulate AMPK
 CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
 CC and its functionally altered mutants are useful for the diagnostic
 CC evaluation, genetic testing and prognosis of a metabolic disorder,
 CC preferably a carbohydrate metabolism disorder. Primers that can detect
 CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
 CC useful for detecting a dysfunction of carbohydrate metabolism resulting
 CC from the expression of a functionally altered allele of PRKAG3.
 CC transgenic animal and host cell transformed with PRKAG3 or a
 CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
 CC screening compounds able to modulate AMPK activity. Nucleic acid
 CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
 CC in a sequence encoding the first cystathione beta synthase (CBS) domain
 CC of PRKAG3 and is useful in gene therapy.
 XX Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;
 SQ Query Match 100.0%; Score 61; DB 22; Length 2109;
 Best Local Similarity 100.0%; Pred. No. 6.1e-10;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACAAGCGAAGTCCGTTGGAGGAGGGAGCCAGGTACAGGGGGAAGTCCCGGTCC 60
 Db |||||||
 QY 100 ACAAGCGAAGTCCGTTGGAGGAGGGAGCCAGGTACAGGGGGAAGTCCCGGTCC 159
 Db |||||||
 QY 61 A 61
 Db 160 A 160
 DE RESULT 3
 AAAD03320
 ID AAAD03320 standard; cDNA; 2115 BP.
 XX
 AC AAAD03320;
 XX

DT 13-JUN-2001 (first entry)
DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
XX
KW Human: gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiac; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1395
FT /*tag= a
FT /product= "Human complete Prkag3 protein"
XX
FT
XX WO200120003-A2.
XX
XX 22-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-EP09896.
XX
XX 10-SEP-1999; 99EP-0402236.
PR 18-MAY-2000; 2000EP-0401388.
XX
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.
PA (LOOF/) LOOFT C.
PA (KALM/) KALM E.
XX
XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
XX WPI; 2001-244810/25.
DR P-PSDB; AAE00223.
XX
XX New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment of disorders
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy .
XX
XX Claim 12; Page 65-68; 71pp; English.
XX
XX The present sequence is a cDNA encoding human adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC complete PRKAG3. Mutation in Prkag3 results in an altered regulation of
CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
CC useful as therapeutic for treating carbohydrate metabolism disorders such
CC as diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX
SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;

Query Match 100.0%; Score 61; DB 22; Length 2115;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGGCAGAGTCGGTGGAGGAGGGAGCCACACAGGTCAGGGGAGGTCCCGGTCC 60
DB 106 ACAAGGCAGAGTCGGTGGAGGAGGGAGCCACACAGGTCAGGGGAGGTCCCGGTCC 165

QY 61 A 61
DB 166 A 166

RESULT 4
AAH43682
ID AAH43682 standard; DNA; 989 BP.
XX
XX AAH43682;
XX
XX 21-JAN-2002 (first entry)
DT
XX
DE PRKAG3 intron 2 - intron 4.
XX
KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
KW metabolic disease; diabetes; obesity; substitution; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT intron 1..21
FT /*tag= a
FT /number= "Intron 2"
FT /note= "3' portion of intron 2"
FT exon 22..177
FT /*tag= b
FT /number= "Exon 3"
FT intron 178..541
FT /*tag= c
FT /number= "Intron 3"
FT exon 542..945
FT /*tag= d
FT /number= "Exon 4"
FT intron 946..989
FT /*tag= e
FT /number= "Intron 4"
FT /note= "5' portion of intron 4"
XX
XX WO200177305-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-SE00765.
XX
XX 07-APR-2000; 2000US-195665P.
XX
XX (AREX-) AREXIS AB.
XX
XX Andersson L, Luthman H, Marklund S;
PI WPI; 2001-657170/75.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
XX Example 1; Fig 2; 25pp; English.
XX
XX The sequences given in AAH43681-84 represents genomic fragments
CC encoding the human AMP-activated protein kinase gamma 3 subunit
CC (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
CC is useful in determining a risk estimate of a metabolic disease,
CC such as diabetes or obesity, in a subject. The variation may occur
CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of
CC a G for a C at nucleotide 320, resulting in the amino acid
CC substitution P71A; in exon 4 variation may be a substitution of a
CC T for a C at nucleotide 550; and in exon 10 variation may be a
CC substitution of a T for a C at nucleotide 1037, resulting in the
CC amino acid substitution R340W. There may also be nucleotide variation
CC in intron 6.

XX SQ Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;

Query Match 83.6%; Score 51; DB 22; Length 989;

Best Local Similarity 100.0%; Pred. No. 7.5e-07;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGCGAAGTCTGGTGGAGGAGGGAGCCACGAGTCAGGGGGAAGGT 51

Db 129 ACAAGCGAAGTCTGGTGGAGGAGGGAGCCACGAGTCAGGGGGAAGGT 179

RESULT 5

AAD03295

ID AAD03295 standard; cDNA; 1867 BP.

XX AC AAD03295;

XX 13-JUN-2001 (first entry)

DE Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.

XX Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;

KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;

KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;

KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;

KW chromosome 15; ss.

XX OS Sus scrofa.

XX FH Key Location/Qualifiers

FT 5'UTR 1..471

FT CDS /tag= a

FT 472..1389

FT /tag= b

FT /product= "Sus scrofa PRKAG3 protein"

FT 3'UTR 1390..1867

FT /tag= c

XX WO200120003-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 2000WO-EP09896.

XX 10-SEP-1999; 99EP-0402236.

XX 18-MAY-2000; 2000EP-0401388.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

PA (ANDE/) ANDERSSON L.

PA (LOOF/) LOOFT C.

PA (KALM/) KALM E.

XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX WPI: 2001-244810/25.

DR P-PSDB; AAE00220.

XX New variants of the gamma subunit of vertebrate adenosine

PT monophosphate-activated kinase for diagnosis or treatment of disorders

PT associated with energy metabolism such as diabetes, obesity, and

PT myopathy -

XX Claim 12; Fig 2; 71pp; English.

XX The present sequence is a cDNA encoding pig adenosine monophosphate

CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,

CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.

CC Mutation in Prkag3 results in an altered regulation of carbohydrate

CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as

CC therapeutic for treating carbohydrate metabolism disorders such as

CC diabetes, obesity, and disorders associated with muscle metabolism

CC such as myopathy and cardiovascular diseases, to modulate AMPK

CC activity, and for restoring a normal AMPK function. PRKAG3 sequence

CC and its functionally altered mutants are useful for the diagnostic

CC evaluation, genetic testing and prognosis of a metabolic disorder,

CC preferably a carbohydrate metabolism disorder. Primers that can detect

CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are

CC useful for detecting a dysfunction of carbohydrate metabolism resulting

CC from the expression of a functionally altered allele of PRKAG3.

CC Transgenic animal and host cell transformed with PRKAG3 or a

CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for

CC screening compounds able to modulate AMPK activity. Nucleic acid

CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or

CC in a sequence encoding the first cystathione beta synthase (CBS) domain

CC of PRKAG3 and is useful in gene therapy.

XX SQ Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;

Query Match 68.5%; Score 41.8; DB 22; Length 1867;

Best Local Similarity 80.3%; Pred. No. 0.00058;

Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ACAAGCGAAGTCTGGTGGAGGAGGGAGCCACGAGTCAGGGGGAAGGTCCCGGTCC 60

Db 100 ACAAGCGAAGTCTGGTGGAGGAGGGAGCCACGAGTCAGGGGGAAGGTCCCGGTCC 159

QY 61 A 61

Db 160 A 160

RESULT 6

AAD03319

ID AAD03319 standard; cDNA; 1873 BP.

XX AC AAD03319;

XX 13-JUN-2001 (first entry)

DE Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.

XX Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;

KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;

KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;

KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;

KW chromosome 15; ss.

XX OS Sus scrofa.

XX FH Key Location/Qualifiers

FT CDS 1..1395

FT /tag= a

FT /product= "Sus scrofa complete Prkag3 protein"

XX WO200120003-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 2000WO-EP09896.

XX 10-SEP-1999; 99EP-0402236.

XX 18-MAY-2000; 2000EP-0401388.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

PA (ANDE/) ANDERSSON L.

PA (LOOF/) LOOFT C.

PA (KALM/) KALM E.

XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX WPI: 2001-244810/25.

DR P-PSDB; AAE00222.

XX


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FT variation replace (89, C)
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX WO200220850-A2.
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
XX 08-JAN-2001; 2001US-260239P.
XX 18-JUN-2001; 2001US-299111P.
XX
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX WPI: 2002-393850/42.
XX P-PSDB; AAE22985.
XX
XX Screening animals to determine those likely to produce larger litters
XX and improved meat quality traits involves assaying for the presence of
XX polymorphisms in the AMP activated protein kinase regulatory gamma
XX subunit gene -
XX
XX Disclosure; Page 89-91; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
XX those more likely to produce large litters and improved meat quality
XX traits. The method involves assaying for the presence of a genotype
XX in the sample of genetic material obtained from animal. The genotype
XX is characterised by polymorphism(s) in the AMP activated protein
XX kinase regulatory gamma subunit (PRKAG3) gene. The method is used
XX for screening animals e.g., pigs to determine those most likely to
XX exhibit improved meat quality traits and to produce larger litters.
XX The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX
XX Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
XX
XX Query Match 68.5%; Score 41.8; DB 24; Length 1873;
XX Best Local Similarity 80.3%; Pred. No. 0.00058;
XX Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX QY 1 ACAAGGCAGAGTCGGTGGAGGAAGGGAGCCACCAGTCTCAGGGGGAAGTCCCGGTCC 60
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 106 ACAAGGCAGAGGATGTAGAGGAAGGGGGCTCCGGGCCCGAGGGAAGTCCCGAGTCC 165
XX
XX QY 61 A 61
XX |
XX Db 166 A 166
XX
XX
XX RESULT 9
XX AAD36459
XX ID AAD36459 standard; DNA; 1873 BP.
XX
XX AC AAD36459;
XX
XX DT 09-AUG-2002 (first entry)
XX
XX DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
XX
XX AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
XX screening; meat quality; single nucleotide polymorphism; SNP; pig;
XX gene; variant; ds.
XX
XX OS Sus scrofa.
XX
XX FH Key Location/Qualifiers
XX CDS 1..1395
XX /tag= a
XX /product= "Pig PRKAG3 polymorphic variant (PRKAG3-199)"
XX
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```
FT variation replace (595, A)
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX WO200220850-A2.
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
XX 08-JAN-2001; 2001US-260239P.
XX 18-JUN-2001; 2001US-299111P.
XX
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX WPI: 2002-393850/42.
XX P-PSDB; AAE22987.
XX
XX Screening animals to determine those likely to produce larger litters
XX and improved meat quality traits involves assaying for the presence of
XX polymorphisms in the AMP activated protein kinase regulatory gamma
XX subunit gene -
XX
XX Disclosure; Page 98-100; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
XX those more likely to produce large litters and improved meat quality
XX traits. The method involves assaying for the presence of a genotype
XX in the sample of genetic material obtained from animal. The genotype
XX is characterised by polymorphism(s) in the AMP activated protein
XX kinase regulatory gamma subunit (PRKAG3) gene. The method is used
XX for screening animals e.g., pigs to determine those most likely to
XX exhibit improved meat quality traits and to produce larger litters.
XX The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
XX
XX Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;
XX
XX Query Match 68.5%; Score 41.8; DB 24; Length 1873;
XX Best Local Similarity 80.3%; Pred. No. 0.00058;
XX Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
XX QY 1 ACAAGGCAGAGTCGGTGGAGGAAGGGAGCCACCAGTCTCAGGGGGAAGTCCCGGTCC 60
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX Db 106 ACAAGGCAGAGGATGTAGAGGAAGGGGGCTCCGGGCCCGAGGGAAGTCCCGAGTCC 165
XX
XX QY 61 A 61
XX |
XX Db 166 A 166
XX
XX
XX RESULT 10
XX AAD36460
XX ID AAD36460 standard; DNA; 1873 BP.
XX
XX AC AAD36460;
XX
XX DT 09-AUG-2002 (first entry)
XX
XX DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
XX
XX AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
XX screening; meat quality; single nucleotide polymorphism; SNP; pig;
XX gene; variant; ds.
XX
XX OS Sus scrofa.
XX
XX FH Key Location/Qualifiers
XX CDS 1..1395
XX /tag= a
XX /product= "Pig PRKAG3 polymorphic variant (PRKAG3-200)"
XX
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FT variation replace (599, A)
FT /*tag= b
XX /standard_name= "single nucleotide polymorphism (SNP)"
PN WO200220850-A2.
XX
XX 14-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciohanu DC, Malek M, Plastow G;
XX
XX WPI; 2002-393850/42.
DR P-PSDB; AAE22988.
XX
XX Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene -
XX
PS Disclosure; Page 102-104; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-200).
XX
SQ Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match 68.5%; Score 41.8; DB 24; Length 1873;
Best Local Similarity 80.3%; Pred. No. 0.00058;
Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGGTGAGGAGGGGAGCCACAGGTCAGGGGAAGGTCCCGGTCC 60
||||||| || ||||||||| ||| || || ||||||||| ||||
Db 106 ACAAGGCAGAGGATGTAGAGGAGGGGGCTCCGGGCCGAGGGAAGGTCCCGGTCC 165

QY 61 A 61
Db 166 A 166

RESULT 11
AAD03321
ID AAD03321 standard; DNA; 2022 BP.
XX
XX AAD03321;
XX
XX 13-JUN-2001 (first entry)
XX
DE Sus scrofa PRKAG3 splice variant DNA.
XX
XX Fig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiatic; gene therapy; ds.
XX
XX Sus scrofa.
XX
XX Key Location/Qualifiers
FH 1..1545
FT /*tag= a

FT /product= "Sus scrofa Prkag3 splice variant"
XX WO200120003-A2.
XX 22-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-EP09896.
XX
XX 10-SEP-1999; 99EP-0402236.
PR 18-MAY-2000; 2000EP-0401388.
XX
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.
PA (LOOF/) LOOFT C.
PA (KALM/) KALM E.
XX
XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
XX WPI; 2001-244810/25.
DR P-PSDB; AAE00224.
XX
XX New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment of disorders
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy -
XX
XX Claim 12; Page 69; 71pp; English.
XX
XX The present sequence is pig adenosine monophosphate (AMP)-activated
CC kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice
CC variant DNA. Prkag3 gene is located in the RN locus of chromosome 15.
CC Mutation in Prkag3 results in an altered regulation of carbohydrate
CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
CC therapeutic for treating carbohydrate metabolism disorders such as
CC diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detection of a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX
SQ Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;

Query Match 68.5%; Score 41.8; DB 22; Length 2022;
Best Local Similarity 80.3%; Pred. No. 0.00059;
Matches 49; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGGTGAGGAGGGGAGCCACAGGTCAGGGGAAGGTCCCGGTCC 60
||||||| || ||||||||| ||| || || ||||||||| ||||
Db 256 ACAAGGCAGAGGATGTAGAGGAGGGGGCTCCGGGCCGAGGGAAGGTCCCGGTCC 315

QY 61 A 61
Db 316 A 316

RESULT 12
AAD36458
ID AAD36458 standard; DNA; 1873 BP.
XX
XX AAD36458;
XX
XX 09-AUG-2002 (first entry)


```
RESULT 14
AAD36462
ID AAD36462 standard; DNA; 808 BP.
XX
AC AAD36462;
XX
DT 09-AUG-2002 (first entry)
XX
DE Pig PRKAG3 gene 5' flanking region including exon and intron.
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; polymorphism; pig; ds.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT exon 19..59
FT /*tag= a
FT /number= 1
FT intron 60..538
FT /*tag= b
FT /number= 1
FT exon 539..692
FT /*tag= c
FT /number= 2
XX
PN WO200220850-A2.
XX
PD 14-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US28283.
XX
PR 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
DR WPI; 2002-393850/42.
XX
PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene -
XX
PS Disclosure; Fig 2B; 109pp; English.
XX
CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 gene 5' flanking region including
CC exon and intron.
XX
SQ Sequence 808 BP; 170 A; 230 C; 199 G; 208 T; 1 other;
Query Match 51.5%; Score 31.4; DB 24; Length 808;
Best Local Similarity 74.5%; Pred. No. 0.94;
Matches 38; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
QY 1 ACAAGGCAGAAATCGGTGGAGGAAGGGAGGCCACCACAGGTTCAGGGGGGAAGT 51
||||| ||| | ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 644 ACAAGCAGGAGGATATAGAGGAAGGGGGCCCTCCGGGCCCGAGGGAAGT 694
||||| ||| | ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 15
```

```
AAS84523
ID AAS84523 standard; cDNA; 2541 BP.
XX
AC AAS84523;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #20327.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG20336.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID NO 20327; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: the sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2541 BP; 476 A; 780 C; 787 G; 498 T; 0 other;
Query Match 43.0%; Score 26.2; DB 23; Length 2541;
Best Local Similarity 67.3%; Pred. No. 43;
Matches 37; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 5 GGCAGAGTCGTGGAGGAGGGGAGCCACCGAGTCAGGGGGAAGTCCCGGTC 59
||||| | ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 1114 GGCAGGGGCGGTGGGGAACACTGTGGCCCGGAGGTCAGGGGTCTCTCCACAGTC 1168
||||| ||| | ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Search completed: June 13, 2003, 02:59:54
Job time : 23.1613 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: June 13, 2003, 02:37:44 ; Search time 151.839 Seconds
(without alignments)
6506.409 Million cell updates/sec

Title: US-09-826-581-5_COPY_200_260
Perfect score: 61
Sequence: 1 acaaggcagaagtcggtgga.....gggggaaggtccccggtcca 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_rrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Match Length	Description
1	38.6	63.3	621 10 BB628877
2	38.6	63.3	655 10 BB629521
3	38.6	63.3	685 10 BB630381
4	37	60.7	399 10 AW356079
5	37	60.7	422 10 AW427435
6	34.2	56.1	444 12 BF690374

7	33.8	55.4	548	13	BI775360
8	32	52.5	516	9	AI664508
c 9	29	47.5	365	9	AA787203
10	28	45.9	618	10	AW693375
11	28	45.9	669	13	BJ080431
c 12	27.8	45.6	808	10	BE306360
13	27.4	44.9	590	13	BM489457
14	27.2	44.6	1029	13	BM466469
15	27	44.3	151	12	BG244994
16	26.6	43.6	611	17	CNS01YJK
17	26.6	43.6	1691	12	BG845439
c 18	26.4	43.3	870	17	AZ166563
c 19	26.4	43.3	935	14	BQ876192
c 20	26.2	43.0	255	10	AW353555
c 21	26.2	43.0	349	12	BE835678
22	26.2	43.0	375	10	AW298840
23	26.2	43.0	475	12	BF773644
24	26.2	43.0	540	13	BI539806
c 25	26.2	43.0	600	17	BH236198
c 26	26.2	43.0	704	17	BH235990
c 27	26.2	43.0	729	17	BH235871
c 28	26	42.6	276	9	AU257757
c 29	26	42.6	312	12	BF904178
c 30	26	42.6	679	10	BB653848
c 31	26	42.6	709	13	BG963198
c 32	26	42.6	991	12	BG324609
c 33	25.8	42.3	459	14	BQ783197
c 34	25.8	42.3	476	12	BG381120
c 35	25.8	42.3	547	10	BE121408
c 36	25.8	42.3	700	9	AL508704
c 37	25.8	42.3	908	14	BQ230020
c 38	25.8	42.3	1157	12	BF674061
c 39	25.6	42.0	467	14	H92825
c 40	25.6	42.0	483	17	AQ169119
c 41	25.6	42.0	501	10	BB823175
c 42	25.6	42.0	590	13	BI507914
c 43	25.6	42.0	629	14	BM702805
c 44	25.6	42.0	716	13	BI085954
c 45	25.6	42.0	1023	14	BQ642252

ALIGNMENTS

RESULT 1
BB628877
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BB628877
RIKEN full-length enriched, 16 days neonate cerebellum Mus
musculus cDNA clone 9630039L22 5', mRNA sequence.
621 bp
linear
EST 31-AUG-2001

GI:15399483

musculus

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 621)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,

Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda

M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,

Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki

D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,

Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,

Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTAAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 148 a 204 c 202 g 101 t
ORIGIN
Query Match 63.3%; Score 38.6; DB 10; Length 655;
Best Local Similarity 77.0%; Pred. No. 0.17;
Matches 47; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ACAGGACAGTTCGGAGGAGGAGGAGCCACCGTTCAGGGGAGGTCCCCGGTCC 60
Db 284 ACAGGACAGGAGCCGTAGAGGAAGCAGAACCCAGGTGTGGGAGAGGTGCCAGTCC 343
QY 61 A 61
Db 344 A 344

RESULT 3
BB630381
LOCUS
DEFINITION BB630381 RIKEN full-length enriched, 6 days neonate skin Mus EST 26-OCT-2001
musculus cDNA clone A030014A04 5', mRNA sequence.
ACCESSION BB630381
VERSION
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 685)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and

Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES
Location/Qualifiers
1..685
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="RIKEN full-length enriched, 6 days neonate skin"
/tissue_type="skin"
/dev_stage="6 days neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATTCGAGTAAATTAATCCCCCCCCCCC 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTAAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 165 a 199 c 198 g 123 t
ORIGIN
Query Match 63.3%; Score 38.6; DB 10; Length 685;
Best Local Similarity 77.0%; Pred. No. 0.17;
Matches 47; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ACAAGGCAGAGTCGTGGAGGAGGAGCCACCGTTCAGGGGAGGTCCCCGGTCC 60
Db 190 ACGAGACAGGAGCCGTAGAGGAAGCAGAACCCAGGTTCGGAGAGGTGCCAGTCC 249
QY 61 A 61
Db 250 A 250

RESULT 4
AW356079
LOCUS
DEFINITION AW356079 38073 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW356079
VERSION
KEYWORDS
SOURCE
ORGANISM
Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
1 (bases 1 to 399)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Lagerfeld,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perteaux,G., Holt,I., Karameycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center

FEATURES	source
Plate: 32	row: F column: 22
seq primer: AATTAGTGACACTATAG.	
Location/Qualifiers	
1. .422	
/organism="Bos taurus"	
/db_xref="taxon:9913"	
/clone_lib="MARC 3Bov"	
/tissue_type="pooled"	
/lab_host="DH10B"	
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."	
102 a	136 c 125 g 59 t
BASE COUNT	

BASE COUNT	102 A	136 C	125 G	59 T
ORIGIN				
Query Match	60.7%; Score 37; DB 10; Length 422;			
Best Local Similarity	75.4%; Pred. No. 0.46;			
Matches	46; Conservative	0; Mismatches	15; Indels	0; Gaps
Qy	1 ACAGGGCAGAAGTCGTTGGAGGAGGGGAGCCACACAGGTCTAGGGGGGAAGTCTCCCCGGTCC 60			
Db	190 AAAAGCCAGGAGGATGTAGAGGAAGGGAGCTGCCAGGCCTGGAGGAGGTCCCAGTCC 249			
Qy	61 A 61			
Db	250 A 250			

RESULT 6	BF890374	444 bp	linear	EST 25-APR-2001
LOCUS	BF890374			
DEFINITION	291826 MARC 3BOV Bos taurus CDNA 5'			
ACCESSION	BF890374			
VERSION	BF890374.1			
KEYWORDS	EST.			
KEYWORDS	GI:12281760			
KEYWORDS	COW.			
KEYWORDS	SOURCE.			

REFERENCE
AUTHORS
1 (bases 1 to 444)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chiklo-McKown, C.G.,
Pertes, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keefe, J.W.

TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL	Genome Res. 11 (4), 626-630 (2001)
MEDLINE	21180013
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390

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FEATURES
  source
    Location/Qualifiers
      1. .444
        /organism="Bos taurus"
        /db_xref="taxon:9913"
        /clone_lib="MARC 30V"
        /tissue_type="pooled"
        /lab_host="DH10B"
        /note="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;

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```

LOCUS      AA787203      365 bp      mRNA      linear      EST 31-JUL-1998
DEFINITION m8d07al.r1 Aspergillus nidulans 24hr asexual developmental and
            vegetative cDNA lambda zap library Emericella nidulans cDNA clone
            m8d07al 5', mRNA sequence.
ACCESSION  AA787203
VERSION    AA787203.1  GI:2847434
KEYWORDS   EST.
SOURCE     Emericella nidulans.
            Emericella nidulans.
REFERENCE  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; Emericella.
            1 (bases 1 to 365)
AUTHORS    Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
            Prade,R. and Roe,R.B.
TITLE      An Aspergillus nidulans EST Database
JOURNAL    Unpublished (1998)
COMMENT    Other ESTs: m8d07al.f1
            Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            We anticipate the future release of the cDNA clones to the Fungal
            Genetics Stock Center
            Seq primer: SK
            High quality sequence stop: 346.
FEATURES   source
            Location/Qualifiers
            1..365
            /organism="Emericella nidulans"
            /strain="FCSC A26"
            /db_xref="taxon:162425"
            /clone="m8d07al"
            /clone_lib="Aspergillus nidulans 24hr asexual
            developmental and vegetative cDNA lambda zap library"
            /tissue_type="vegetative mycelia, asexual structures"
            /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
            XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
            3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 93 a 118 c 96 g 58 t
ORIGIN
Query Match 47.5%; Score 29; DB 9; Length 365;
Best Local Similarity 67.2%; Pred. No. 95;
Matches 41; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ACAAGCCAGCAACTCGCTCGAGAGCGGACCACCAAGTCAGCGGGAAGTCCCGTCC 60
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 ACAAGCCCGTCTCGCGCGAGAGAGCGGACTCAGCAGGAGCGGAAAGAGGTAGCTGTC 3

QY 61 A 61
    |
Db 2 A 2

RESULT 10
AW693375
LOCUS      AW693375      618 bp      mRNA      linear      EST 20-DEC-2000
DEFINITION NF063H10STF1000 Developing stem Medicago truncatula cDNA clone
            NF063H10ST 5', mRNA sequence.
ACCESSION  AW693375
VERSION    AW693375.2  GI:11933844
KEYWORDS   EST.
SOURCE     barrel medic.
            Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
            1 (bases 1 to 618)
REFERENCE  He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
            C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon

```

```

,R.A.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library
Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7568111.
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert length: 660 Std Error: 0.00
Plate: 063 row: H column: 10
Seq primer: TCACACAGGAACACAGCTATGAC.
FEATURES   source
            Location/Qualifiers
            1..618
            /organism="Medicago truncatula"
            /db_xref="taxon:3880"
            /clone="NF063H10ST"
            /clone_lib="Developing stem"
            /tissue_type="stem"
            /dev_stage="Pooled developmental"
            /note="Vector: Lambda zap; Contains a mixture of
            internodal stem segments"
BASE COUNT 174 a 107 c 137 g 200 t
ORIGIN
Query Match 45.9%; Score 28; DB 10; Length 618;
Best Local Similarity 77.3%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ACAAGCCAGCAAGTCTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 44
    ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 76 ACAGGCCAAGAGTGTGGTGGAGAGTGTGTCTACTAGCTCATGG 119

RESULT 11
BJ080431
LOCUS      BJ080431      669 bp      mRNA      linear      EST 12-DEC-2001
DEFINITION BJ080431 NIBB Mochii normalized Xenopus tailbud library Xenopus
            laevis cDNA clone XL075j16 3', mRNA sequence.
ACCESSION  BJ080431
VERSION    BJ080431.1  GI:17574127
KEYWORDS   EST.
SOURCE     African clawed frog.
            Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
            Xenopodinae; Xenopus.
            1 (bases 1 to 669)
REFERENCE  Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
            Y.
            Expressed genes in X. laevis embryo
            Unpublished (2001)
            Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
            1..669
            /organism="Xenopus laevis"
            /db_xref="taxon:8355"
            /clone="XL075j16"
            /clone_lib="NIBB Mochii normalized Xenopus tailbud
            library"
            /tissue_type="whole embryo"
            /dev_stage="stage 25"
            /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
            were oligo-dT primed and directionally cloned. Staging

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BASE COUNT	194 a	128 c	196 g	150 t	1 others	
ORIGIN						
Query Match	45.9%;	Score 28;	DB 13;	Length 569;		
Best local Similarity	66.7%;	Pred. No. 2e+02;				
Matches	40;	Conservative	0;	Mismatches 20;	Indels 0;	Gaps 0;
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Db	592	ACAAGGCCACAGGGGTTGAGGCATGTGGAATACCAAGGTCAGTGTGACTGTCCTCCATAC	651			
RESULT 12						
BE306360/c						
LOCUS	BE306360	808 bp	mRNA	linear	EST 26-OCT-2000	
DEFINITION	601101079F1 NC1_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3493458					
ACCESSION	BE306360					
VERSION	BE306360					
KEYWORDS	EST.					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
TITLE	1 (bases 1 to 808)					
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .					
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM8540 row: n column: 19 High quality sequence stop: 552. Location/Qualifiers 1. .808 /organism="Mus musculus" /strain="CZECH II" /db_xref="taxon:10090" /clone="IMAGE:3493458" /clone_lib="NC1_CGAP_Lu29" /tissue_type="spontaneous tumor, metastatic to mammary." /stem_cell_origin="Stem cell origin." /lab_host="DH10B" /note="Organ: lung; Vector: pCMV-SPORT6; Site:1: SalI; Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"					
BASE COUNT	163 a	243 c	241 g	161 t		
ORIGIN						
Query Match	45.6%;	Score 27.8;	DB 10;	Length 808;		
Best local Similarity	69.1%;	Pred. No. 2.4e+02;				
Matches	38;	Conservative	0;	Mismatches 17;	Indels 0;	Gaps 0;
QY	7	CAGAAGTCGTGGAGAGGGAGGCCACCAAGTCAGGGGGAAGTCTCCCGGTCCA	61			
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RESULT 13						
BM489457						
LOCUS	BM489457	590 bp	mRNA	linear	EST 07-FEB-2002	
DEFINITION	pgm2n.pk010.p18 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA					

Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12336 row: c column: 01
High quality sequence stop: 681.
Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5579448"
/clone_lib="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

BASE COUNT 308 a 249 c 295 g 174 t 3 others
ORIGIN

Query Match 44.6%; Score 27.2; DB 13; Length 1029;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 3 AAGGCAGCAAGTCGTCGAGGAAGGGAGCCACCAGGTCAGGGGAAGGT 51
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Db 762 AAGACAGAAACGACAGGAGGAGGAGGAGGCANNAGGACAGGAGATGAT 810

RESULT 15
BG244994 151 bp mRNA linear EST 13-FEB-2001
LOCUS 602358260F1 NCL_CGAP_Maml Mus musculus cDNA clone IMAGE:4486719 5',
DEFINITION mRNA sequence.
ACCESSION BG244994
VERSION BG244994.1 GI:12754809
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cyapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10330 row: h column: 16
High quality sequence stop: 151.
Location/Qualifiers

FEATURES

source
1. .151
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4486719"
/clone_lib="NCL_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator

BASE COUNT 21 a 38 c 70 g 22 t
ORIGIN
Query Match 44.3%; Score 27; DB 12; Length 151;
Best Local Similarity 66.1%; Pred. No. 3.2e+02;
Matches 39; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ACAAGGCAGAAGTCGTCGAGGAAGGGAGCCACCAGGTCAGGGGAAGGTTCGCCGGTC 59
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Db 73 ACTCGGCAGACGCCCGGTGGAGGTGAGGATCACCCCGGAAGGGGGGACGACGTGGGTC 131

Search completed: June 13, 2003, 05:58:24
Job time : 155.839 secs

Db 667 ACACAGCAGAAGCCGGCTGCAGAACTGGGAACAAGCATCCCCCTGGGGAAAAATGCCC 721

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RESULT 5
US-08-815-652B-1
; Sequence 1, Application US/08815652B
; Patent No. 6034062
; GENERAL INFORMATION:
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony
; APPLICANT: Song, Jeffrey
; APPLICANT: Thies, R. Scott
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,652B
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5186D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: C57B6xCBA
; TISSUE TYPE: liver
; IMMEDIATE SOURCE:
; LIBRARY: Mouse liver cDNA
; CLONE: ML14A
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1564..1893
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 610..1896
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 1..2447
; US-08-815-652B-1

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Best Local Similarity 65.5%; Pred. No. 20;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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RESULT 6
US-08-254-353A-1
; Sequence 1, Application US/08254353A
; Patent No. 6287816
; GENERAL INFORMATION:
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Song, Jeffrey
; APPLICANT: Thies, Scott
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254.353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/POCKET NUMBER: GI 5186B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: C57B46xCBA
; TISSUE TYPE: liver
; IMMEDIATE SOURCE:
; LIBRARY: Mouse liver cDNA
; CLONE: ML14A
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1564..1893
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 610..1896
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 1..2447
; US-08-254-353A-1

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Query Match 40.3%; Score 24.6; DB 4; Length 2447;
Best Local Similarity 65.5%; Pred. No. 20;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY
db

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Best Local Similarity 65.5%; Pred. No. 20;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Db      667 ACACAGCAGAGCCGCTCCAGAACTGGACACAGCATCCCCGGGGAATGCC 721

RESULT 9
US-09-750-580-4
; Sequence 4, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:

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APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bihain, Bernard
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89 US2.CIP
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB99/02058
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 49/469/099
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 4
LENGTH: 5381
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 919..930
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 1442..1498
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 1613..1724
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 2243..3940
OTHER INFORMATION: exon 4
NAME/KEY: misc.feature
LOCATION: 3941..5381
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 319
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 3213
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: conflict
LOCATION: 1241
OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: conflict
LOCATION: 1447
OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
NAME/KEY: primer_bind
LOCATION: 1..11022
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 553..11575
OTHER INFORMATION: 17-42.tp complement
NAME/KEY: primer_bind
LOCATION: 899..11920
OTHER INFORMATION: 17-39.pu
NAME/KEY: primer_bind
LOCATION: 1246..12267

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NAME/KEY: misc.binding
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NAME/KEY: misc.binding
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US-09-750-580-4
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Best Local Similarity 70.2%; Pred.No.22;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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Db 613 TCTCTGTTGGTGGGCCAGCCAGGTCTCAGTGGGAAGGTTAAAGGTC 659
RESULT 10
US-08-451-777A-7/C
Sequence 7, Application US/08451777A
Patent No. 5789223
GENERAL INFORMATION:
APPLICANT: Bergsma, Derk J.
APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Human Galactokinase Gene
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road/JW2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,777A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10825
FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Eagle, Alissa M.

Db 5363 AAGGAACAACCTAGTGTGGGCGCGCCAGCCAGTCAAGAGCATGGGCCCTGG 5309

RESULT 12

US-08-998-208-7/c

Sequence 7, Application US/08998208

Patent No. 5880105

GENERAL INFORMATION:

APPLICANT: Bergsma, Derk J.

APPLICANT: Stambolian, Dwight

TITLE OF INVENTION: Human Galactokinase Gene

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: 709 Swedeland Road/UW2220

CITY: King of Prussia

COUNTRY: Pennsylvania

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,208

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/451,777

FILING DATE: 26-MAY-1995

APPLICATION NUMBER: PCT/US94/10825

FILING DATE: 23-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Eagle, Alissa M.

REGISTRATION NUMBER: 37,126

REFERENCE/DOCKET NUMBER: P50268-1B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5364

TELEFAX: 610-270-5090

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 7676 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-998-208-7

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Best Local Similarity 65.5%; Pred. No. 23;

Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0

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Db 5363 AAGGAACAACCTAGTGTGGGCGCGCCAGCCAGTCAAGAGCATGGGCCCTGG 5309

RESULT 13

PCT-US95-06743-7/c

Sequence 7, Application PC/TUS9506743

GENERAL INFORMATION:

APPLICANT: Bergsma, Derk J.

APPLICANT: Stambolian, Dwight

TITLE OF INVENTION: Human Galactokinase Gene

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corp./Corporate

ADDRESSEE: Intellectual Property

STREET: 709 Swedeland Road/UW2220

CITY: King of Prussia

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_NA:*
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 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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 - 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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 - 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	51	83.6	989	10	US-09-826-581-2
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4	27	44.3	74868	9	US-10-175-523-67
5	25	41.0	560	9	US-09-995-793A-32
6	25	41.0	1188	9	US-09-995-793A-30
7	25	41.0	4034	10	US-09-967-768A-301
8	25	41.0	8670	9	US-09-373-658-69
9	24.8	40.7	33795	10	US-09-880-107-2184
10	24.6	40.3	2996	10	US-09-822-830A-179
11	24.6	40.3	5312	9	US-10-091-572-817
12	24.6	40.3	5312	9	US-09-764-891-9241
13	24.6	40.3	5381	9	US-09-842-364-4
14	24.6	40.3	5381	10	US-09-751-877-4
15	24.6	40.3	8095	10	US-09-880-107-2228
16	24.6	40.3	81001	9	US-09-842-364-1
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18	24.4	40.0	14040	9	US-09-764-891-5478
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c	20	24.4	40.0	302250	10	US-09-962-832-154	Sequence 154, App
	21	24.2	39.7	139	10	US-09-864-761-19511	Sequence 19511, A
	22	24.2	39.7	263	10	US-09-294-093B-950	Sequence 950, App
	23	24.2	39.7	451	10	US-09-864-761-5	Sequence 5, Appli
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	26	24	39.3	131	10	US-09-864-761-19652	Sequence 19652, A
	27	24	39.3	506	9	US-10-198-846-9038	Sequence 9038, Ap
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	31	24	39.3	2608	9	US-10-054-988-16	Sequence 16, Appl
	32	24	39.3	2608	10	US-09-739-254-16	Sequence 16, Appl
	33	24	39.3	2608	10	US-09-904-615-16	Sequence 16, Appl
	34	23.8	39.0	1942	9	US-09-800-274-1	Sequence 1, Appli
c	35	23.8	39.0	6456	12	US-10-044-090-71	Sequence 71, Appl
c	36	23.8	39.0	14738	9	US-09-764-891-5637	Sequence 5637, Ap
c	37	23.8	39.0	14738	9	US-09-764-891-5639	Sequence 5639, Ap
c	38	23.6	38.7	308	10	US-09-960-352-9061	Sequence 9061, Ap
c	39	23.6	38.7	2193	10	US-09-822-849A-49	Sequence 49, Appl
	40	23.6	38.7	2421	10	US-09-815-242-7677	Sequence 7677, Ap
c	41	23.6	38.7	2692	9	US-09-992-598-298	Sequence 298, App
c	42	23.6	38.7	2692	9	US-09-989-293A-298	Sequence 298, App
c	43	23.6	38.7	2692	9	US-09-989-735-298	Sequence 298, App
c	44	23.6	38.7	2692	9	US-09-990-444-298	Sequence 298, App
c	45	23.6	38.7	2692	9	US-09-989-730-298	Sequence 298, App

ALIGNMENTS

RESULT 1
US-09-826-581-5
; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5

Query Match 100.0%; Score 61; DB 10; Length 1647;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGGTGGAGGAGGGAGCCACCAGGTCTAGGGGAGGTCCCGGTCC 60
|||||
Db 200 ACAAGGCAGAGTCGGTGGAGGAGGGAGCCACCAGGTCTAGGGGAGGTCCCGGTCC 259

QY 61 A 61
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Db 260 A 260

RESULT 2
US-09-826-581-2
; Sequence 2, Application US/09826581
; Patent No. US20020142310A1

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; GENERAL INFORMATION:
; APPLICANT: Andersson, Lelf
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-2

Query Match      83.6%; Score 51; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.8e+08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGGTGGAGAGGGGAGGCCACCGAGTCAGGGGGAAGGT 51
    |||||
Db 129 ACAAGGCAGAGTCGGTGGAGAGGGGAGGCCACCGAGTCAGGGGGAAGGT 179

RESULT 3
US-09-960-352-1640
; Sequence 1640, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Ningping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 1640
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 08-L1H188-005-Q1-K1-B7
US-09-960-352-1640

Query Match      44.9%; Score 27.4; DB 10; Length 382;
Best Local Similarity 65.6%; Pred. No. 2.9;
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ACAAGGCAGAGTCGGTGGAGAGGGGAGGCCACCGAGTCAGGGGGAAGGTCCCGGTCC 60
    |||||
Db 128 ACAAGGCAGAGTCGGTGGAGAGGGGAGGCCACCGAGTCAGGGGGAAGGTCCCGGTCC 187

QY 61 A 61
Db 188 A 188

RESULT 4
US-10-175-523-67/c
; Sequence 67, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
```

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; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/UJ95-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 74868
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-175-523-67

Query Match      44.3%; Score 27; DB 9; Length 74868;
Best Local Similarity 85.7%; Pred. No. 2.2;
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 AAGGCAGAGTCGGTGGAGAGGGGAGGCCACCGAG 37
    |||||
Db 73759 AAGGCAGAGTCGGTGGAGAGGGGAGGCCACCGAG 73725

RESULT 5
US-09-995-793A-32
; Sequence 32, Application US/09995793A
; Publication No. US20030054446A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Bernard H.F.
; APPLICANT: Stoehr, Heidi
; TITLE OF INVENTION: No. US20030054446A1 retina-specific human proteins C7orf9,
; FILE REFERENCE: 033488-001
; CURRENT APPLICATION NUMBER: US/09/995,793A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/253,751
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; OTHER INFORMATION: genomic DNA, Exon from 101 to 460
US-09-995-793A-32

Query Match      41.0%; Score 25; DB 9; Length 560;
Best Local Similarity 64.9%; Pred. No. 17;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 CAAGGCAGAGTCGGTGGAGAGGGGAGGCCACCGAGTCAGGGGGAAGGTCCCGGT 58
    |||||
Db 249 CAAGGCAGAGGGGAGGCCACCGAGTCAGGGGGAAGGTCCCGGT 305

RESULT 6
US-09-995-793A-30
; Sequence 30, Application US/09995793A
; Publication No. US20030054446A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Bernard H.F.
```



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; TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polyptides
; FILE REFERENCE: 1488-1070006
; CURRENT APPLICATION NUMBER: US/09/373,658
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 8670
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Unknown
US-09-373-658-69

Query Match          41.0%; Score 25; DB 9; Length 8670;
Best Local Similarity 64.9%; Pred. No.12;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 5 GCAGAAAGTCGGTGGAGGAAGGCGACCCAGGTCTAGGGGGAAGGTCCCCGGTCCA 61
      ||||| || ||||||||| ||||| || | | | | | | | | | | | | | | | | | |
Db 6571 GCCAGGAGCGGTGGAGGAGGTGGAGCAGCGGTATCATGAAACAGAGCCCCCGGCCA 6515

RESULT 9
US-09-880-107-2184
; Sequence 2184, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2184
; LENGTH: 33795
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L25680
US-09-880-107-2184

Query Match          40.7%; Score 24.8; DB 10; Length 33795;
Best Local Similarity 67.3%; Pred. No.12;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 7 CAGAAGTCGGTGGAGGAAGGCGACCCAGGTCTAGGGGGAAGGTCCCCGGT 58
      ||| ||| || | | | | | | | | | | | | | | | | | | | | | | | |
Db 999 CAGCAGTGGGCCCAAGCAAATGTAGCCACAGGTCTGGGGCACAGCACCGGT 1050

RESULT 10
US-09-822-830A-179
; Sequence 179, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakr
; APPLICANT: Graham, James R.
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; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 2996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-179

Query Match          40.38; Score 24.6; DB 10; Length 2996;
Best Local Similarity 65.59; Pred. No. 19;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY      5  GCACGAAGTCGGTGGAGGAGGGAGCCACCAAGGTCAGGGGAGGTCCCGCGTC 59
          ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db      1568  GCCAGAGAGCTCTTTGGGAAGAGTGTCCCGCGTCAGGTGGTCCCGCGTC 1622

RESULT 11
US-10-091-572-817
; Sequence 817, Application US/10091572
; Publication No. US20030054373A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAl18C1
; CURRENT APPLICATION NUMBER: US/10/091,572
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,850
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,245
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
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; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08

Query Match      40.3%; Score 24.6; DB 9; Length 5312;
Best Local Similarity 65.5%; Pred. No. 18;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      5  GCGAAGTCGGTGGAGGAGGAGCCACAGGTCAGGGGAAGGTCCCGGTC 59
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1867 GCGAGGAGGCTCTTTGGGAAGAGTGTGCCCGGTCAGGTGGTCCGCTCCCGTC 1921

RESULT 12
US-09-764-891-9241
; Sequence 9241, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9241
; LENGTH: 5312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9241

Query Match      40.3%; Score 24.6; DB 9; Length 5312;
Best Local Similarity 65.5%; Pred. No. 18;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      5  GCGAAGTCGGTGGAGGAGGAGCCACAGGTCAGGGGAAGGTCCCGGTC 59
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1867 GCGAGGAGGCTCTTTGGGAAGAGTGTGCCCGGTCAGGTGGTCCGCTCCCGTC 1921

RESULT 13
US-09-842-364-4
; Sequence 4, Application US/09842364
; Publication No. US20030032783A1
; GENERAL INFORMATION:
; APPLICANT: Yen-Potin, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: APOLIPOPROTEIN A-IV-RELATED PROTEIN: POLYPEPTIDE, POLYNUCLEOTI
; FILE REFERENCE: GENSET 50CP2C
; CURRENT APPLICATION NUMBER: US/09/842,364
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 09/469,099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
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; SEQ ID NO 4
; LENGTH: 5381
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..918
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 919..930
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 1442..1498
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 1613..1724
; NAME/KEY: exon
; LOCATION: 2243..3940
; OTHER INFORMATION: exon 4
; NAME/KEY: misc.feature
; LOCATION: 3941..5381
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 319
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 3213
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: conflict
; LOCATION: 1241
; OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
; NAME/KEY: conflict
; LOCATION: 1447
; OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
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; OTHER INFORMATION: 17-42.pu
; NAME/KEY: primer_bind
; LOCATION: 533..11575
; OTHER INFORMATION: 17-42.rp complement
; NAME/KEY: primer_bind
; LOCATION: 899..11920
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; NAME/KEY: primer_bind
; LOCATION: 1441..12461
; OTHER INFORMATION: 17-39.rp complement
; NAME/KEY: primer_bind
; LOCATION: 1632..12651
; OTHER INFORMATION: 17-40.rp complement
; NAME/KEY: primer_bind
; LOCATION: 2964..13984
; OTHER INFORMATION: 17-41.pu
; NAME/KEY: primer_bind
; LOCATION: 3432..14454
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; NAME/KEY: primer_bind
; LOCATION: 300..318
; OTHER INFORMATION: 17-42-319.mis
; NAME/KEY: primer_bind
; LOCATION: 320..338
; OTHER INFORMATION: 17-42-319.mis complement
; NAME/KEY: primer_bind
; LOCATION: 3194..3212
; OTHER INFORMATION: 17-41-250.mis
; NAME/KEY: primer_bind
; LOCATION: 3214..3232
; OTHER INFORMATION: 17-41-250.mis complement
; NAME/KEY: misc_binding
; LOCATION: 307..331
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; NAME/KEY: misc_binding
; LOCATION: 3201..3225
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Best Local Similarity 70.2%; Pred. No. 18;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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US-09-751-877-4
; Sequence 4, Application US/09751877
; Patent No. US2002014294A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duciert, Aymeric
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89.US3.REG
; CURRENT APPLICATION NUMBER: US/09/751,877
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 4
; LENGTH: 5381
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 919..930
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 1442..1498
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 1613..1724
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 2243..3940
; OTHER INFORMATION: exon 4
; NAME/KEY: misc.feature
; LOCATION: 3941..5381
; OTHER INFORMATION: 3'regulatory region
; NAME/KEY: allele
; LOCATION: 319
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; NAME/KEY: primer_bind
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; OTHER INFORMATION: 17-41-250.mis
; NAME/KEY: primer_bind
; LOCATION: 3214..3232
; OTHER INFORMATION: 17-41-250.mis complement
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; LOCATION: 3201..3225
; OTHER INFORMATION: 17-41-250.probe
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on: June 13, 2003, 01:49:14 ; Search time 192.613 Seconds
(without alignments)
9216.782 Million cell updates/sec
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries

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- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
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- 16: em.fun.*
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- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.man.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	61	100.0	989	6	AX281579	AX281579 Sequence
2	61	100.0	1647	6	AX281582	AX281582 Sequence
3	61	100.0	2109	6	AX099776	AX099776 Sequence
4	61	100.0	2115	6	AX099802	AX099802 Sequence
5	61	100.0	2115	9	AF214519	AF214519 Homo sapi
6	61	100.0	152129	2	AC027416	AC027416 Homo sapi
c	61	100.0	206854	9	AC009974	AC009974 Homo sapi
8	57.8	94.8	2290	9	HS249977	AJ249977 Homo sapi
9	48.2	79.0	1867	6	AX099774	AX099774 Sequence
10	48.2	79.0	1873	4	AF214520	AF214520 Sus scrofa
11	48.2	79.0	1873	6	AX099800	AX099800 Sequence
12	48.2	79.0	1873	6	AX398331	AX398331 Sequence
13	48.2	79.0	1873	6	AX398333	AX398333 Sequence
14	48.2	79.0	1873	6	AX398335	AX398335 Sequence
15	48.2	79.0	1873	6	AX398337	AX398337 Sequence
16	48.2	79.0	1873	6	AX398339	AX398339 Sequence
17	48.2	79.0	2022	6	AX099804	AX099804 Sequence
18	48.2	79.0	5888	4	AF214521	AF214521 Sus scrofa
c	47.2	77.4	227724	2	AF36361	AF36361 Mus muscu
19	41.8	68.5	146577	2	AC128070	AC128070 Rattus no
20	41.8	68.5	190183	2	AC129703	AC129703 Rattus no
21	41.8	68.5	192968	2	AC127107	AC127107 Rattus no
22	41.8	68.5	192968	2	AC127107	AC127107 Rattus no
23	27.4	44.9	29641	3	AC005802	AC005802 Leishmani
c	27.4	44.9	35018	3	AC005893	AC005893 Leishmani
24	27.4	44.9	110000	3	AC125735_0	AC125735 Leishmani
25	26.8	43.9	10346	1	AE009112	AE009112 Agrobacte
26	26.8	43.9	14856	1	AE008077	AE008077 Agrobacte
27	26.8	43.0	79397	2	AC115385	AC115385 Rattus no
c	26.2	43.0	14101	1	AE009874	AE009874 Pyrobacul
28	26.2	43.0	14101	1	AE009874	AE009874 Pyrobacul
29	26.2	43.0	79397	2	AC115385	AC115385 Rattus no
30	25.8	42.3	1917	10	AF002245	AF002245 Cricetulu
31	25.8	42.3	4279	10	AF039574	AF039574 Mus muscu
32	25.8	42.3	5253	10	AF112855	AF112855 Mus muscu
c	25.8	42.3	17570	1	AE007063	AE007063 Mycobacte
33	25.8	42.3	39430	1	MFCY49	273966 Mycobacteri
c	25.8	42.3	183496	2	AC125075	AC125075 Mus muscu
34	25.6	42.0	217	11	HSJ11082	AL159376 Sfs from
35	25.6	42.0	38819	3	AC091120	AC091120 Leishmani
c	25.6	42.0	92750	2	AC121230	AC121230 Leishmani
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37	25.6	41.6	15586	1	AE000078	AE000078 Rhizobium
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38	25.4	41.6	140053	2	AC007873	AC007873 Homo sapi
c	25.4	41.6	158075	2	AC131311	AC131311 Homo sapi
39	25.4	41.6	158082	2	AC106429	AC106429 Rattus no
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ALIGNMENTS

RESULT 1	AX281579	AX281579	989 bp	DNA	linear	PAT 02-NOV-2001
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DEFINITION	AX281579	Sequence 2 from Patent WO0177305.				
ACCESSION	AX281579					
VERSION	AX281579.1	GI:16608830				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Andersson,L., Luthman,H. and Marklund,S.					
TITLE	Variants of the human amp-activated protein kinase gamma 3 subunit					
JOURNAL	Patent: WO 0177305-A 2 18-OCT-2001;					

FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
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Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 822 GGGCTGGGATGACGAACCGCGGCCGAGATCTACATGCGCTTCATGCAGGA 881
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QY 61 G 61
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Db 882 G 882

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DEFINITION Sequence 5 from Patent WO0177305.
ACCESSION AX281582
VERSION AX281582.1 GI:16608833
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Andersson, L., Luthman, H. and Marklund, S.
Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: WO 0177305-A 5 18-OCT-2001;
Arexis AB (SE)
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1. .1647
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Best Local Similarity 100.0%; Pred. No. 3.3e-10;
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Db 529 GGGCTGGGATGACGAACCGCGGCCGAGATCTACATGCGCTTCATGCAGGA 588
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QY 61 G 61
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Db 589 G 589

RESULT 3
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LOCUS AX099776 2109 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 3 from Patent WO0120003.
ACCESSION AX099776
VERSION AX099776.1 GI:13538810
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
Location/Qualifiers
1. .2109
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QY 61 G 61
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Db 489 G 489

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LOCUS
DEFINITION Sequence 29 from Patent WO0120003.
ACCESSION AX099802
VERSION AX099802.1 GI:13538836
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
Location/Qualifiers
1. .2115
/organism="Homo sapiens"
/db_xref="taxon:9606"

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DB 435 GGGCTGGGATGACGAACCTCGGAAACCCGGCCGACATCTACATCGGCTTCATGCAGGA 494
QY 61 G 61
DB 495 G 495

RESULT 5
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LOCUS      AF214519      2115 bp      mRNA      linear      PRI 03-JUN-2000
DEFINITION Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
mRNA, complete cds.
ACCESSION      AF214519
VERSION      AF214519.1      GI:8215681
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2115)
AUTHORS      Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gallard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
and Andersson,L.
TITLE      A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle
JOURNAL      Science 288 (5469), 1248-1251 (2000)
MEDLINE      20280150
PUBMED      10818001
REFERENCE
2 (bases 1 to 2115)
AUTHORS      Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gallard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P.P., Chardon,P. and Andersson,L.
TITLE      Direct Submission
JOURNAL      Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden
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DB 435 GGGCTGGGATGACGAACCTCGGAAACCCGGCCGACATCTACATCGGCTTCATGCAGGA 494
QY 61 G 61
DB 495 G 495

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AC027416
LOCUS      AC027416      152129 bp      DNA      linear      HTG 07-JUN-2000
DEFINITION Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
unordered pieces.
ACCESSION      AC027416
VERSION      AC027416.2      GI:8317289
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 152129)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens, clone RP11-504G11
JOURNAL      Unpublished
REFERENCE
2 (bases 1 to 152129)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castelle,A., Choquel,Y., Colangelo,M., Collins,S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,M., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Olivier,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
JOURNAL      Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RN/RepeatMasker.html
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----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information

Center project name: L7458
Center clone name: 504_G_11
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135376 bases at least Q40
Consensus quality: 143264 bases at least Q30
Consensus quality: 146503 bases at least Q20
Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1006 1105: gap of 100 bp
* 1106 2402: contig of 1297 bp in length
* 2403 2502: gap of 100 bp
* 2503 3823: contig of 1321 bp in length
* 3824 3923: gap of 100 bp
* 3924 5020: contig of 1097 bp in length
* 5021 5120: gap of 100 bp
* 5121 6161: contig of 1041 bp in length
* 6162 6261: gap of 100 bp
* 6262 7547: contig of 1286 bp in length
* 7548 7647: gap of 100 bp
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* 9984 10083: gap of 100 bp
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* 12557 12656: gap of 100 bp
* 12657 15043: contig of 2387 bp in length
* 15044 15143: gap of 100 bp
* 15144 17123: contig of 1980 bp in length
* 17124 17223: gap of 100 bp
* 17224 19466: contig of 2243 bp in length
* 19467 19566: gap of 100 bp
* 19567 21928: contig of 2362 bp in length
* 21929 22028: gap of 100 bp
* 22029 24319: contig of 2291 bp in length
* 24320 24419: gap of 100 bp
* 24420 27059: contig of 2640 bp in length
* 27060 27159: gap of 100 bp
* 27160 30170: contig of 3011 bp in length
* 30171 30270: gap of 100 bp
* 30271 33968: contig of 3698 bp in length
* 33969 34068: gap of 100 bp
* 34069 38179: contig of 4111 bp in length
* 38180 38279: gap of 100 bp
* 38280 42366: contig of 4087 bp in length
* 42367 42466: gap of 100 bp
* 42467 46365: contig of 3899 bp in length
* 46366 46465: gap of 100 bp
* 46466 51285: contig of 4820 bp in length
* 51286 51385: gap of 100 bp
* 51386 55871: contig of 4486 bp in length
* 55872 55971: gap of 100 bp
* 55972 60595: contig of 4624 bp in length
* 60596 60695: gap of 100 bp
* 60696 66595: contig of 5900 bp in length

* 66596 66695: gap of 100 bp
* 66696 73218: contig of 6523 bp in length
* 73219 73318: gap of 100 bp
* 73319 77115: contig of 3797 bp in length
* 77116 77215: gap of 100 bp
* 77216 85022: contig of 7807 bp in length
* 85023 85122: gap of 100 bp
* 85123 93314: contig of 8192 bp in length
* 93315 93414: gap of 100 bp
* 93415 101193: contig of 7779 bp in length
* 101194 101293: gap of 100 bp
* 101294 113090: contig of 11797 bp in length
* 113091 113190: gap of 100 bp
* 113191 123496: contig of 10306 bp in length
* 123497 123596: gap of 100 bp
* 123597 137837: contig of 14241 bp in length
* 137838 137937: gap of 100 bp
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2503. .3823
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3924. .5020
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 Best Local Similarity 100.0%; Pred. No. 4.1e-10;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 38106 CGCTCGGATGACGAACCTGGGAACCGCGCCAGATCTACATGCGCTTCATGCAGGA 38047
QY 61 G 61
DB 38046 G 38046

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RESULT 7
AC009974/c
LOCUS AC009974 206854 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
ACCESSION AC009974
VERSION AC009974.9 GI:16799058
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 206854)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 206854)
AUTHORS Harris,A. and Cotton,M.
TITLE The sequence of Homo sapiens BAC clone RP11-459119
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 206854)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Nov 8, 2001 this sequence version replaced gi:13431203.
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Center: Washington University Genome Sequencing Center
Center code: WUGSC

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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0459119
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPC1-11 human BAC library was made from the blood of one male donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,B., Tateo,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

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misc_feature	1..37 /notes="match to EST AW880850 (NID:g8042860)"
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QY 61 G 61
Db 168125 G 168125
RESULT 8
HSA249977 HSA249977 2290 bp mRNA linear PRI 07-APR-2000
LOCUS Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
DEFINITION (AMPK gamma 3 gene).
ACCESSION AJ249977
VERSION AJ249977.1 GI:6688200
KEYWORDS AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2290)
AUTHORS Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D.
TITLE Characterization of AMP-activated protein kinase gamma-subunit
isoforms and their role in AMP binding
JOURNAL Biochem. J. 346 Pt 3, 659-669 (2000)
MEDLINE 20164049
PUBMED 10698692
REFERENCE 2 (bases 1 to 2290)
AUTHORS Carling, D.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, W12 0NN, UNITED KINGDOM
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ORIGIN

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Db 531 GGGCTGGGATGACGAACTGCGAAACCGCGCCAGATCTACATGCGCTTCATGACGAGGA 590

QY 61 G 61
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Db 591 G 591

RESULT 9
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DEFINITION Sequence 1 from Patent WO0120003.
ACCESSION AX099774
VERSION    AX099774.1 GI:13538808
KEYWORDS   .
SOURCE     pig.
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 1867)
AUTHORS    Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
            Rogel-Gaillard,C., Jannuccelli,N., Gellin,J., le Roy,P. and
            Chardon,P.
TITLE      Variants of the gamma chain of ampk, dna sequences encoding the
            same, and uses thereof
JOURNAL    Patent: WO 0120003-A 1 22-MAR-2001;
            INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
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                        YRTIDGLIGTFRDLAVLETAFTALDIFVDRRVSALPVVNETGQVGLYSRFDI
                        HLAQQTYNHLDMNVGALRQTLICLGLVLSQPHETLGEVIDRIVREQVHRLVLWDE
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BASE COUNT  380 a 583 c 529 g 375 t
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Best Local Similarity 86.9%; Pred. No. 7.2e-06;
Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGGCTGGGATGACGAACTGCGAAACCGCGCCAGATCTACATGCGCTTCATGACGAGGA 60
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Db 429 GGGCTGGGATGACGAACTGCGAAACCGCGCCAGATCTACATGCGCTTCATGACGAGGA 488

QY 61 G 61
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Db 489 G 489

RESULT 10
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LOCUS      1873 bp      mRNA      linear      MAM 03-JUN-2000
DEFINITION Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
            mRNA, complete cds.
ACCESSION  AF214520
VERSION     AF214520.1 GI:8215683
KEYWORDS    .
SOURCE      pig.
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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SOURCE           Sus scrofa.
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE        1 (bases 1 to 1873)
AUTHORS          Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
                  Rogel-Gaillard,C., Paul,S., Jannuccelli,N., Rask,L., Ronne,H.,
                  Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                  and Andersson,L.
TITLE            A mutation in PRKAG3 associated with excess glycogen content in pig
                  skeletal muscle
JOURNAL          Science 288 (5469), 1248-1251 (2000)
MEDLINE         20280150
PUBMED          10818001
REFERENCE        2 (bases 1 to 1873)
AUTHORS          Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
                  Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
                  Kalm,E., le Roy,P., Chardon,P. and Andersson,L.
TITLE            Direct Submission
JOURNAL          Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
                  University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                  Sweden
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                        /map="15q"
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            CDS              1..1395
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DEFINITION Sequence 27 from Patent WO0120003.
ACCESSION  AX099800
VERSION     AX099800.1 GI:13538834
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SOURCE      pig.
ORGANISM    Sus scrofa
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REFERENCE 1 (bases 1 to 1873)
AUTHORS Anderson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Charodon, P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Institut National de la Recherche Agronomique (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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ACCESSION AX398331
VERSION AX398331.1 GI:21261106
KEYWORDS
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Rothschild, M.F., Giobanu, D.C., Malek, M. and Plastow, G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 1 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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VERSION AX398333.1 GI:21261108
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REFERENCE 1
AUTHORS Rothschild, M.F., Giobanu, D.C., Malek, M. and Plastow, G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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VERSION AX398335.1 GI:21261110
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 5 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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ACCESSION AX398337
VERSION AX398337.1 GI:21261112
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REFERENCE
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 7 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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SUMMARIES

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4	61	100.0	2115	AAD03320	Human AMPK gamma s
5	48.2	79.0	1867	AAD03295	Pig AMPK gamma sub
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c 21	24.8	40.7	7818	22	AAK51950	Human polynucleoti
c 22	24.8	40.7	14533	23	AA656883	DNA encoding novel
c 23	24.8	40.7	14917	24	AAD32338	Human lung specif
c 24	24.4	40.0	1406	23	ABL19505	Drosophila melanog
c 25	24.4	40.0	2327	17	AA703736	Phytase gene, Asp
c 26	24.4	40.0	2327	20	AA227414	A. terreus phytase
c 27	24.4	40.0	3406	23	ABL19504	Drosophila melanog
c 28	24.4	40.0	3593	23	ABL19502	Drosophila melanog
c 29	24.2	39.7	433	23	AA574013	DNA encoding novel
c 30	24.2	39.7	664	22	AAH99539	Human protein enco
c 31	24.2	39.7	747	23	AA574015	DNA encoding novel
c 32	24.2	39.7	999	23	AA574014	DNA encoding novel
c 33	24.2	39.7	2147	21	AA258309	Human peptidase NA
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c 36	24.2	39.7	2229	21	AA258308	Human peptidase NA
c 37	24.2	39.7	2320	21	AA258304	Human peptidase NA
c 38	24.2	39.7	2395	21	AA258311	Human peptidase NA
c 39	24.2	39.7	2402	21	AA258310	Human peptidase NA
c 40	24.2	39.7	2689	23	AA574016	DNA encoding novel
c 41	24.2	39.7	2702	21	AA258307	Human peptidase NA
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c 44	24	39.3	1089	21	AAA47543	Primate GPR2 seque
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ALIGNMENTS

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ID AAH43682 standard; DNA; 989 BP.

XX AC AAH43682;

XX DT 21-JAN-2002 (first entry)

XX DE PRKAG3 intron 2 - intron 4.

XX KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
XX LW metabolic disease; diabetes; obesity; substitution; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

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FT FT /number= "Intron 4"

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FT  /note= "5' portion of intron 4"
XX
PN W0200177305-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-SE00765.
XX
XX 07-APR-2000; 2000US-195665P.
XX
XX (AREX-) AREXIS AB.
XX
XX Andersson L, Luthman H, Marklund S;
XX
XX WPI; 2001-657170/75.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
XX associated with a metabolic disease e.g. diabetes or obesity and method
XX for determining a risk estimate of diseases in subject by detecting the
XX variant -
XX
XX Example 1; Fig 2; 25pp; English.
XX
XX The sequences given in AAH43681-84 represents genomic fragments
XX encoding the human AMP-activated protein kinase gamma 3 subunit
XX (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
XX is useful in determining a risk estimate of a metabolic disease,
XX such as diabetes or obesity, in a subject. The variation may occur
XX in exons 3, 4 or 10. In exon 3 variation may be a substitution of
XX a G for a C at nucleotide 320, resulting in the amino acid
XX substitution P71A; in exon 4 variation may be a substitution of a
XX T for a C at nucleotide 550; and in exon 10 variation may be a
XX substitution of a T for a C at nucleotide 1037, resulting in the
XX amino acid substitution R340W. There may also be nucleotide variation
XX in intron 6.
XX
XX Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 61; DB 22; Length 989;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-12;
XX Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGCTGGGATGACGAACCTGGGAACCGCGGCCAGATCTACATCGCGTTCATGCAGGA 60
XX |
XX Db 822 GGGCTGGGATGACGAACCTGGGAACCGCGGCCAGATCTACATCGCGTTCATGCAGGA 881
XX
XX QY 61 G 61
XX |
XX Db 882 G 882
XX
XX
XX RESULT 2
XX AAH43685
XX ID AAH43685 standard; cDNA; 1647 BP.
XX
XX AC AAH43685;
XX
XX 21-JAN-2002 (first entry)
XX
XX PRKAG3 cDNA.
XX
XX DE
XX KW Human: AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
XX metabolic disease; diabetes; obesity; substitution; ss.
XX
XX OS Homo sapiens.
XX
XX XX Key Location/Qualifiers
XX FH CDS 20..1489
XX FT /*tag= a
XX FT /product= "PRKAG3"
XX FT variation 230
XX FT /*tag= b
XX FT /label= "C230G"
XX FT

```

```

FT variation /note= "Causes P71A"
XX 559
XX FT /*tag= C
XX FT /label= "T559C"
XX FT /note= "Silent variation"
XX 1037
XX FT /*tag= d
XX FT /label= "C1037T"
XX FT /note= "Causes R340W"
XX
XX W0200177305-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-SE00765.
XX
XX 07-APR-2000; 2000US-195665P.
XX
XX (AREX-) AREXIS AB.
XX
XX Andersson L, Luthman H, Marklund S;
XX
XX WPI; 2001-657170/75.
XX
XX P-PSDB; Q0847679.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
XX associated with a metabolic disease e.g. diabetes or obesity and method
XX for determining a risk estimate of diseases in subject by detecting the
XX variant -
XX
XX Disclosure; Fig 5; 25pp; English.
XX
XX This sequence represents the full length cDNA encoding the human
XX AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
XX the presence of the PRKAG3 DNA, or a variant, is useful in determining
XX a risk estimate of a metabolic disease, such as diabetes or obesity,
XX in a subject. The variation may occur in exons 3, 4 or 10. In exon
XX 3 variation may be a substitution of a G for a C at nucleotide 320,
XX resulting in the amino acid substitution P71A; in exon 4 variation may
XX be a substitution of a T for a C at nucleotide 550; and in exon 10
XX variation may be a substitution of a T for a C at nucleotide 1037,
XX resulting in the amino acid substitution R340W. There may also be
XX nucleotide variation in intron 6. The numbering of these
XX variations is based on the full length cDNA as given, rather than on
XX position 1 of the open reading frame.
XX
XX Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
XX
XX Query Match 100.0%; Score 61; DB 22; Length 1647;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-12;
XX Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGCTGGGATGACGAACCTGGGAACCGCGGCCAGATCTACATCGCGTTCATGCAGGA 60
XX |
XX Db 529 GGGCTGGGATGACGAACCTGGGAACCGCGGCCAGATCTACATCGCGTTCATGCAGGA 588
XX
XX QY 61 G 61
XX |
XX Db 589 G 589
XX
XX
XX RESULT 3
XX AAD03296
XX ID AAD03296 standard; DNA; 2109 BP.
XX
XX AC AAD03296;
XX
XX 13-JUN-2001 (first entry)
XX
XX Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
XX
XX Human: gamma subunit; adenosine monophosphate-activated kinase; AMPK;
XX PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
XX

```


KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 XX 5'UTR 1..471
 FT /*tag= a
 FT CDS 472..1389
 FT /*tag= b
 FT /product= "Human Prkag3 protein"
 FT 3'UTR 1390..2109
 FT /*tag= c
 XX

PN WO200120003-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 2000WO-EP09896.

XX 10-SEP-1999; 99EP-0402236.

XX 18-MAY-2000; 2000EP-0401388.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX (ANDE/) ANDERSSON L.

XX (LOOF/) LOOFT C.

XX (KALM/) KALM E.

XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX WPI; 2001-244810/25.

XX P-PSDB; AAE00223.

XX New variants of the gamma subunit of vertebrate adenosine

XX monophosphate-activated kinase for diagnosis or treatment of disorders
 XX associated with energy metabolism such as diabetes, obesity, and
 XX myopathy -
 XX Claim 12; Fig 2; 71pp; English.
 XX The present sequence is a cDNA encoding human adenosine monophosphate
 XX (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
 XX PRKAG3. Mutation in Prkag3 results in an altered regulation of
 XX carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
 XX useful as therapeutic for treating carbohydrate metabolism disorders such
 XX as diabetes, obesity, and disorders associated with muscle metabolism
 XX such as myopathy and cardiovascular diseases, to modulate AMPK
 XX activity, and for restoring a normal AMPK function. PRKAG3 sequence
 XX and its functionally altered mutants are useful for the diagnostic
 XX evaluation, genetic testing and prognosis of a metabolic disorder,
 XX preferably a carbohydrate metabolism disorder. Primers that can detect
 XX a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
 XX useful for detecting a dysfunction of carbohydrate metabolism resulting
 XX from the expression of a functionally altered allele of PRKAG3.
 XX Transgenic animal and host cell transformed with PRKAG3 or a
 XX heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
 XX screening compounds able to modulate AMPK activity. Nucleic acid
 XX encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
 XX in a sequence encoding the first cystathione beta synthase (CBS) domain
 XX of PRKAG3 and is useful in gene therapy.

XX Sequence 2109 BP; 458 A; 521 C; 560 G; 470 T; 0 other;

Query Match 100.0%; Score 61; DB 22; Length 2109;
 Best Local Similarity 100.0%; Pred. No. 1.8e-12;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCTGGATGACGAATCGGGAACCCGGCGCCGATCATCGCTTCATCGAGA 60

|||||

429 GGGCTGGATGACGAATCGGGAACCCGGCGCCGATCATCGCTTCATCGAGA 488

61 G 61

Db 489 G 489

RESULT 4

AA03320

ID AAD03320 standard; cDNA; 2115 BP.

XX AAD03320;

XX 13-JUN-2001 (first entry)

XX Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.

XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;

XX PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;

XX genetic testing; carbohydrate metabolism disorder; skeletal muscle;

XX cystathione beta synthase; CBS; cardiant; gene therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX 1..1395

XX /*tag= a

XX /product= "Human complete Prkag3 protein"

XX WO200120003-A2.

XX 22-MAR-2001.

XX 11-SEP-2000; 2000WO-EP09896.

XX 10-SEP-1999; 99EP-0402236.

XX 18-MAY-2000; 2000EP-0401388.

XX (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX (ANDE/) ANDERSSON L.

XX (LOOF/) LOOFT C.

XX (KALM/) KALM E.

XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX WPI; 2001-244810/25.

XX P-PSDB; AAE00223.

XX New variants of the gamma subunit of vertebrate adenosine

XX monophosphate-activated kinase for diagnosis or treatment of disorders

XX associated with energy metabolism such as diabetes, obesity, and

XX myopathy -

XX Claim 12; Page 65-68; 71pp; English.

XX The present sequence is a cDNA encoding human adenosine monophosphate

XX (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,

XX complete PRKAG3. Mutation in Prkag3 results in an altered regulation of

XX carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is

XX useful as therapeutic for treating carbohydrate metabolism disorders such

XX as diabetes, obesity, and disorders associated with muscle metabolism

XX such as myopathy and cardiovascular diseases, to modulate AMPK

XX activity, and for restoring a normal AMPK function. PRKAG3 sequence

XX and its functionally altered mutants are useful for the diagnostic

XX evaluation, genetic testing and prognosis of a metabolic disorder,

XX preferably a carbohydrate metabolism disorder. Primers that can detect

XX a genetic polymorphic marker linked to a sequence encoding PRKAG3, are

XX useful for detecting a dysfunction of carbohydrate metabolism resulting

XX from the expression of a functionally altered allele of PRKAG3.

XX Transgenic animal and host cell transformed with PRKAG3 or a

XX heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for

XX screening compounds able to modulate AMPK activity. Nucleic acid

XX encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or

XX in a sequence encoding the first cystathione beta synthase (CBS) domain

XX of PRKAG3 and is useful in gene therapy.

```

XX SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
Query Match 100.0%; Score 61; DB 22; Length 2115;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCTGGGATGACGAACTGGCGAAACCCGGCGCCAGATCTACATGCGCTTCATGCAGGA 60
DB 435 GGGCTGGGATGACGAACTGGCGAAACCCGGCGCCAGATCTACATGCGCTTCATGCAGGA 494
QY 61 G 61
DB 495 G 495

RESULT 5
ID AAD03295 standard; cDNA; 1867 BP.
XX AC AAD03295;
XX DT 13-JUN-2001 (first entry)
XX DE Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 CDNA.
XX KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
XX KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
XX KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
XX KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
XX KW chromosome 15; ss.
XX OS Sus scrofa.
XX FH Key Location/Qualifiers
XX FT 5'UTR 1..471
XX FT /*tag= a
XX FT CDS 472..1389
XX FT /*tag= b
XX FT /*product= "Sus scrofa PRKAG3 protein"
XX FT 3'UTR 1390..1867
XX FT /*tag= c
XX WO200120003-A2.
XX PN 22-MAR-2001.
XX PD
XX PF 11-SEP-2000; 2000WO-EP09896.
XX PR 10-SEP-1999; 99EP-0402236.
XX PR 18-MAY-2000; 2000EP-0401388.
XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX PA (ANDE/) ANDERSSON L.
XX PA (LOOF/) LOOFT C.
XX PA (KALM/) KALM E.
XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX DR WPI; 2001-244810/25.
XX DR P-FSDB; ANE00220.
XX XX
XX PT New variants of the gamma subunit of vertebrate adenosine
XX PT monophosphate-activated kinase for diagnosis or treatment of disorders
XX PT associated with energy metabolism such as diabetes, obesity, and
XX PT myopathy -
XX XX
XX PS Claim 12; Fig 2; 71pp; English.
XX CC The present sequence is a cDNA encoding pig adenosine monophosphate
XX CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
XX CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.

```

```

CC Mutation in Prkag3 results in an altered regulation of carbohydrate
CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
CC therapeutic for treating carbohydrate metabolism disorders such as
CC diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX SQ Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;
Query Match 79.0%; Score 48.2; DB 22; Length 1867;
Best Local Similarity 86.9%; Pred. No. 7.6e-08;
Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGGCTGGGATGACGAACTGGCGAAACCCGGCGCCAGATCTACATGCGCTTCATGCAGGA 60
DB 429 GGGCTGGGATGACGAACTGGCGAAACCCGGCGCCAGATCTACATGCGCTTCATGCAGGA 488
QY 61 G 61
DB 489 G 489

RESULT 6
AAD03319
ID AAD03319 standard; cDNA; 1873 BP.
XX AC AAD03319;
XX DT 13-JUN-2001 (first entry)
XX DE Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 CDNA.
XX KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
XX KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
XX KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
XX KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
XX KW chromosome 15; ss.
XX OS Sus scrofa.
XX FH Key Location/Qualifiers
XX FT CDS 1..1395
XX FT /*tag= a
XX FT /*product= "Sus scrofa complete Prkag3 protein"
XX WO200120003-A2.
XX PN 22-MAR-2001.
XX PD
XX PF 11-SEP-2000; 2000WO-EP09896.
XX PR 10-SEP-1999; 99EP-0402236.
XX PR 18-MAY-2000; 2000EP-0401388.
XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX PA (ANDE/) ANDERSSON L.
XX PA (LOOF/) LOOFT C.
XX PA (KALM/) KALM E.
XX PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;

```

XX WPI; 2001-244810/25.
 DR P-PSDB; AAE00222.
 XX
 PT New variants of the gamma subunit of vertebrate adenosine
 PT monophosphate-activated kinase for diagnosis or treatment of disorders
 PT associated with energy metabolism such as diabetes, obesity, and
 myopathy .
 PT
 XX
 PS Claim 12; Page 62-64; 71pp; English.
 XX
 CC The present sequence is a cDNA encoding pig adenosine monophosphate
 CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
 CC complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome
 CC 15. Mutation in Prkag3 results in an altered regulation of carbohydrate
 CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
 CC therapeutic for treating carbohydrate metabolism disorders such as
 CC diabetes, obesity, and disorders associated with muscle metabolism
 CC such as myopathy and cardiovascular diseases, to modulate AMPK
 CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
 CC and its functionally altered mutants are useful for the diagnostic
 CC evaluation, genetic testing and prognosis of a metabolic disorder,
 CC preferably a carbohydrate metabolism disorder. Primers that can detect
 CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
 CC useful for detecting a dysfunction of carbohydrate metabolism resulting
 CC from the expression of a functionally altered allele of PRKAG3.
 CC Transgenic animal and host cell transformed with PRKAG3 or a
 CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
 CC screening compounds able to modulate AMPK activity. Nucleic acid
 CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
 CC in a sequence encoding the first cystathione beta synthase (CBS) domain
 CC of PRKAG3 and is useful in gene therapy.
 XX
 SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 79.0%; Score 48.2; DB 22; Length 1873;
 Best Local Similarity 86.9%; Pred. No. 7.6e-08;
 Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1 GGGCTGGATGACGAACTCGGAAACCGCGGCCGACATCTACATGCGCTTCATGCAGGA 60
 Db 435 GGGCTGGATGATGAGCTGCAGAGCCGGGGGCCAGGTCTACATGCTTCATGCAGGA 494
 QY 61 G 61
 Db 495 G 495

RESULT 7
 AAD36456
 ID AAD36456 standard; DNA; 1873 BP.
 XX
 AC AAD36456;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Pig wild-type PRKAG3 gene.
 XX
 KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
 KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
 KW gene; ds.
 XX
 OS Sus scrofa.
 XX
 EH Key Location/Qualifiers
 FT CDS 1..1395
 FT /*tag= a
 FT /product= "Pig PRKAG3 wild-type protein"
 FT replace (89, C)
 FT /*tag= b
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 FT replace (154, A)
 FT /*tag= c

FT variation /standard_name= "Single nucleotide polymorphism (SNP)"
 FT replace (595, A
 FT /*tag= d
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 FT replace (399, A)
 FT /*tag= e
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 XX
 PN WO200220850-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US28283.
 XX
 PR 08-SEP-2000; 2000US-231045P.
 PR 08-JAN-2001; 2001US-260239P.
 PR 18-JUN-2001; 2001US-299111P.
 XX
 PA (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX
 PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
 XX
 DR WPI; 2002-393850/42.
 DR P-PSDB; AAE22984.
 XX
 PT Screening animals to determine those likely to produce larger litters
 PT and improved meat quality traits involves assaying for the presence of
 PT polymorphisms in the AMP activated protein kinase regulatory gamma
 PT subunit gene .
 PT
 PS Claim 17; Fig 1; 109pp; English.
 XX
 CC The invention relates to a method for screening animals to determine
 CC those more likely to produce large litters and improved meat quality
 CC traits. The method involves assaying for the presence of a genotype
 CC in the sample of genetic material obtained from animal. The genotype
 CC is characterised by polymorphism(s) in the AMP activated protein
 CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
 CC for screening animals e.g., pigs to determine those most likely to
 CC exhibit improved meat quality traits and to produce larger litters.
 CC The present sequence is pig wild-type PRKAG3 gene.
 XX
 SQ Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 79.0%; Score 48.2; DB 24; Length 1873;
 Best Local Similarity 86.9%; Pred. No. 7.6e-08;
 Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGGCTGGATGACGAACTCGGAAACCGCGGCCGACATCTACATGCGCTTCATGCAGGA 60
 Db 435 GGGCTGGATGATGAGCTGCAGAGCCGGGGGCCAGGTCTACATGCTTCATGCAGGA 494
 QY 61 G 61
 Db 495 G 495

RESULT 8
 AAD36457
 ID AAD36457 standard; DNA; 1873 BP.
 XX
 AC AAD36457;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
 XX
 KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
 KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
 KW gene; variant; ds.
 XX
 OS Sus scrofa.

```

FH Key Location/Qualifiers
FT CDS 1..1395
FT /*tag= a
FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
FT variation replace (89, C)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
FN W0200220850-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
XX 08-JAN-2001; 2001US-260239P.
XX 18-JUN-2001; 2001US-299111P.
XX
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
XX WPI: 2002-393850/42.
XX P-PSDB; AAE22985.
XX
XX Screening animals to determine those likely to produce larger litters
XX and improved meat quality traits involves assaying for the presence of
XX polymorphisms in the AMP activated protein kinase regulatory gamma
XX subunit gene -
XX
XX Disclosure; Page 89-91; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
XX those more likely to produce large litters and improved meat quality
XX traits. The method involves assaying for the presence of a genotype
XX in the sample of genetic material obtained from animal. The genotype
XX is characterised by polymorphism(s) in the AMP activated protein
XX kinase regulatory gamma subunit (PRKAG3) gene. The method is used
XX for screening animals e.g.; pigs to determine those most likely to
XX exhibit improved meat quality traits and to produce larger litters.
XX The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX
XX Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;

Query Match 79.0%; Score 48.2; DB 24; Length 1873;
Best Local Similarity 86.9%; Pred. No. 7.6e-08;
Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGGCTGGGATGACCAACTCGGAACCCGGCGCCAGATCTACATCGCTTCATCAGGA 60
|||||
DB 435 GGGCTGGGATGATGAGCTGCAGAACCCGGGGCCAGGTCTACATGCACTTCATCAGGA 494

QY 61 G 61
|
DB 495 G 495

RESULT 9
AAD36458
ID AAD36458 standard; DNA; 1873 BP.
XX
XX AAD36458;
XX
XX 09-AUG-2002 (first entry)
XX
XX Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
XX
XX AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
XX screening; meat quality; single nucleotide polymorphism; SNP; pig;
XX gene; variant; ds.
XX
XX Sus scrofa.
XX

```

```

FH Key Location/Qualifiers
FT CDS 1..1395
FT /*tag= a
FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
FT variation replace (154, A)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX W0200220850-A2.
XX
XX 14-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
XX 08-JAN-2001; 2001US-260239P.
XX 18-JUN-2001; 2001US-299111P.
XX
XX (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
XX WPI: 2002-393850/42.
XX P-PSDB; AAE22986.
XX
XX Screening animals to determine those likely to produce larger litters
XX and improved meat quality traits involves assaying for the presence of
XX polymorphisms in the AMP activated protein kinase regulatory gamma
XX subunit gene -
XX
XX Claim 34; Page 93-95; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
XX those more likely to produce large litters and improved meat quality
XX traits. The method involves assaying for the presence of a genotype
XX in the sample of genetic material obtained from animal. The genotype
XX is characterised by polymorphism(s) in the AMP activated protein
XX kinase regulatory gamma subunit (PRKAG3) gene. The method is used
XX for screening animals e.g.; pigs to determine those most likely to
XX exhibit improved meat quality traits and to produce larger litters.
XX The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
XX
XX Sequence 1873 BP; 383 A; 580 C; 534 G; 376 T; 0 other;

Query Match 79.0%; Score 48.2; DB 24; Length 1873;
Best Local Similarity 86.9%; Pred. No. 7.6e-08;
Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGGCTGGGATGACCAACTCGGAACCCGGCGCCAGATCTACATCGCTTCATCAGGA 60
|||||
DB 435 GGGCTGGGATGATGAGCTGCAGAACCCGGGGCCAGGTCTACATGCACTTCATCAGGA 494

QY 61 G 61
|
DB 495 G 495

RESULT 10
AAD36459
ID AAD36459 standard; DNA; 1873 BP.
XX
XX AAD36459;
XX
XX 09-AUG-2002 (first entry)
XX
XX Pig PRKAG3 polymorphic variant DNA (PRKAG3-199).
XX
XX AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
XX screening; meat quality; single nucleotide polymorphism; SNP; pig;
XX gene; variant; ds.
XX
XX Sus scrofa.
XX

```



```
XX FH Key Location/Qualifiers
XX CDS 1..1545
XX FT /*tag= a
XX FT /product= "Sus scrofa Prkag3 splice variant"
XX PN
XX PN WO200120003-A2.
XX PD 22-MAR-2001.
XX PF 11-SEP-2000; 2000WO-EP09896.
XX PR 10-SEP-1999; 99EP-0402236.
XX PR 18-MAY-2000; 2000EP-0401388.
XX XX
XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX PA (ANDE/) ANDERSSON L.
XX PA (LOOF/) LOOFT C.
XX PA (KALM/) KALM E.
XX PI Andersson L, Loof C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX DR WPI; 2001-244810/25.
XX DR P-PSDB; AAE00224.
XX XX
XX XX New variants of the gamma subunit of vertebrate adenosine
XX PT monophosphate-activated kinase for diagnosis or treatment of disorders
XX PT associated with energy metabolism such as diabetes, obesity, and
XX PT myopathy
XX XX
XX PS Claim 12; page 69; 71pp; English.
XX CC
XX CC The present sequence is pig adenosine monophosphate (AMP)-activated
XX CC kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice
XX CC variant DNA. Prkag3 gene is located in the RN locus of chromosome 15.
XX CC Mutation in Prkag3 results in an altered regulation of carbohydrate
XX CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
XX CC therapeutic for treating carbohydrate metabolism disorders such as
XX CC diabetes, obesity, and disorders associated with muscle metabolism
XX CC such as myopathy and cardiovascular diseases, to modulate AMPK
XX CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
XX CC and its functionally altered mutants are useful for the diagnostic
XX CC evaluation, genetic testing and prognosis of a metabolic disorder,
XX CC preferably a carbohydrate metabolism disorder. Primers that can detect
XX CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
XX CC useful for detecting a dysfunction of carbohydrate metabolism resulting
XX CC from the expression of a functionally altered allele of PRKAG3.
XX CC Transgenic animal and host cell transformed with PRKAG3 or a
XX CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
XX CC screening compounds able to modulate AMPK activity. Nucleic acid
XX CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
XX CC in a sequence encoding the first cystathione beta synthase (CBS) domain
XX CC of PRKAG3 and is useful in gene therapy.
XX SQ Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;

Query Match 79.0%; Score 48.2; DB 22; Length 2022;
Best Local Similarity 86.9%; Pred. No. 7.7e-08;
Matches 53; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGCTGGATGACGACGCGGAACCGCGCCCGACATCTACATGCGCTTCATGACGGA 60
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
585 GGCTGGATGATGACGTCGAGAAGCGGGGCCCGAGGTCATACATGCTTCATGACGGA 644
QY 61 G 61
DB 645 G 645

RESULT 13
AAA64328
ID AAA64328 standard; cDNA; 5259 BP.
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XX AC AAA64328;
XX DT 20-DEC-2000 (first entry)
XX DE cDNA sequence encoding a Ste20-related protein kinase called SMAK.
XX KW Mouse; Ste20-related protein kinase; SMAK; caspase-3-cleavage;
XX KW caspase activated protein kinase; apoptosis; neoplasia development;
XX KW actin stress fiber dissolution; lymphoproliferative condition;
XX KW inflammation; ischemia; stroke; autoimmune disease; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX CDS 66..3674
XX FT /*tag= a
XX FT /transl_except= (pos: 4..5, aa: Ser)
XX FT /transl_except= (pos: 1373..1376, aa: Xaa)
XX FT /product= "SMAK"
XX FT /note= "Xaa is the termination codon"
XX PN WO200049139-A2.
XX PD 24-AUG-2000.
XX PF 18-FEB-2000; 2000WO-CA00165.
XX PR 19-FEB-1999; 99US-0120784.
XX PA (UYMC-) UNIV MCMASTER.
XX PI Rudnicki MA, Sabourin LA;
XX DR WPI; 2000-538295/51.
XX DR P-PSDB; AAB08521.
XX PT Nucleic acids encoding a Ste20-related protein kinase designated SMAK,
XX PT useful for the prevention, diagnosis and treatment of neoplasia
XX PT development, lymphoproliferative conditions, inflammation, ischemia or
XX PT strokes and autoimmune diseases
XX PS Claim 4; Fig 1; 78pp; English.
XX CC The present sequence encodes a murine Ste20-related protein kinase
XX CC designated SMAK. SMAK is a caspase activated protein kinase. SMAK
XX CC activates 2 signalling pathways that are involved in mediating apoptosis.
XX CC It also mediates actin stress fiber dissolution through
XX CC caspase-3-cleavage and functions to activate the stress activated
XX CC protein kinases (cjun-amino terminal kinase (JNK) signalling pathway).
XX CC SMAX protein and polynucleotides may be used in the prevention,
XX CC treatment and diagnosis of diseases associated with inappropriate SMAX
XX CC expression. The SMAX polypeptides may be used as antigens in the
XX CC production of antibodies, and in assays to identify modulators
XX CC (agonists and antagonists) of SMAX expression and activity. The SMAX
XX CC protein is associated with apoptosis and may play a role in preventing
XX CC neoplasia development, lymphoproliferative conditions, inflammation,
XX CC ischemia or strokes and autoimmune diseases.
XX SQ Sequence 5259 BP; 1744 A; 980 C; 1250 G; 1285 T; 0 other;

Query Match 42.3%; Score 25.8; DB 21; Length 5259;
Best Local Similarity 67.9%; Pred. No. 11;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 9 ATGACCACTCGGGAACCGCGCCCGACATCTACATGCGCTTCATGACGAGG 61
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2604 ATGGGAACCTGCAGCAGCAGCGGACCATCTTTCAGCGCTTTCAGCAGGAG 2656

RESULT 14
AAA64328
ID AAI99683/c
AAI99683 standard; DNA; 4403765 BP.
```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:37:44 ; Search time 151.839 Seconds
(without alignments)
6506.409 Million cell updates/sec

Title: US-09-826-581-5_Copy_529_589

Perfect score: 61
Sequence: 1 gggctggatgcgaactgc.....acatggcttcattgcaggag 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- BST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_esthum:*
 - 4: em_esthum:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: gb_gss:*
 - 18: em_gss_hum:*
 - 19: em_gss_inv:*
 - 20: em_gss_pln:*
 - 21: em_gss_vrt:*
 - 22: em_gss_fun:*
 - 23: em_gss_man:*
 - 24: em_gss_mus:*
 - 25: em_gss_other:*
 - 26: em_gss_pro:*
 - 27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45.6	74.8	444	12	BF890374 291826 MA
2	45.6	74.8	548	13	BF1775360 467815 MA
3	44	72.1	685	10	BB630381 BB630381
4	27.4	44.9	910	17	AL212510 Tetraodon
5	27.4	44.9	1010	17	CNS03856
6	27.2	44.6	955	12	BG394974 602457369

7	26.8	43.9	581	13	BJ005207
8	26.4	43.3	442	17	AQ641446
9	26	42.6	248	10	BB711478
10	26	42.6	349	9	AI606158
11	26	42.6	580	17	BH140228
12	26	42.6	593	17	BH140663
13	25.8	42.3	648	10	AW024446
14	25.8	42.3	680	10	BE198231
15	25.8	42.3	738	13	BG918873
16	25.8	42.3	986	12	BF120119
17	25.6	42.0	738	13	BM006421
18	25.6	42.0	812	9	AA519383
19	25.6	42.0	1004	17	CNS0385
20	25.4	41.6	1000	13	BM468546
21	25.2	41.3	369	14	W68459
22	25.2	41.3	432	13	BI616099
23	25.2	41.3	482	13	BI537568
24	25	41.0	481	10	AW488804
25	25	41.0	636	13	B060200
26	25	41.0	1083	12	BF135856
27	24.8	40.7	339	12	BF773519
28	24.8	40.7	414	10	AW501053
29	24.8	40.7	567	10	AV392022
30	24.8	40.7	591	14	BM707454
31	24.8	40.7	605	9	AA195150
32	24.8	40.7	658	13	BI719961
33	24.8	40.7	707	17	AG130442
34	24.8	40.7	718	10	AV753229
35	24.8	40.7	738	12	BG700791
36	24.8	40.7	742	10	BE394076
37	24.8	40.7	888	13	BM011144
38	24.8	40.7	904	12	BF033403
39	24.6	40.3	284	17	CNS03WV1
40	24.6	40.3	481	14	BQ508350
41	24.6	40.3	509	13	BM088002
42	24.6	40.3	532	12	BG599496
43	24.6	40.3	532	14	BQ508349
44	24.6	40.3	542	12	BE809466
45	24.6	40.3	554	12	BE755789

ALIGNMENTS

RESULT 1	BF890374	444 bp	mRNA	linear	EST 25-APR-2001
LOCUS	291826 MARC 3BOV Bos taurus	cdna 5'	mrna	sequence.	
DEFINITION	BF890374				
ACCESSION	BF890374				
VERSION	BF890374.1				GI:12281760
KEYWORDS	EST.				
SOURCE	COW.				
ORGANISM	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 444)				
AUTHORS	Smith, I.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, G., Perle, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.				
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cdna libraries and construction of a gene index for cattle				
JOURNAL	Genome Res. 11 (4), 626-630 (2001)				
MEDLINE	21180013				
COMMENT	Contact: Smith tpL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smth@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred				

sequencing pipeline with 384 multicapillary sequencer . Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
e mouse tissues.

```

FEATURES             Location/Qualifiers
     1..248
         /organism="Mus musculus"
         /db_xref="taxon:10090"
         /clone="B020024106"
         /clone_lib="RIKEN full-length enriched, 2 cells egg"
         /tissue_type="egg"
         /dev_stage="2 cells"
         /lab_host="DH10B"
         /note="Site_1: Salt; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in RIKEN
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGATCCACAGACTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGATCTCGAGATTCAATAAATTAATCCCCCCCCCCC 3']. cDNA
was cleaved with XhoI and BamHI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT          92 a   47 c   33 g   76 t
ORIGIN

Query Match      42.6%; Score 26; DB 10; Length 248;
Best Local Similarity 65.5%; Pred. No. 1.1e+02;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY    3  GCTGGGATGACGAATCTCGGAAACC CGGCCCATCATGC GTTCATCAGGA 60
       |||||  |  |||  |||||  |||||  |||  |||  |||||  |||||  |||
Db     52  GCTGTAACAACAACAGAGAACAGGTAC CCGTACTCCCATCTGCTTCAAACA 109
       |||||  |  |||  |||||  |||||  |||  |||  |||||  |||||  |||

AI060158              349 bp mRNA linear EST 21-APR-1999
IMAGE:1049954 3', mRNA sequence.
AI060158
AI060158.1 GI:4615325
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 349)
Marra.M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen.M., Bowers.Y., Person
,B., Swaller,T., Gibbons.M., Pape,D., Harvey.N., Schurk.R., Ritter
,E., Kohn.S., Shin.T., Jackson.Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL : contact the

```


Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@remail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:953633
Seq primer: -40RP from Gibco
High quality sequence stop: 472.
Location/Qualifiers
1. .680
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="IMAGE:1548285"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p773 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
253 a 137 c 187 g 103 t
BASE COUNT
ORIGIN
Query Match 42.3%; Score 25.8; DB 10; Length 680;
Best Local Similarity 67.9%; Pred. No. 1.6e-02;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 9 ATGACGAAGTGGGAAACCCGCCAGATCTACATCGCTTCATCGAGG 61
|||||
Db 19 ATGGGAAGTGCAGCAGCGGGAGCAGATCTTCAGCGCTTGACGAGG 71
|||||
RESULT 15
BG918873 738 bp mRNA linear EST 05-JUN-2001
LOCUS
DEFINITION
BG918873.1 GI:14299349
VERSION
BG918873.1
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 738)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10899 row: p column: 20
High quality sequence stop: 715.
Location/Qualifiers
1. .738
/organism="Mus musculus"
/strain="FVB/N"
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/sex="female, virgin"
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FEATURES
source

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/dev_stage="5 months"
/lab_host="PH108"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT      257 a      150 c      216 g      115 t
ORIGIN

Query Match      42.3%; Score 25.8; DB 13; Length 738;
Best Local Similarity 67.9%; Pred. No. 1.6e+02;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY      9 ATGACGAACGTGGGAAACCCGCCAGATCTACATGGCTTCATGCAGGAG 61
      ||| ||||| | | | ||||| | | ||||| ||||| |||||
Db      146 ATGGRAACTGCAGCAGCAGCGGAGCAGATCTTCAGCGCTTTGAGCAGGAG 198
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Search completed: June 13, 2003, 05:58:28
Job time : 155.839 secs

Best Local Similarity	73.8%;	Pred. No. 5.2;	
Matches	31;	Conservative	0; Mismatches 11; Indels 0; Gaps 0
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Db	822	ACCAGCTGCGGAGATCTGGGCGCCAGTTCTACGAGCGCTACA	863
<p>RESULT 4</p> <p>US-08-744-231-1</p> <p>: Sequence 1, Application US/08744231</p> <p>: Patent No. 6358722</p> <p>: GENERAL INFORMATION:</p> <p>: APPLICANT: Van Loon, Adolphus</p> <p>: APPLICANT: Mitchell, David</p> <p>: TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY</p> <p>: NUMBER OF SEQUENCES: 35</p> <p>: CORRESPONDENCE ADDRESS:</p> <p>: ADDRESSEE: Hoffmann-La Roche Inc.</p> <p>: STREET: 340 Kingsland Street</p> <p>: CITY: Nutley</p> <p>: STATE: New Jersey</p> <p>: COUNTRY: United States of America</p> <p>: ZIP: 07110</p> <p>: COMPUTER READABLE FORM:</p> <p>: MEDIUM TYPE: Floppy disk</p> <p>: COMPUTER: IBM PC compatible</p> <p>: OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>: SOFTWARE: PatentIn Release #1.0, Version #1.25</p> <p>: CURRENT APPLICATION DATA:</p> <p>: APPLICATION NUMBER: US/08/744,231</p> <p>: FILING DATE:</p> <p>: CLASSIFICATION: 435</p> <p>: PRIOR APPLICATION DATA:</p> <p>: APPLICATION NUMBER: 08/424,757</p> <p>: FILING DATE: 18-APR-1995</p> <p>: ATTORNEY/AGENT INFORMATION:</p> <p>: NAME: Kass, Alan P</p> <p>: REGISTRATION NUMBER: 32142</p> <p>: REFERENCE/DOCKET NUMBER: Case Docket 9339</p> <p>: TELECOMMUNICATION INFORMATION:</p> <p>: TELEPHONE: (201) 235-4205</p> <p>: TELEFAX: (201) 235-2363</p> <p>: INFORMATION FOR SEQ ID NO: 1:</p> <p>: SEQUENCE CHARACTERISTICS:</p> <p>: LENGTH: 2327 base pairs</p> <p>: TYPE: nucleic acid</p> <p>: STRANDEDNESS: double</p> <p>: TOPOLOGY: linear</p> <p>: MOLECULE TYPE: DNA (genomic)</p> <p>: FEATURE:</p> <p>: NAME/KEY: CDS</p> <p>: LOCATION: join(374..420, 469..1819)</p> <p>US-08-744-231-1</p> <p>Query Match 40.0%; Score 24.4; DB 4; Length 2327;</p> <p>Best Local Similarity 73.8%; Pred. No. 5.2;</p> <p>Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0</p>			
QY	12	ACGACTGCGGAACCCGCCGCCAGATCTACATGCGCTTCA	53
Db	822	ACCAGCTGCGGAGATCTGGGCGCCAGTTCTACGAGCGCTACA	863
<p>RESULT 5</p> <p>US-09-518-914-1</p> <p>: Sequence 1, Application US/09518914</p> <p>: Patent No. 6413731</p> <p>: GENERAL INFORMATION:</p> <p>: APPLICANT: Borowsky, Beth E.</p> <p>: APPLICANT: Ogozalek, Kristine L.</p> <p>: APPLICANT: Lakhiani, Parul P.</p> <p>: APPLICANT: Adham, Nika</p>			

;; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS

;; FILE REFERENCE: 59138-A/JPW
;; CURRENT APPLICATION NUMBER: US/09/518,914
;; EARLIER FILING DATE: 2000-03-03
;; EARLIER APPLICATION NUMBER: US 09/303,593
;; EARLIER FILING DATE: 1999-05-03
;; NUMBER OF SEQ ID NOS: 44
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 1508
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-518-914-1

Query Match 38.4%; Score 23.4; DB 4; Length 1508;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 11 GACGAACCTGCGGAACCGCGCCGACGATCTACATGCGCTTCATCGAGG 59

Db 652 GAGGGGTGCTGACATCTCTGCTCGGACACTACATGAGCTTCACGCCGG 700

RESULT 6

US-09-518-914-3

;; Sequence 3, Application US/09518914

;; Patent No. 6413731

;; GENERAL INFORMATION:

;; APPLICANT: Borowsky, Beth E.

;; APPLICANT: Ogozalek, Kristine L.

;; APPLICANT: Lakhiani, Parul P.

;; APPLICANT: Adham, Nika

;; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS

;; FILE REFERENCE: 59138-A/JPW

;; CURRENT APPLICATION NUMBER: US/09/518,914

;; EARLIER FILING DATE: 2000-03-03

;; EARLIER APPLICATION NUMBER: US 09/303,593

;; EARLIER FILING DATE: 1999-05-03

;; NUMBER OF SEQ ID NOS: 44

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 3

;; LENGTH: 1541

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-09-518-914-3

Query Match 38.4%; Score 23.4; DB 4; Length 1541;

Best Local Similarity 67.3%; Pred. No. 11;

Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 11 GACGAACCTGCGGAACCGCGCCGACGATCTACATGCGCTTCATCGAGG 59

Db 685 GAGGGGTGCTGACATCTCTGCTCGGACACTACATGAGCTTCACGCCGG 733

RESULT 7

US-08-804-227C-7

;; Sequence 7, Application US/08804227C

;; Patent No. 5876991

;; GENERAL INFORMATION:

;; APPLICANT: DeHoff, Bradley S.

;; APPLICANT: Kuhstoss, Stuart A.

;; APPLICANT: Rostock, Paul R., Jr.

;; APPLICANT: Sutton, Kimberly L.

;; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES

;; NUMBER OF SEQUENCES: 15

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: THOMAS G. PLANT 1501

;; STREET: LILLY CORPORATE CENTER

;; CITY: INDIANAPOLIS

;; STATE: IN

;; COUNTRY: USA

;; ZIP: 46285

;;

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: MS-DOS

;; SOFTWARE: ASCII(DOS) Text only

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/804,227C

;; FILING DATE: February 21, 1997

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Plant, Thomas, G.

;; REGISTRATION NUMBER: 35,784

;; REFERENCE/DOCKET NUMBER: X-8231

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 317-276-2459

;; INFORMATION FOR SEQ ID NO: 7:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 44377 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: DNA (genomic)

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 350..14002

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 14046..20036

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 20110..31284

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 31329..36071

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 36155..41830

US-08-804-227C-7

Query Match

Best Local Similarity 38.0%; Score 23.2; DB 2; Length 44377;

Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGCTGGGATGACGAACCTGCGGAACCCGCGCCCGCAGATCTACA 44

Db 27492 GGGCAGCGCGTCGACACTGCGGAGTCCGGTGACCGGATGTACA 27535

RESULT 8

US-08-804-198-1

;; Sequence 1, Application US/08804198

;; Patent No. 5945320

;; GENERAL INFORMATION:

;; APPLICANT: Burgett, Stanley G.

;; APPLICANT: Kuhstoss, Stuart A.

;; APPLICANT: Rao, Nagaraja R.

;; APPLICANT: Richardson, Mark A.

;; APPLICANT: Rostock, Paul R., Jr.

;; TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE

;; NUMBER OF SEQUENCES: 6

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: PAUL R. CANTRELL 1138

;; STREET: LILLY CORPORATE CENTER

;; CITY: INDIANAPOLIS

;; STATE: IN

;; COUNTRY: USA

;; ZIP: 46285

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: Macintosh

;; OPERATING SYSTEM: Macintosh 7.0

;; SOFTWARE: Microsoft Word 5.1

;; CURRENT APPLICATION DATA:

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1  APPLICATION NUMBER:  US/08/804,198
2  FILING DATE:
3  CLASSIFICATION:  435
4  ATTORNEY/AGENT INFORMATION:
5  NAME:  GANTRELL, PAUL R.
6  REGISTRATION NUMBER:  36,470
7  REFERENCE/DOCKET NUMBER:  P9113
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE:  317-276-3885
10 INFORMATION FOR SEQ ID NO:  1:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH:  44377 base pairs
13 TYPE:  nucleic acid
14 STRANDEDNESS:  single
15 TOPOLOGY:  linear
16 MOLECULE TYPE:  DNA (genomic)
17 FEATURE:
18 NAME/KEY:  CDS
19 LOCATION:  350..14002
20 FEATURE:
21 NAME/KEY:  CDS
22 LOCATION:  14046..20036
23 FEATURE:
24 NAME/KEY:  CDS
25 LOCATION:  20110..31284
26 FEATURE:
27 NAME/KEY:  CDS
28 LOCATION:  31329..36071
29 FEATURE:
30 NAME/KEY:  CDS
31 LOCATION:  36155..41830
32 US-08-804-198-1

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Query Match 38.0%; Score 23.2; DB 2; Length 44377;
Best Local Similarity 70.5%; Pred. No. 26;
Matches 31; Conservative 0; Mismatches 13; Indels 0;

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1  RESULT 9
2  US-09-221-654-1
3  ; Sequence 1, Application US/09221654
4  ; Patent No. 6054306
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Lassen, Soren
7  ; APPLICANT: Bech, Lisbeth
8  ; APPLICANT: Fuglsang, Claus
9  ; APPLICANT: Ohmann, Anders
10 ; APPLICANT: Breinholt, Jens
11 ; APPLICANT: Ostergaard, Peter
12 ; TITLE OF INVENTION: Peniophora Phytase
13 ; NUMBER OF SEQUENCES: 2
14 ; CORRESPONDENCE ADDRESS:
15 ; ADDRESSEE: No. 60543060 No. 6054306disk of No. 6054306th America, Inc.
16 ; STREET: 405 Lexington Avenue
17 ; CITY: New York
18 ; STATE: NY
19 ; COUNTRY: U.S.A.
20 ; ZIP: 10174
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: Diskette
23 ; COMPUTER: IBM Compatible
24 ; OPERATING SYSTEM: DOS
25 ; SOFTWARE: FastSEO for Windows Version 2.0
26 ; CURRENT APPLICATION DATA:
27 ; APPLICATION NUMBER: US/09/221,654
28 ; FILING DATE:
29 ; CLASSIFICATION:
30 ; PRIOR APPLICATION DATA:
31 ; APPLICATION NUMBER: 08/989,358
32 ;

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> FILING DATE: 12-DEC-1997
> APPLICATION NUMBER: 0529/97
> FILING DATE: 07-MAY-1997
> APPLICATION NUMBER: 60/046,081
> FILING DATE: 09-MAY-1997
> ATTORNEY/AGENT INFORMATION:
> NAME: Gregg, Valeta A
> REGISTRATION NUMBER: 35,127
> REFERENCE/DOCKET NUMBER: 5101.200-US
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 212-867-0123
> TELEFAX: 212-878-9655
> TELEX:
> INFORMATION FOR SEQ ID NO: 1:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 1320 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: cdna
> US-09-221-654-1

Query Match 37.4%; Score 22.8; DB 3; Length 1320;
Best Local Similarity 66.0%; Pred.No.18;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0

QY 4 CTGGGATGACGAAGTCCGGAACCGCGGCCAGATCTACATGCGCTTCA 53
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Db 360 CGGGGCTAACCATCCACCAACCGGCACCGATATGTATACGGCTACA 409

RESULT 10
US-08-989-358A-1
> Sequence 1, Application us/08989358A
> Patent No. 6060298
> GENERAL INFORMATION:
> APPLICANT: Lassen, Soren
> APPLICANT: Bech, Lisbeth
> APPLICANT: Fuglsang, Claus
> APPLICANT: Ohmann, Anders
> APPLICANT: Breinholt, Jens
> APPLICANT: Ostergaard, Peter
> TITLE OF INVENTION: Peniophora Phytase
> NUMBER OF SEQUENCES: 3
> CORRESPONDENCE ADDRESS:
> ADDRESSEE: NO. 6060298o No. 6060298disk of No. 6060298th America, Inc.
> STREET: 405 Lexington Avenue
> CITY: New York
> STATE: NY
> COUNTRY: U.S.A.
> ZIP: 10174
> COMPUTER READABLE FORM:
> MEDIUM TYPE: Diskette
> COMPUTER: IBM Compatible
> OPERATING SYSTEM: DOS
> SOFTWARE: FastSeq for Windows Version 2.0
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/08/989,358A
> FILING DATE: 12-DEC-1997
> CLASSIFICATION: 435
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: 1481/96
> FILING DATE: 20-DEC-1996
> APPLICATION NUMBER: 0529/97
> FILING DATE: 07-MAY-1997
> APPLICATION NUMBER: 60/046,081
> FILING DATE: 09-MAY-1997
> ATTORNEY/AGENT INFORMATION:
> NAME: Gregg, Valeta A
> REGISTRATION NUMBER: 35,127
> REFERENCE/DOCKET NUMBER: 5101.200-US
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 212-867-0123

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; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-989-359A-1

Query Match 37.4%; Score 22.8; DB 3; Length 1320;
Best Local Similarity 66.0%; Pred. No. 18;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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QY 4 CTGGGATGACGAATCGGGAACCGGGCCCGGATCATCGGCTTCA 53
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Db 360 CGGGGCTAACCAATCGCACCAACCGGACCGGATATGATATACGCGTACA 409
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RESULT 11
US-08-993-359-23
; Sequence 23, Application US/08993359A
; Patent No. 6039942
; GENERAL INFORMATION:
; APPLICANT: Lassen, Soren F.
; APPLICANT: Bech, Lisbeth
; APPLICANT: Ohmann, Anders
; APPLICANT: Breinholt, Jens
; APPLICANT: Fuglsang, Claus C.
; APPLICANT: Ostergaard, Peter R.
; TITLE OF INVENTION: Phytase Polypeptides
; FILE REFERENCE: 5383.500-US
; CURRENT APPLICATION NUMBER: US/08/993,359A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 1480/96
; EARLIER FILING DATE: 1996-12-20
; EARLIER APPLICATION NUMBER: 1481/96
; EARLIER FILING DATE: 1996-12-20
; EARLIER APPLICATION NUMBER: 0301/97
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 0529/97
; EARLIER FILING DATE: 1997-05-07
; EARLIER APPLICATION NUMBER: 1388/97
; EARLIER FILING DATE: 1997-12-01
; EARLIER APPLICATION NUMBER: 60/046,082
; EARLIER FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Peniophora lycii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (123)...(1439)
; NAME/KEY: sig_peptide
; LOCATION: (123)...(212)
; NAME/KEY: mat_peptide
; LOCATION: (213)...(1439)
US-08-993-359-23
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Query Match 37.4%; Score 22.8; DB 3; Length 1593;
Best Local Similarity 66.0%; Pred. No. 18;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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QY 4 CTGGGATGACGAATCGGGAACCGGGCCCGGATCATCGGCTTCA 53
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Db 482 CGGGGCTAACCAATCGCACCAACCGGACCGGATATGATATACGCGTACA 531
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RESULT 12
US-08-362-670B-27/c
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; Sequence 27, Application US/08362670B
; Patent No. 5658882
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,670B
; FILING DATE: December 22, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1233 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
; CLONE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1233
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 847..1233
US-08-362-670B-27
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Query Match 37.0%; Score 22.6; DB 1; Length 1233;
Best Local Similarity 64.2%; Pred. No. 21;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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Db 135 GGCTGGGATGAGGGGGCGGCCGACGACGCGCGGAACTTCCTGCGGCCCA 83
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RESULT 13
US-08-333-576C-27/c
; Sequence 27, Application US/08333576C
; Patent No. 6027919
; GENERAL INFORMATION:
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Wozney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomsen, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
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NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,576C
FILING DATE: No. 6027919ember 2, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1233 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
CLONE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1233
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 847..1233
US-08-333-576C-27

Query Match 37.0%; Score 22.6; DB 3; Length 1233;
Best Local Similarity 64.2%; Pred. No. 21;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 GGGCTGGGATGACGAACTCGGAAACCCGGCGCCAGATCTACATGCGCTTCA 53
|||||
Db 135 GGGCTGGGATGAGGGCGCGCGAGCGCGGCGGAACTTCTCTGCGGCCCA 83

RESULT 14
US-08-324-27/c
Sequence 27, Application US/08808324
Patent No. 6284572
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1233 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
CLONE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1233
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 847..1233
US-08-808-324-27

Query Match 37.0%; Score 22.6; DB 4; Length 1233;
Best Local Similarity 64.2%; Pred. No. 21;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 GGGCTGGGATGACGAACTCGGAAACCCGGCGCCAGATCTACATGCGCTTCA 53
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Db 135 GGGCTGGGATGAGGGCGCGCGAGCGCGGCGGAACTTCTCTGCGGCCCA 83

RESULT 15
PCT-US94-14030A-27/c
Sequence 27, Application PC/TUS9414030A
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:

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; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202D-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1233 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: DNA encoding BMP2 propeptide/BMP-12 mature
; CLONE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1233
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 847..1233
PCT-US94-14030A-27

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Query Match      37.0%; Score 22.6; DB 5; Length 1233;
Best Local Similarity 64.2%; Pred. NO. 21;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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Db      135 GGGCTGGGATGAGGGGGCGCGGACGACGCGCGCGGAACCTTCTGCGGCCCA 83

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Search completed: June 13, 2003, 06:01:13
Job time : 11.6452 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 04:39:50 ; Search time 19.2903 Seconds
(without alignments)
4579.068 Million cell updates/sec

Title: US-09-826-581-5_COPY_529_589

Perfect score: 61

Sequence: 1 ggcctgggatgcgaactgc.....acatcgcttcacgagag 61

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 72403093 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications.NA:*

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- 3: /cgn2.6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 11: /cgn2.6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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- 13: /cgn2.6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2.6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	989	10	US-09-826-581-2
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c 4	25	41.0	1473	10	US-09-815-242-8004
c 5	24.8	40.7	14917	9	US-09-909-567B-11
c 6	24	39.3	1086	10	US-09-931-381A-19
c 7	24	39.3	1089	9	US-09-898-751A-1
c 8	24	39.3	1244	10	US-09-931-381A-17
c 9	23.8	39.0	600	10	US-09-764-864-166
c 10	23.6	38.7	573	9	US-10-108-605-84
c 11	23.6	38.7	2760	10	US-09-934-868-51
c 12	23.4	38.4	1508	9	US-10-146-835-1
c 13	23.4	38.4	1541	9	US-10-146-835-3
c 14	23.2	38.0	1323	10	US-09-917-800A-1694
c 15	23.2	38.0	3627	9	US-09-927-827-4
c 16	23.2	38.0	4204	9	US-10-007-270-23
c 17	23.2	38.0	7356	9	US-09-927-827-1
c 18	23.2	38.0	27847	9	US-10-265-593-3
c 19	23	37.7	242	10	US-09-960-352-12740

c 20	23	37.7	416	9	US-09-764-891-6224	Sequence 6224, Ap
c 21	23	37.7	416	9	US-09-764-891-6227	Sequence 6227, Ap
c 22	23	37.7	5535	9	US-09-373-658-67	Sequence 67, Appl
c 23	22.8	37.4	232	10	US-09-923-876-2303	Sequence 2303, Ap
c 24	22.8	37.4	240	10	US-09-764-864-602	Sequence 602, App
c 25	22.8	37.4	8907	9	US-09-738-626-934	Sequence 934, App
c 26	22.8	37.4	3309400	9	US-09-738-626-1	Sequence 1, Appli
c 27	22.6	37.0	1233	9	US-09-945-182-27	Sequence 27, Appl
c 28	22.6	37.0	1260	7	US-08-957-425-4	Sequence 4, Appli
c 29	22.6	37.0	1547	9	US-10-044-716-1	Sequence 1, Appli
c 30	22.6	37.0	1607	9	US-09-804-625-3	Sequence 3, Appli
c 31	22.6	37.0	4839	9	US-10-073-961-476	Sequence 476, App
c 32	22.6	37.0	4839	10	US-09-764-887-476	Sequence 1, Appli
c 33	22.6	37.0	14759	10	US-09-952-360-1	Sequence 1, Appli
c 34	22.4	36.7	363	10	US-09-878-574-5173	Sequence 5173, Ap
c 35	22.4	36.7	471	9	US-09-918-995-29143	Sequence 29143, A
c 36	22.4	36.7	1089	9	US-09-898-751A-3	Sequence 3, Appli
c 37	22.4	36.7	1451	10	US-09-822-830A-330	Sequence 330, App
c 38	22.4	36.7	2175	9	US-09-764-891-7546	Sequence 7546, Ap
c 39	22.4	36.7	3432	9	US-10-300-834-4	Sequence 4, Appli
c 40	22.2	36.4	303	10	US-09-923-876-3718	Sequence 3718, Ap
c 41	22.2	36.4	984	10	US-09-815-242-7872	Sequence 7872, Ap
c 42	22	36.1	238	10	US-09-923-876-2600	Sequence 2600, Ap
c 43	22	36.1	306	10	US-09-284-093B-79	Sequence 79, Appl
c 44	22	36.1	531	9	US-09-918-995-31548	Sequence 31548, A
c 45	21.8	35.7	261	10	US-09-886-607-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-826-581-2
; Sequence 2, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SU
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-2

Query Match	100.0%	Score 61;	DB 10;	Length 989;
Best Local Similarity	100.0%;	Pred. No. 3.4e-14;		
Matches 61;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy	61	G 61		
Db	882	G 882		

RESULT 2

US-09-826-581-5
; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger

```
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(1486)
US-09-826-581-5

Query Match          100.0%; Score 61; DB 10; Length 1647;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTGGGATGACGAAGTGGGAACCGCGCGCCGAGATCTACATGGCTTCATGCAGGA 60
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Db 529 GGCTGGGATGACGAAGTGGGAACCGCGCGCCGAGATCTACATGGCTTCATGCAGGA 588

QY 61 G 61
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Db 589 G 589

RESULT 3
US-09-939-964-1/c
; Sequence 1, Application US/09939964
; Publication No. US2003005422A1
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; TITLE OF INVENTION: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; FILE REFERENCE: CAP0068
; CURRENT APPLICATION NUMBER: US/09/939,964
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/214,808
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1

Query Match          41.6%; Score 25.4; DB 9; Length 536165;
Best Local Similarity 64.4%; Pred. No. 3.1;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 GGCTGGGATGACGAAGTGGGAACCGCGCGCCGAGATCTACATGGCTTCATGCAGGA 60
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RESULT 4
US-09-815-242-8004/c
; Sequence 8004, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
```

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; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8004
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1473)
US-09-815-242-8004

Query Match          41.0%; Score 25; DB 10; Length 1473;
Best Local Similarity 64.9%; Pred. No. 2.7;
Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 GGCTGGGATGACGAAGTGGGAACCGCGCGCCGAGATCTACATGGCTTCATGCAG 58
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Db 792 GTGCGGAAGATGATCAGCGGGGACTTGGCGCCGAGCTCCATGGTCACTCTCTTCAG 736

RESULT 5
US-09-909-567B-11
; Sequence 11, Application US/09909567B
; Publication No. US2003002257A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto A.
; APPLICANT: Naier, Mano
; APPLICANT: Chen, Selyu
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: DEX-0214
; CURRENT APPLICATION NUMBER: US/09/909,567B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,834
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 14917
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-909-567B-11

Query Match          40.7%; Score 24.8; DB 9; Length 14917;
Best Local Similarity 67.3%; Pred. No. 4;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 8 GATGACGAAGTGGGAACCGCGCGCCGAGATCTACATGGCTTCATGCAGG 59
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Db 2869 GAAGAGGACCTGCAGAACCTCTGTGACAGACCCAGCATGATCCCGAGG 2920
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Db      82 GCGAGCGCCCTACCACTGCGCGGAGTCCGGCAGCGCTTCACGCGAAG 132

RESULT 10
US-10-108-605-84
; Sequence 84, Application US/10108605
; Patent No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/176,418
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-108-605-84

Query Match      38.7%; Score 23.6; DB 9; Length 573;
Best Local Similarity 64.8%; Pred. No. 8.8;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      8 GATGACGACGTCGCGAACCAGCCGCCAGATCTACATGCGCTTCATGCGAGG 61
      ||||| || ||| || || || || || || || || || || || || || || || ||
Db      68 GATGGCGTCCAGCGCGGCGCTCGTCGCGCAAGATCATCGAGCGCTTCGAGCAGAAG 121

RESULT 11
US-09-934-868-51/c
; Sequence 51, Application US/09934868
; Patent No. US20020137190A1
; GENERAL INFORMATION:
; APPLICANT: Koffas, Mattheos
; APPLICANT: Odum, James M
; APPLICANT: Schenzle, Andreas J
; TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
; FILE REFERENCE: CL1596 US NA
; CURRENT APPLICATION NUMBER: US/09/934,868
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 51
; LENGTH: 2760
; TYPE: DNA
; ORGANISM: Methylomonas 16a
; FEATURE:
; OTHER INFORMATION: ORF7
; OTHER INFORMATION: nasa gene
US-09-934-868-51

Query Match      38.7%; Score 23.6; DB 10; Length 2760;
Best Local Similarity 64.8%; Pred. No. 10;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      1 GGCTGGGATGACGAACTCGCGAACCAGCCGCCAGATCTACATGCGCTTCAT 54
      ||||| || ||| || || || || || || || || || || || || || || || ||
Db      1123 GGGCGACGGTGTGCGGTTTGCCAAACAGCGCGACTCTATCGACATGCGCTGGAT 1070

RESULT 12
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US-10-146-835-1
; Sequence 1, Application US/10146835
; Publication No. US20030073167A1
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhiani, Parul P.
; APPLICANT: Adham, Nika
; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
; FILE REFERENCE: 59138-A/JPW
; CURRENT APPLICATION NUMBER: US/10/146,835
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: US/09/518,914
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/303,593
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-835-1

Query Match      38.4%; Score 23.4; DB 9; Length 1508;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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      || || || || || || || || || || || || || || || || || || || || ||
Db      652 GAGGGGTTCGTGACATCTCTCTCTGGGACTACATGAGCTTCACGCCGG 700

RESULT 13
US-10-146-835-3
; Sequence 3, Application US/10146835
; Publication No. US20030073167A1
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhiani, Parul P.
; APPLICANT: Adham, Nika
; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
; FILE REFERENCE: 59138-A/JPW
; CURRENT APPLICATION NUMBER: US/10/146,835
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: US/09/518,914
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/303,593
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-835-3

Query Match      38.4%; Score 23.4; DB 9; Length 1541;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY      11 GACGAACCTCGGAAACCGCGGCCAGATCTACATGCGCTTCATGCGAGG 59
      || || || || || || || || || || || || || || || || || || || || ||
Db      685 GAGGGGTTCGTGACATCTCTCTCTGGGACTACATGAGCTTCACGCCGG 733

RESULT 14
US-09-917-800A-1694
; Sequence 1694, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

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35: em_htg_rod:*

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37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	61	100.0	2115	6	AX099802	Sequence
4	61	100.0	2115	9	AF214519	Homo sapi
5	61	100.0	2290	9	HS8249977	Homo sapi
6	56.2	92.1	1867	6	AX099774	Sequence
7	56.2	92.1	1873	4	AF214520	Sus scrofa
8	56.2	92.1	1873	6	AX099800	Sequence
9	56.2	92.1	1873	6	AX398331	Sequence
10	56.2	92.1	1873	6	AX398333	Sequence
11	56.2	92.1	1873	6	AX398335	Sequence
12	56.2	92.1	1873	6	AX398337	Sequence
13	56.2	92.1	1873	6	AX398339	Sequence
14	56.2	92.1	2022	6	AX099804	Sequence
15	46.2	75.7	1722	6	AX281580	Sequence
16	46.2	75.7	152129	2	AC027416	Homo sapi
17	46.2	75.7	206854	9	AC009974	Homo sapi
18	43.4	71.1	5888	4	AF214521	Sus scrofa
19	41.2	67.5	146577	2	AC128070	Rattus no
20	41.2	67.5	190183	2	AC129703	Rattus no
21	41.2	67.5	192968	2	AC127107	Rattus no
22	41.2	67.5	227724	2	AF336381	Mus muscu
23	29.8	48.9	196208	2	AC129702	Rattus no
24	29.2	47.9	1681	4	AF334948	Canis fam
25	29.2	47.9	107799	2	AC112601	Rattus no
26	29.2	47.9	166397	2	AC112066	Rattus no
27	29.2	47.9	178452	2	AC096427	Rattus no
28	28.2	46.2	249536	10	AL663072	Mouse DNA
29	28	45.9	143720	10	AC087332	Mus Muscu
30	28	45.9	153605	2	AC019360	Homo sapi
31	28	45.9	154746	2	AC063943	Homo sapi
32	28	45.9	183861	2	HS75N14	Homo sapien
33	28	45.9	187546	2	AC129236	Homo sapi
34	28	45.9	195325	2	AC125616	Homo sapi
35	28	45.9	204767	2	AL772255	Mus muscu
36	28	45.9	209336	2	AL845470	Mus muscu
37	27.8	45.6	71165	2	AC101452	Mus muscu
38	27.6	45.2	75131	2	AC023022	Homo sapi
39	27.6	45.2	115004	2	AC108872	Oryza sat
40	27.6	45.2	119563	9	HSJ894D12	Human DNA
41	27.6	45.2	140181	2	AC025266	Homo sapi
42	27.6	45.2	141990	9	AC004691	Homo sapi
43	27.6	45.2	143277	2	AC105743	Oryza sat
44	27.6	45.2	153170	9	HS1103G7	Homo DNA
45	27.6	45.2	156335	9	AC018818	Homo sapi

ALIGNMENTS

RESULT 1
AX281582
LOCUS AX281582 1647 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 5 from Patent WO0177305.
ACCESSION AX281582
VERSION AX281582.1 GI:16608833
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Andersson, L., Luthman, H. and Marklund, S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 5 18-OCT-2001;

Araxis AB (SE)
Location/Qualifiers
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/db_xref="taxon:9606"
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/note="unnamed protein product"
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/db_xref="GI:16608834"
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Query Match 100.0%; Score 61; DB 6; Length 1647;
Best Local Similarity 100.0%; Pred. No. 9.5e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1007 TTCTCGACATCTTTGGTTCCCTGCTGCCCGCCCTCTCTCTACGCACTATCCAA 1066
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QY 61 G 61
Db 1067 G 1067

RESULT 2
AX099776
LOCUS 2109 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 3 from Patent WO0120003.
ACCESSION AX099776
VERSION AX099776.1 GI:13538810
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2109)
AUTHORS Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Galliard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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source Location/Qualifiers
1. .2109
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BASE COUNT 458 a 621 c 560 g 470 t
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Query Match 100.0%; Score 61; DB 6; Length 2109;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 907 TTCTCGACATCTTTGGTTCCCTGCTGCCCGCCCTCTCTCTACGCACTATCCAA 966
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QY 61 G 61
Db 967 G 967

RESULT 3
AX099802
LOCUS 2115 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 29 from Patent WO0120003.
ACCESSION AX099802
VERSION AX099802.1 GI:13538836
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2115)
AUTHORS Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Galliard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
FEATURES
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1. .i395
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ITDFILVHRYSPLVQIYEIOHKLETWREIYLOGCFKPLVSI SPNDSLFEAVYTL
IKNRHRLPVLDPVSGNVHLHILTHKRLKFLHIFGSLIRPSFLYRTIQDQIGTFRDL
AVVLETPALITDIFVDRRVSALPVNCGQVGLYSRFDVIHLAAQTYNHLDMVS
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BASE COUNT 460 a 622 c 562 g 471 t
ORIGIN

Query Match 100.0%; Score 61; DB 6; Length 2115;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTCGACATCTTTGGTTCCCTGCTGCCCGCCCTCTCTCTACGCACTATCCAA 60
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Db 913 TTCTCGACATCTTTGGTTCCCTGCTGCCCGCCCTCTCTCTACGCACTATCCAA 972
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QY 61 G 61
Db 973 G 973

RESULT 4
AF214519
LOCUS 2115 bp mRNA linear PRI 03-JUN-2000
DEFINITION Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
AF214519
ACCESION AF214519
RNA, complete cds.

VERSION AF214519.1 GI:8215681
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2115)
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M.,
Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Resk, D., Ronne, H.,
Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
and Andersson, L.
TITLE A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle
JOURNAL Science 288 (5469), 1248-1251 (2000)
MEDLINE 20280150
PUBMED 10818001
REFERENCE 2 (bases 1 to 2115)
AUTHORS Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden
FEATURES
source Location/Qualifiers
1..2115
/organism="Homo sapiens"
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/chromosome="2"
/map="2p"
/tissue.type="skeletal muscle"
gene 1..2115
/gene="PRKAG3"
CDS 1..1395
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TFILVRLYRSPILQIYEIOHKIETWREIYLOCCFKPLVSIISPNDLSFEAVYTLI
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BASE COUNT 460 a 622 c 562 g 471 l
ORIGIN
Query Match 100.0%; Score 61; DB 9; Length 2115;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTGCACATCTTTGGTTCCTGCTGCCGCCGCCCTCTCTCTACCGCACTATCCAA 60
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DB 913 TTCTGCACATCTTTGGTTCCTGCTGCCGCCGCCCTCTCTCTACCGCACTATCCAA 972
QY 61 G 61
DB 973 G 973
RESULT 5
HSA249977
LOCUS HSA249977 2290 bp mRNA linear PRI 07-APR-2000
DEFINITION Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit
(AMPK gamma 3 gene).
ACCESSION AJ249977
VERSION AJ249977.1 GI:6688200
KEYWORDS AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.

SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2290)
Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D.
TITLE Characterization of AMP-activated protein kinase gamma-subunit
isoforms and their role in AMP binding
JOURNAL Biochem. J. 346 Pt 3, 659-669 (2000)
MEDLINE 20164049
PUBMED 10698692
REFERENCE 2 (bases 1 to 2290)
AUTHORS Carling, D.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC
Clinical Sciences Centre, Hammersmith Hospital, DuCane Road,
London, W12 0NN, UNITED KINGDOM
FEATURES
source Location/Qualifiers
1..2290
/organism="Homo sapiens"
/db_xref="taxon:9606"
22..1500
/gene="AMPK gamma 3"
22..1500
/gene="AMPK gamma 3"
/function="AMP-activated protein kinase regulatory
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/evidence=experimental
/product="AMP-activated protein kinase gamma 3 subunit"
/protein_id="CAB65117.1"
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GSLPRLPSFLYRTIQDLGIGTFRDLAVLEATPIL/ALDIFVDRVSAIPVNVCCQV
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BASE COUNT 501 a 674 c 617 g 498 t
ORIGIN
Query Match 100.0%; Score 61; DB 9; Length 2290;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTGCACATCTTTGGTTCCTGCTGCCGCCGCCCTCTCTCTACCGCACTATCCAA 60
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DB 1009 TTCTGCACATCTTTGGTTCCTGCTGCCGCCGCCCTCTCTCTACCGCACTATCCAA 1068
QY 61 G 61
DB 1069 G 1069
RESULT 6
AX099774
LOCUS AX099774 1867 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 1 from Patent WO0120003.
ACCESSION AX099774
VERSION AX099774.1 GI:13538808
KEYWORDS pig.
SOURCE Sus scrofa
ORGANISM Sus scrofa
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1867)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the

same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
Location/Qualifiers
source 1. .1867
/organism="Sus scrofa"
/db_xref="taxon:9823"
472. .1389
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YNTIIDLIGIFRDLAWLETAPILTALDIFVDRRVSAIPVWNETGVVGLYSRFDVI
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TQHLLGVVSLSDILOALVLSFAGIDALGA"
BASE COUNT 380 a 583 c 529 g 375 t
ORIGIN
Query Match 92.1%; Score 56.2; DB 6; Length 1867;
Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTCTGCACATCTTTGGTTCCTGCTGCGCGCCCTCTCTCTACCGCATATCCAA 60
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Db 907 TTCTGCACATCTTTGGCACCTGCTGCGCGCCCTCTCTCTACCGCATATCCAA 966
QY 61 G 61
Db 967 G 967
RESULT 7
AF214520
LOCUS AF214520 1873 bp mRNA linear MAM 03-JUN-2000
DEFINITION Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
mRNA, complete cds.
ACCESSION AF214520
VERSION AF214520.1 GI:8215683
KEYWORDS
SOURCE
ORGANISM
Sus scrofa.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
and Andersson,L.
A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle
JOURNAL Science 288 (5469), 1248-1251 (2000)
MEDLINE 20280150
PUBMED 10818001
AUTHORS 2 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
Sweden
Location/Qualifiers
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/chromosome="15"
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1. .1873
gene

/gene="PRKAG3"
1. .1395
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/product="AMP-activated protein kinase gamma subunit"
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/db_xref="GI:8215684"
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HFMOEHTCYDAMATSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKKQSFVGMIT
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ALVLSFAGIDALGA"
BASE COUNT 382 a 580 c 535 g 376 t
ORIGIN
Query Match 92.1%; Score 56.2; DB 4; Length 1873;
Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTCTGCACATCTTTGGTTCCTGCTGCGCGCCCTCTCTCTACCGCATATCCAA 60
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Db 913 TTCTGCACATCTTTGGCACCTGCTGCGCGCCCTCTCTCTACCGCATATCCAA 972
QY 61 G 61
Db 973 G 973
RESULT 8
AX099800
LOCUS AX099800 1873 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 27 from Patent WO0120003.
ACCESSION AX099800
VERSION AX099800.1 GI:13538834
KEYWORDS
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and
Chardon,P.
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
Location/Qualifiers
source 1. .1873
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/codon_start=1
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/db_xref="GI:13538835"
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BASE COUNT 382 a 580 c 535 g 376 t
ORIGIN

Query Match 92.1%; Score 56.2; DB 6; Length 1873;
Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTGACATCTTTGGTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCAA 60
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QY 61 G 61
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Db 973 G 973

RESULT 9
AX398331
LOCUS
DEFINITION Sequence 1 from Patent WO220850.
ACCESSION AX398331
VERSION AX398331.1 GI:21261106
KEYWORDS
SOURCE
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 1 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)

FEATURES
source
1. .1873
/organism="Sus scrofa"
/db_xref="taxon:9823"
1. .1395
/note="unnamed protein product"
/codon_start=1
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ALVLSAPGIDALGA"

BASE COUNT 382 a 580 c 535 g 376 t

ORIGIN
Query Match 92.1%; Score 56.2; DB 6; Length 1873;
Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTGACATCTTTGGTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCAA 60
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Db 913 TTCTGACATCTTTGGCACCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCAA 972

QY 61 G 61
|
Db 973 G 973

RESULT 10
AX398333
LOCUS
DEFINITION Sequence 3 from Patent WO220850.
ACCESSION AX398333
VERSION AX398333.1 GI:21261108
KEYWORDS
SOURCE pig.

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 3 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)

FEATURES
source
1. .1873
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1. .1395
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HFMEQHTCYDAMATSSKLIVFTDMLTLEIKKAFFALVANGVRAAPLWDSKKQSFVGLTI
TDFILVLRYYRSPVQIYEIEHKIETWREIYLQGCPLVSI SPNDSLFEAVYALI
KNRIHLRVLDPVSGAVLHILTHKRLLFHFGTLPRPSFLYRT IQDLGIGTFRDL
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ALVLSAPGIDALGA"

BASE COUNT 381 a 581 c 535 g 376 t

ORIGIN
Query Match 92.1%; Score 56.2; DB 6; Length 1873;
Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTGACATCTTTGGTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCAA 60
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Db 913 TTCTGACATCTTTGGCACCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCAA 972

QY 61 G 61
|
Db 973 G 973

RESULT 11
AX398335
LOCUS
DEFINITION Sequence 5 from Patent WO0220850.
ACCESSION AX398335
VERSION AX398335.1 GI:21261110
KEYWORDS
SOURCE pig.

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1
AUTHORS Rothschild,M.F., Ciobanu,D.C., Malek,M. and Plastow,G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 5 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)

FEATURES
source
1. .1873
/organism="Sus scrofa"
/db_xref="taxon:9823"
1. .1395
/note="unnamed protein product"
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HFMEQHTCYDAMATSSKLIVFTDMLTLEIKKAFFALVANGVRAAPLWDSKKQSFVGLTI

AX398339
LOCUS AX398339 1873 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 9 from Patent WO0220850.
ACCESSION AX398339
VERSION AX398339.1 GI:21261114
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
AUTHORS Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 9 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
FEATURES
source
1. .1873
/organism="Sus scrofa"
/db_xref="taxon:9823"
1. .1395
/note="unnamed protein product"
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HFMEQHTCDAMATSKLVIDPMLKKAFFALVANGVQAAPLWDSKKSFGVGLTI
TDFILVHRYRSPPLVQIYEIEHKIETWREIYLOGCFKPLVISPNDLSFEAYALI
KNRIHLPLVDPSGAVLHILTHKRLKELHIFGTLPRPSFLYRTIQDLIGTFRDL
AVYLETAPILTALDIFDVRVSALPVVNETGVVGLYSRFDVIHLAAQQYINHLDMNV
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ALVISPAGIDALGA"

BASE COUNT 383 a 580 c 534 g 376 t
ORIGIN
Query Match 92.1%; Score 56.2; DB 6; Length 1873;
Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTCCTGCACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCAAA 60
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Db 913 TTCCTGCACATCTTTGGCACCTGCTGCCCGGCCCTCTCTCTACCGCACTATCAAA 972
Qy 61 G 61
|
Db 973 G 973

RESULT 12
AX398337
LOCUS AX398337 1873 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 7 from Patent WO0220850.
ACCESSION AX398337
VERSION AX398337.1 GI:21261112
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
AUTHORS Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 7 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
FEATURES
source
1. .1873
/organism="Sus scrofa"
/db_xref="taxon:9823"
1. .1395
/note="unnamed protein product"
/codon_start=1
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ALVISPAGIDALGA"

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Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTCCTGCACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCAAA 60
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Db 913 TTCCTGCACATCTTTGGCACCTGCTGCCCGGCCCTCTCTCTACCGCACTATCAAA 972
Qy 61 G 61
|
Db 973 G 973

RESULT 13
AX398337
LOCUS AX398337 1873 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 7 from Patent WO0220850.
ACCESSION AX398337
VERSION AX398337.1 GI:21261112
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
AUTHORS Rothschild, M.F., Ciobanu, D.C., Malek, M. and Plastow, G.
TITLE Novel prkag3 alleles and use of the same as genetic markers for
reproductive and meat quality traits
JOURNAL Patent: WO 0220850-A 7 14-MAR-2002;
Iowa State University Research Foundation, Inc. (US)
FEATURES
source
1. .1873
/organism="Sus scrofa"
/db_xref="taxon:9823"
1. .1395
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD32628.1"
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ALVISPAGIDALGA"

BASE COUNT 383 a 580 c 534 g 376 t
ORIGIN
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Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTCCTGCACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCAAA 60
|||||
Db 913 TTCCTGCACATCTTTGGCACCTGCTGCCCGGCCCTCTCTCTACCGCACTATCAAA 972
Qy 61 G 61
|
Db 973 G 973

RESULT 14
AX099804
LOCUS AX099804 2022 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 31 from Patent WO0120003.
ACCESSION AX099804
VERSION AX099804.1 GI:13538838
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 2022)
AUTHORS Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
Chardon, P.
TITLE Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL Patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
FEATURES
source
1. .2022
/organism="Sus scrofa"

BASE COUNT 383 a 580 c 534 g 376 t
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Query Match 92.1%; Score 56.2; DB 6; Length 1873;
Best Local Similarity 95.1%; Pred. No. 3.5e-08;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTCCTGCACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCAAA 60
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Db 913 TTCCTGCACATCTTTGGCACCTGCTGCCCGGCCCTCTCTCTACCGCACTATCAAA 972
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Db 973 G 973

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        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY      61 G 61
Db      1123 G 1123

RESULT 15
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LOCUS      AX281580      1722 bp      DNA      linear      PAT 03-NOV-2001
DEFINITION Sequence 3 from Patent WO0177305.
ACCESSION  AX281580
VERSION     AX281580.1 GI:16608831
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Andersson,L., Luthman,H. and Marklund,S.
TITLE      Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL    Patent: WO 0177305-A 3 18-OCT-2001;
            Arexis AB (SE)
FEATURES
            Location/Qualifiers
            source
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              /db_xref="taxon:9606"
BASE COUNT    321 a  504 c  534 g  363 t
ORIGIN

Query Match      75.7%; Score 46.2; DB 6; Length 1722;
Best Local Similarity 86.4%; Pred. No. 6.4e-05;
Matches 51; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      3 CCTGCCACATCTTTGGTTCCTTCCTCCCGCGCCCTCCTTCCTCTACCGCAGTATCCAAAG 61
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1510 CCATCCTTAACACAGCTTCCCTCCCTCCCGCGCCCTCCTTCCTCTACCGCAGTATCCAAAG 1568
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Search completed: June 13, 2003, 04:39:46
Job time : 194.613 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 01:37:39 ; Search time 22.1613 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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22:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	547	22	Human AMP-activate
2	61	100.0	1647	22	PRKAG3 cDNA. Homo
3	61	100.0	2109	22	Human AMPK gamma s
4	61	100.0	2115	22	Human AMPK gamma s
5	56.2	92.1	1867	22	Pig AMPK gamma sub
6	56.2	92.1	1873	22	Pig AMPK gamma sub
7	56.2	92.1	1873	24	Pig wild-type PRKA
8	56.2	92.1	1873	24	AA036456
9	56.2	92.1	1873	24	AA036457
					Pig PRKAG3 polymor

10	56.2	92.1	1873	24	AAD36459	Pig PRKAG3 polymor	
11	56.2	92.1	1873	24	AAD36460	Pig PRKAG3 polymor	
12	56.2	92.1	2022	22	AAD03321	Sus scrofa PRKAG3	
13	46.2	75.7	1722	22	AAH43683	PRKAG3 intron 4 -	
c	14	28	45.9	3238	23	AAH77333	DNA encoding novel
15	28	45.9	9979	22	AAK81194	Human immune/haema	
16	28	45.9	13673	22	AAK76548	Human immune/haema	
17	28	45.9	13673	22	AAK81195	Human immune/haema	
c	18	27.4	44.9	566	22	AA055559	Mammalian vestibul
c	19	27.4	44.9	2289	23	ABL08199	Drosophila melanog
c	20	27.4	44.9	4363	23	ABL08198	Drosophila melanog
21	26.8	43.9	4984	23	AA07842	Nucleotide sequenc	
22	26.6	43.6	2322	21	AAC64727	Mouse tumour suppr	
23	26.6	43.6	2416	21	AAC64726	Mouse tumour suppr	
24	26	42.6	1176	23	ABI97971	Non-endogenous hum	
25	26	42.6	1231	17	AAT38911	B2'-bradykinin rece	
26	26	42.6	1231	17	AAT38912	B2'-bradykinin rece	
27	26	42.6	1231	21	AAF20881	Human bradykinin r	
28	26	42.6	1231	21	AAF20882	Human bradykinin r	
29	26	42.6	1231	21	AAF20890	Human bradykinin r	
30	26	42.6	1231	21	AAF20891	Human bradykinin r	
31	26	42.6	1231	21	AAA34759	Human adenosine re	
32	26	42.6	1231	21	AAA34760	Human adenosine re	
33	26	42.6	1231	21	AAA34768	Human adenosine re	
34	26	42.6	1231	21	AAA34769	Human adenosine re	
35	26	42.6	1378	17	AAT10666	Human bradykinin B	
36	26	42.6	1682	21	AAC98901	Human pancreatic c	
37	26	42.6	2239	21	AAF20879	Human bradykinin r	
38	26	42.6	2239	21	AAF20888	Human bradykinin r	
39	26	42.6	2239	21	AAA34757	Human adenosine re	
40	26	42.6	2239	21	AAA34766	Human adenosine re	
41	26	42.6	2478	21	AAF20880	Human bradykinin r	
42	26	42.6	2478	21	AAF20889	Human bradykinin r	
43	26	42.6	2478	21	AAA34758	Human adenosine re	
44	26	42.6	2478	21	AAA34767	Human adenosine re	
45	26	42.6	7328	21	AAF20874	Human bradykinin r	

ALIGNMENTS

RESULT 1

AB08485

ID ABA08485 standard; cDNA; 547 BP.

AC ABA08485;

DT 11-JAN-2002 (first entry)

DE Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261.

XX

Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibito; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteoplastic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnary; antiulcer; ss.

OS Homo sapiens.

XX

WO200157188-A2.

PN

XX

09-AUG-2001.

PD

XX

05-FEB-2001; 2001WO-US03800.

PF

XX

```
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PA (HYSE-) HYSEQ INC.
XX
XX
PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457740/49.
DR P-PSDB; ABB11241.
XX
XX Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
XX Claim 1; Page 429; 1963pp; English.
XX
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
SQ Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
Query Match 100.0%; Score 61; DB 22; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTGACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCAA 60
DB 270 TTCTGACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCAA 329
QY 61 G 61
DB 330 G 330
DB
RESULT 2
AAH43685
ID AAH43685 standard; cDNA; 1647 BP.
XX
```

```
AC AAH43685;
XX 21-JAN-2002 (first entry)
XX
XX PRKAG3 CDNA.
XX
XX Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
KW metabolic disease; diabetes; obesity; substitution; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 20..1489
XX FT /tag= a
XX FT /product= "PRKAG3"
XX FT variation 230
XX FT /tag= b
XX FT /label= "C230G"
XX FT /note= "Causes P71A"
XX FT variation 559
XX FT /tag= c
XX FT /label= "T559C"
XX FT /note= "Silent variation"
XX FT variation 1037
XX FT /tag= d
XX FT /label= "C1037T"
XX FT /note= "Causes R340W"
XX WO200177305-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-SE00765.
XX
XX 07-APR-2000; 2000US-195665P.
XX
XX (AREX-) AREXIS AB.
XX
XX Andersson L, Luthman H, Marklund S;
XX WPI; 2001-657170/75.
XX P-PSDB; QQB47679.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
XX Disclosure; Fig 5; 25pp; English.
XX
XX This sequence represents the full length cDNA encoding the human
CC AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
CC the presence of the PRKAG3 DNA, or a variant, is useful in determining
CC a risk estimate of a metabolic disease, such as diabetes or obesity,
CC in a subject. The variation may occur in exons 3, 4 or 10. In exon
CC 3 variation may be a substitution of a G for a C at nucleotide 320,
CC resulting in the amino acid substitution P71A; in exon 4 variation may
CC be a substitution of a T for a C at nucleotide 550; and in exon 10
CC variation may be a substitution of a T for a C at nucleotide 1037,
CC resulting in the amino acid substitution R340W. There may also be
CC nucleotide variation in intron 6. The numbering of these
CC variations is based on the full length cDNA as given, rather than on
CC position 1 of the open reading frame.
XX
SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
Query Match 100.0%; Score 61; DB 22; Length 1647;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTGACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCAA 60
DB 1007 TTCTGACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTACCGCACTATCCAA 1066
```


CC complete PRKAG3. Mutation in Prkag3 results in an altered regulation of
CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
CC useful as therapeutic for treating carbohydrate metabolism disorders such
CC as diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.

XX
SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;

Query Match 100.0%; Score 61; DB 22; Length 2115;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGTCACATCTTTGGTTCCCTGCTGCGCGCGCCCTCTCCCTACCGCACTATCCAA 60
|||||
DB 913 TTCTGTCACATCTTTGGTTCCCTGCTGCGCGCGCCCTCTCCCTACCGCACTATCCAA 972
|||||

QY 61 G 61
DB 973 G 973

RESULT 5
AAD03295
ID AAD03295 standard; cDNA; 1867 BP.

XX
AC AAD03295;

DT 13-JUN-2001 (first entry)

DE Pig AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.

XX
KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
KW chromosome 15; ss.

OS
Sus scrofa.

Key Location/Qualifiers
5'UTR 1..471
CDS /tag= a
472..1389
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/product= "Sus scrofa PRKAG3 protein"
1390..1867
/tag= c

3'UTR

WO200120003-A2.

22-MAR-2001.

11-SEP-2000; 2000WO-EP09896.

10-SEP-1999; 99EP-0402236.

18-MAY-2000; 2000EP-0401388.

(INRG) INRA INST NAT RECH AGRONOMIQUE.
(ANDE/) ANDERSSON L.
(LOOF/) LOOFT C.

(KALM/) KALM E.

Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
Iannuccielli N, Gellin J, Le Roy P, Chardon P;
WPI: 2001-244810/25.
P-PSDB; AAE00220.

New variants of the gamma subunit of vertebrate adenosine
monophosphate-activated kinase for diagnosis or treatment of disorders
associated with energy metabolism such as diabetes, obesity, and
myopathy -

Claim 12; Fig 2; 7lpp; English.

The present sequence is a cDNA encoding pig adenosine monophosphate
(AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.
Mutation in Prkag3 results in an altered regulation of carbohydrate
metabolism, particularly in skeletal muscle. PRKAG3 is useful as
therapeutic for treating carbohydrate metabolism disorders such as
diabetes, obesity, and disorders associated with muscle metabolism
such as myopathy and cardiovascular diseases, to modulate AMPK
activity, and for restoring a normal AMPK function. PRKAG3 sequence
and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic disorder,
preferably a carbohydrate metabolism disorder. Primers that can detect
a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
useful for detecting a dysfunction of carbohydrate metabolism resulting
from the expression of a functionally altered allele of PRKAG3.
Transgenic animal and host cell transformed with PRKAG3 or a
heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
screening compounds able to modulate AMPK activity. Nucleic acid
encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
in a sequence encoding the first cystathione beta synthase (CBS) domain
of PRKAG3 and is useful in gene therapy.

Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;

Query Match 92.1%; Score 56.2; DB 22; Length 1867;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTGTCACATCTTTGGTTCCCTGCTGCGCGCGCCCTCTCCCTACCGCACTATCCAA 60
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DB 907 TTCTGTCACATCTTTGGTACCCCTGCTGCGCGCGCCCTCTCCCTACCGCACTATCCAA 966
61 G 61
967 G 967

RESULT 6
AAD03319
ID AAD03319 standard; cDNA; 1873 BP.

XX
AC AAD03319;

DT 13-JUN-2001 (first entry)

DE Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.

XX
KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
KW chromosome 15; ss.

OS
Sus scrofa.

Key Location/Qualifiers
FH 1..1395
FT CDS /tag= a

FT XX /product= "Sus scrofa complete Prkg3 protein"
PN XX
XX WO200120003-A2.
PD 22-MAR-2001.
XX
XX 11-SEP-2000; 2000WO-EP09896.
XX
XX 10-SEP-1999; 99EP-0402236.
PR 18-MAY-2000; 2000EP-0401388.
XX
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.
PA (LOOE/) LOOFT C.
PA (KALM/) KALM E.
XX
XX Andersson L, Loofft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
XX WPI: 2001-244810/25.
DR P-PSDB; AAE00222.
XX
XX New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment of disorders
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy -
XX
PS Claim 12; Page 62-64; 71pp; English.
XX
XX The present sequence is a cDNA encoding pig adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC complete PRKAG3. Prkg3 gene is located in the RN locus of chromosome
CC 15. Mutation in prkg3 results in an altered regulation of carbohydrate
CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
CC therapeutic for treating carbohydrate metabolism disorders such as
CC diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkg3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX
XX Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
Query Match 92.1%; Score 56.2; DB 22; Length 1873;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTCTGCGACATCTTTGGTTCCTGCTGCCGCCGCCCTCTCTCTACCGCATTCCAA 60
DB 913 TTCTGCGACATCTTTGGCACCTGCTGCCGCCGCCCTCTCTCTACCGCATTCCAA 972
QY 61 G 61
DB 973 G 973
RESULT 7
AAD36456
ID AAD36456 standard; DNA; 1873 BP.
XX
AC AAD36456;
XX
DT 09-AUG-2002 (first entry)

XX Pig wild-type PRKAG3 gene.
DE
XX
XX AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; ds.
XX
XX Sus scrofa.
OS
XX
FH Key Location/Qualifiers
FT CDS 1..1395
FT /tag= a
FT /product= "Pig PRKAG3 wild-type protein"
FT replace (89, C)
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (154, A)
FT /tag= c
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (395, A)
FT /tag= d
FT /standard_name= "Single nucleotide polymorphism (SNP)"
FT replace (599, A)
FT /tag= e
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200220850-A2.
XX
XX 14-MAR-2002.
PD
XX 10-SEP-2001; 2001WO-US28283.
XX
XX 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
XX Rothschild MF, Globanu DC, Malek M, Plastow G;
PI
XX WPI: 2002-393850/42.
DR P-PSDB; AAE22984.
XX
XX Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene -
XX
XX Claim 17; Fig 1; 109pp; English.
XX
XX The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g. pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig wild-type PRKAG3 gene.
XX
XX Sequence 1873 BP; 382 A; 580 C; 535 G; 376 T; 0 other;
Query Match 92.1%; Score 56.2; DB 24; Length 1873;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTCTGCGACATCTTTGGTTCCTGCTGCCGCCGCCCTCTCTCTACCGCATTCCAA 60
DB 913 TTCTGCGACATCTTTGGCACCTGCTGCCGCCGCCCTCTCTCTACCGCATTCCAA 972
QY 61 G 61
DB 973 G 973

```
RESULT 8
AAD36457
ID AAD36457 standard; DNA; 1873 BP.
XX
AC AAD36457;
XX
DT 09-AUG-2002 (first entry)
XX
DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; variant; ds.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT CDS 1..1395
FT /tag= a
FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-30)"
FT replace (89, C)
FT /tag= b
FT variation
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200220850-A2.
XX
PD 14-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US28283.
XX
PR 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
DR WPI; 2002-393850/42.
DR P-PSDB; AAE22985.
XX
PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene
XX
PS Disclosure; Page 89-91; 109pp; English.
XX
CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-30).
XX
SQ Sequence 1873 BP; 382 A; 535 C; 376 T; 0 other;
```

```
Query Match 92.1%; Score 56.2; DB 24; Length 1873;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 TTCTCGACATCTTGGTTCCTGCTGCCCGCCCTCTTCCTACCGCACTATCCAA 60
|||||
Db 913 TTCTCGACATCTTGGACACCTGCTGCCCGCCCTCTTCCTACCGCACTATCCAA 972
|||||
QY 61 G 61
|
Db 973 G 973
```

```
RESULT 9
AAD36458
ID AAD36458 standard; DNA; 1873 BP.
XX
AC AAD36458;
XX
DT 09-AUG-2002 (first entry)
XX
DE Pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
XX
KW AMP activated protein kinase regulatory gamma subunit; PRKAG3 gene;
KW screening; meat quality; single nucleotide polymorphism; SNP; pig;
KW gene; variant; ds.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT CDS 1..1395
FT /tag= a
FT /product= "Pig PRKAG3 polymorphic variant (PRKAG3-52)"
FT replace (154, A)
FT /tag= b
FT variation
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200220850-A2.
XX
PD 14-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US28283.
XX
PR 08-SEP-2000; 2000US-231045P.
PR 08-JAN-2001; 2001US-260239P.
PR 18-JUN-2001; 2001US-299111P.
XX
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
PI Rothschild MF, Ciobanu DC, Malek M, Plastow G;
XX
DR WPI; 2002-393850/42.
DR P-PSDB; AAE22986.
XX
PT Screening animals to determine those likely to produce larger litters
PT and improved meat quality traits involves assaying for the presence of
PT polymorphisms in the AMP activated protein kinase regulatory gamma
PT subunit gene
XX
PS Claim 34; Page 93-95; 109pp; English.
XX
CC The invention relates to a method for screening animals to determine
CC those more likely to produce large litters and improved meat quality
CC traits. The method involves assaying for the presence of a genotype
CC in the sample of genetic material obtained from animal. The genotype
CC is characterised by polymorphism(s) in the AMP activated protein
CC kinase regulatory gamma subunit (PRKAG3) gene. The method is used
CC for screening animals e.g., pigs to determine those most likely to
CC exhibit improved meat quality traits and to produce larger litters.
CC The present sequence is pig PRKAG3 polymorphic variant DNA (PRKAG3-52).
XX
SQ Sequence 1873 BP; 383 A; 580 C; 376 T; 0 other;
```

```
Query Match 92.1%; Score 56.2; DB 24; Length 1873;
Best Local Similarity 95.1%; Pred. No. 6.2e-09;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 TTCTCGACATCTTGGTTCCTGCTGCCCGCCCTCTTCCTACCGCACTATCCAA 60
|||||
Db 913 TTCTCGACATCTTGGACACCTGCTGCCCGCCCTCTTCCTACCGCACTATCCAA 972
|||||
QY 61 G 61
|
Db 973 G 973
```


RESULT 12
 AAD03321
 ID AAD03321 standard; DNA; 2022 BP.
 XX
 AC AAD03321;
 XX
 DT 13-JUN-2001 (first entry)
 XX
 DE Sus scrofa PRKAG3 splice variant DNA.
 XX
 KW Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiatic; gene therapy; ds.
 XX
 OS Sus scrofa.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..1545
 FT /*tag= a
 FT /product= "Sus scrofa Prkag3 splice variant"
 XX
 PN WO200120003-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 11-SEP-2000; 2000WO-EF09896.
 XX
 PR 10-SEP-1999; 99EP-0402236.
 PR 18-MAY-2000; 2000EP-0401388.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (ANDE/) ANDERSSON L.
 PA (LOOF/) LOOFT C.
 PA (KALM/) KALM E.
 XX
 PI Andersson L, Loof C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
 PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
 XX
 DR WPI: 2001-244810/25.
 DR P-PSDB; AAE00224.
 XX
 PT New variants of the gamma subunit of vertebrate adenosine
 PT monophosphate-activated kinase for diagnosis or treatment of disorders
 PT associated with energy metabolism such as diabetes, obesity, and
 PT myopathy
 XX
 PS Claim 12; Page 69; 71pp; English.
 XX
 CC The present sequence is pig adenosine monophosphate (AMP)-activated
 CC kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice
 CC variant DNA. Prkag3 gene is located in the RN locus of chromosome 15.
 CC Mutation in prkag3 results in an altered regulation of carbohydrate
 CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as
 CC therapeutic for treating carbohydrate metabolism disorders such as
 CC diabetes, obesity, and disorders associated with muscle metabolism
 CC such as myopathy and cardiovascular diseases, to modulate AMPK
 CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
 CC and its functionally altered mutants are useful for the diagnostic
 CC evaluation, genetic testing and prognosis of a metabolic disorder,
 CC preferably a carbohydrate metabolism disorder. Primers that can detect
 CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
 CC useful for detecting a dysfunction of carbohydrate metabolism resulting
 CC from the expression of a functionally altered allele of PRKAG3.
 CC Transgenic animal and host cell transformed with PRKAG3 or a
 CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
 CC screening compounds able to modulate AMPK activity. Nucleic acid
 CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
 CC in a sequence encoding the first cystathione beta synthase (CBS) domain
 CC of PRKAG3 and is useful in gene therapy.

XX

SQ Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
 Query Match 92.1%; Score 56.2; DB 22; Length 2022;
 Best Local Similarity 95.1%; Pred. No. 6.2e-09;
 Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TTCTGACATCTTGGTTCCTGCTGCGCGCGCTCTCTCTACCGCAGTATCCAA 60
 Db 1063 TTCTGACATCTTGGCACCCTGCTGCGCGCGCTCTCTCTACCGCAGTATCCAA 1122
 QY 61 G 61
 Db 1123 G 1123
 RESULT 13
 AAH43683
 ID AAH43683 standard; DNA; 1722 BP.
 XX
 AC AAH43683;
 XX
 DT 21-JAN-2002 (first entry)
 XX
 DE PRKAG3 intron 4 - intron 10.
 XX
 KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
 KW metabolic disease; diabetes; obesity; substitution; ds.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Intron 1..13
 FT /*tag= a
 FT /number= "Intron 4"
 FT /note= "3' portion of Intron 4"
 FT exon 14..95
 FT /*tag= b
 FT /number= "Exon 5"
 FT /tag= c
 FT /number= "Intron 5"
 FT exon 553..611
 FT /*tag= d
 FT /number= "Exon 6"
 FT intron 612..736
 FT /*tag= e
 FT /number= "Intron 6"
 FT exon 737..782
 FT /*tag= f
 FT /number= "Exon 7"
 FT intron 783..986
 FT /*tag= g
 FT /number= "Intron 7"
 FT exon 987..1041
 FT /*tag= h
 FT /number= "Exon 8"
 FT intron 1042..1242
 FT /*tag= i
 FT /number= "Intron 8"
 FT exon 1243..1369
 FT /*tag= j
 FT /number= "Exon 9"
 FT intron 1370..1522
 FT /*tag= k
 FT /number= "Intron 9"
 FT exon 1523..1688
 FT /*tag= l
 FT /number= "Exon 10"
 FT intron 1689..1722
 FT /*tag= i
 FT /number= "Intron 10"
 FT /note= "5' portion of intron 10"
 XX

PN WO200177305-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-SB00765.
XX
PR 07-APR-2000; 2000US-195665P.
XX
PA (AREX-) AREXIS AB.
XX
XX Andersson L, Luthman H, Marklund S;
XX WPI; 2001-657170/75.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
XX Example 1; Fig 3; 25pp; English.
XX
XX The sequences given in AH43681-84 represents genomic fragments
CC encoding the human AMP-activated protein kinase gamma 3 subunit
CC (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
CC is useful in determining a risk estimate of a metabolic disease,
CC such as diabetes or obesity, in a subject. The variation may occur
CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of
CC a G for a C at nucleotide 320, resulting in the amino acid
CC substitution P71A; in exon 4 variation may be a substitution of a
CC T for a C at nucleotide 550; and in exon 10 variation may be a
CC substitution of a T for a C at nucleotide 1037, resulting in the
CC amino acid substitution R340W. There may also be nucleotide variation
CC in intron 6.
XX
XX Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0 other;
SQ Query Match 75.7%; Score 46.2; DB 22; Length 1722;
Best Local Similarity 86.4%; Pred. No. 1e-05;
Matches 51; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CCTGCACATCTTTGGTTCCTGCTGCCCGCCCTCTTCTACCGCACTATCCAAAG 61
|| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1510 CCATCCTAACGAGGTTCCCTGCTGCCCGCCCTCTTCTACCGCACTATCCAAAG 1568

RESULT 14
AAS77333/c
XX ID AAS77333 standard; cDNA; 3238 BP.
XX AC AAS77333;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #13137.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX

DR WPI; 2001-639362/73.
DR P-PSDB; ABG13146.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 1; SEQ ID No 13137; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 3238 BP; 926 A; 915 C; 858 G; 539 T; 0 other;
SQ Query Match 45.9%; Score 28; DB 23; Length 3238;
Best Local Similarity 66.7%; Pred. No. 8.6;
Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TCCTGCACATCTTTGGTTCCTGCTGCCCGCCCTCTTCTACCGCACTATCCAAAG 61
|| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2820 TGTGCGACCTCACCGGTTACGATCTGCGAGTGCACCTCTTTCTGCGCACTGCCCATG 2761

RESULT 15
AAK81194
XX ID AAK81194 standard; DNA; 9979 BP.
XX AC AAK81194;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36006.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX OS Homo sapiens.
XX PN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01354.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0215647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.

PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUNA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 36006; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased

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OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:37:44 ; Search time 151.839 Seconds
(without alignments)
6506.409 Million cell updates/sec

Title: US-09-826-581-5_COPY_1007_1067
Perfect score: 61
Sequence: 1 ttcctgcacatcttggttc.....cctctaccgcactatccaag 61

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmt.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_estl.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56.2	92.1	572	BI344527	BI344527 373008 MA
2	29.4	48.2	1173	BM556730	BM556730 AGENCOURT
3	28	45.9	389	AQ997354	AQ997354 RPT-23-2
4	27.6	45.2	626	BF528264	BF528264 602043043
5	27.4	44.9	619	BE978092	BE978092 bs73q07.y
6	27.4	44.9	701	BE408262	BE408262 601302612

C 7	27.4	44.9	706	12	BG744371
C 8	27.4	44.9	715	12	BF488250
C 9	27.4	44.9	754	9	A1063338
C 10	27.4	44.9	757	12	BG479057
C 11	27.4	44.9	913	12	BG290491
C 12	27.4	44.9	921	10	BE275257
C 13	27.4	44.9	926	12	BG291149
C 14	27.2	44.6	569	14	BQ048516
C 15	27.2	44.6	887	12	BG174779
C 16	26.8	43.9	442	9	A1583845
C 17	26.8	43.9	543	14	W03359
C 18	26.8	43.9	606	13	BI735773
C 19	26.8	43.9	617	13	BI526922
C 20	26.8	43.9	668	10	BE307400
C 21	26.8	43.9	693	13	BG974543
C 22	26.8	43.9	720	13	BI155021
C 23	26.8	43.9	815	13	BI664379
C 24	26.8	43.9	836	12	BF136865
C 25	26.8	43.9	970	12	BG288506
C 26	26.8	43.9	973	14	BQ715536
C 27	26.8	43.9	1060	12	BF581580
C 28	26.8	43.9	1088	12	BF788164
C 29	26.8	43.9	1106	14	BM917705
C 30	26.8	43.9	1647	13	BM564338
C 31	26.8	43.9	1794	11	BC014747
C 32	26.6	43.6	322	10	AW486152
C 33	26.6	43.6	324	14	W53632
C 34	26.6	43.6	343	10	AW478129
C 35	26.6	43.6	392	9	AA009100
C 36	26.6	43.6	432	9	AA030295
C 37	26.6	43.6	504	12	BF470814
C 38	26.6	43.6	517	9	A1746867
C 39	26.6	43.6	526	9	A1509176
C 40	26.6	43.6	527	10	BE030622
C 41	26.6	43.6	553	12	BE948793
C 42	26.6	43.6	556	9	AL661556
C 43	26.6	43.6	606	13	BI134085
C 44	26.6	43.6	611	10	BB618484
C 45	26.6	43.6	643	9	A1726042

ALIGNMENTS

RESULT 1
BI344527
LOCUS 373008 MARC 2PTG Sus scrofa cDNA 5', mRNA linear EST 30-JUL-2001
DEFINITION 373008 MARC 2PTG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BI344527
VERSION BI344527.1 GI:15037807
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 572)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keefe,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGACACGCTATGACCAT

BACKWARD: GTTTCCTCCACTCAGCAGC
Plate: 119 row: I column: 11
Seq primer: AFTTAGTGACACTATAG.
Location/Qualifiers
1. .572
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 106 a 190 c 151 g 124 t 1 others
ORIGIN

Query Match 92.1%; Score 56.2; DB 13; Length 572;
Best Local Similarity 95.1%; Pred. No. 4.3e-06;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTCGACATCTTGGTTCCTGCTGCGCGCCCTCTTCTCTACCGCACTATCCAA 60
|||||
Db 169 TTCTCGACATCTTGGCACCTGCTGCGCGCCCTCTTCTCTACCGCACTATCCAA 228
|||||

QY 61 G 61
|
Db 229 G 229

RESULT 2
BM556730/c
LOCUS
DEFINITION BM556730.1 1173 bp mRNA linear EST 20-FEB-2002
AGENCOURT_6540753 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737918
5', mRNA sequence.
ACCESSION BM556730
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12748 row: m column: 23
High quality sequence stop: 473.
Location/Qualifiers
1. .1173
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5737918"
/clone_lib="NIH_MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
BASE COUNT 218 a 400 c 377 g 175 t 3 others
ORIGIN

Query Match 48.2%; Score 29.4; DB 13; Length 1173;
Best Local Similarity 57.1%; Pred. No. 1.1e-02;
Matches 37; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Best Local Similarity 70.9%; Pred. No. 1.5e-02;
Matches 39; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 5 TGCACATCTTGGTTCCTGCTGCGCGCCCTCTTCTCTACCGCACTATCCAA 59
|||||
Db 897 TGCACATCTTGGTTCCTGCGCGCCCTCTTCTCTACCGCACTATCCAA 843
|||||

RESULT 3
AQ997354
LOCUS
DEFINITION AQ997354.1 389 bp DNA linear GSS 24-FEB-2000
RPCI-23-271P21-TV RPCI-23 Mus musculus genomic clone RPCI-23-271P21
DNA sequence.
ACCESSION AQ997354
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Aklnret
B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-271P21.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (Info@resgen.com). BAC end page:
http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
Plate: 271 row: P column: 21
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .389
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-271P21"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 99 a 106 c 96 g 88 t
ORIGIN

Query Match 45.9%; Score 28; DB 17; Length 389;
Best Local Similarity 71.2%; Pred. No. 3.1e-02;
Matches 37; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 TCTCGACATCTTGGTTCCTGCTGCGCGCCCTCTTCTCTACCGCACTATCCGAC 53
|||||
Db 54 TCTCGACATCTTGGTTCCTGCTGCGCGCCCTCTTCTCTACCGCACTATCCGAC 105
|||||

RESULT 4
BF528264/c

LOCUS BF528264 626 bp mRNA linear EST 11-DEC-2000
 DEFINITION 602043043F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180619
 5', mRNA sequence.
 ACCESSION BF528264
 VERSION BF528264.1 GI:11615627
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 626)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM9492 row: f column: 12
 High quality sequence start: 130
 High quality sequence stop: 605.
 Location/Qualifiers
 1..626
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4180619"
 /clone_lib="NCL_CGAP_Brn67"
 /tissue_type="anaplastic oligodendroglioma with lp/19q loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: brain; Vector: pCMV-Sport6; Site.1: NotI; Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCL_CGAP Library."
 BASE COUNT 146 a 157 c 187 g 136 t
 ORIGIN
 Query Match 45.2%; Score 27.6; DB 12; Length 626;
 Best Local Similarity 67.2%; Pred. No. 4.3e+02;
 Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 TTCTCGACATCTTTGGTTCCTCTGCGCCGCCCTCTCTCTACCGCATATCC 58
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 169 TGGTTGGCATCTAGCATGCTGTCGCCGCCCTCTCTCTCTACCGCATATCC 112
 RESULT 5
 BE978092/c
 LOCUS BE978092 619 bp mRNA linear EST 04-OCT-2000
 DEFINITION bs73q07.v1 Drosophila melanogaster adult testis library Drosophila melanogaster cDNA clone bs73q07 5', mRNA sequence.
 ACCESSION BE978092
 VERSION BE978092.1 GI:10609221
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 619)
 AUTHORS Andrews, J., Bouffard, G. and Oliver, B.
 TITLE Drosophila melanogaster testis expressed sequence tags
 JOURNAL Unpublished (1999)
 COMMENT Contact: Brian Oliver
 Laboratory of Cellular and Developmental Biology
 NIDDK, National Institutes of Health
 6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
 Fax: (301) 496 5239

LOCUS BF528264 626 bp mRNA linear EST 11-DEC-2000
 DEFINITION 602043043F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180619
 5', mRNA sequence.
 ACCESSION BF528264
 VERSION BF528264.1 GI:11615627
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 626)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM9492 row: f column: 12
 High quality sequence start: 130
 High quality sequence stop: 605.
 Location/Qualifiers
 1..626
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4180619"
 /clone_lib="NCL_CGAP_Brn67"
 /tissue_type="anaplastic oligodendroglioma with lp/19q loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: brain; Vector: pCMV-Sport6; Site.1: NotI; Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCL_CGAP Library."
 BASE COUNT 146 a 157 c 187 g 136 t
 ORIGIN
 Query Match 45.2%; Score 27.6; DB 12; Length 626;
 Best Local Similarity 67.2%; Pred. No. 4.3e+02;
 Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 TTCTCGACATCTTTGGTTCCTCTGCGCCGCCCTCTCTCTACCGCATATCC 58
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 169 TGGTTGGCATCTAGCATGCTGTCGCCGCCCTCTCTCTCTACCGCATATCC 112
 RESULT 5
 BE978092/c
 LOCUS BE978092 619 bp mRNA linear EST 04-OCT-2000
 DEFINITION bs73q07.v1 Drosophila melanogaster adult testis library Drosophila melanogaster cDNA clone bs73q07 5', mRNA sequence.
 ACCESSION BE978092
 VERSION BE978092.1 GI:10609221
 KEYWORDS EST.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 619)
 AUTHORS Andrews, J., Bouffard, G. and Oliver, B.
 TITLE Drosophila melanogaster testis expressed sequence tags
 JOURNAL Unpublished (1999)
 COMMENT Contact: Brian Oliver
 Laboratory of Cellular and Developmental Biology
 NIDDK, National Institutes of Health
 6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
 Fax: (301) 496 5239

Email: oliver@helix.nih.gov
 http://www.niddk.nih.gov/intram/people/boliver.htm
 Tissue isolation and library construction performed at the National Institute of Diabetes and Digestive and Kidney Diseases, NIH (see http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov).
 Plate: 73 row: g column: 07
 Seq primer: M13RPI reverse primer (ABI).
 Location/Qualifiers
 1..619
 /organism="Drosophila melanogaster"
 /strain="y[*] w[67cl]/Y"
 /db_xref="taxon:7227"
 /clone="bs73q07"
 /sex="male"
 /dev_stage="1-5 day adult"
 /lab_host="SOLR (Stratagene)"
 /note="Organ: testis; Vector: pBlueScript SK (Stratagene); Site.1: EcoR I; Site.2: Xho I; Testes dissected from 1-5 day adult y[*] w[67cl]/Y males raised at 25°C. RNA isolated using Trizol (Life Technologies) and a single round of Poly(A)+ selection using Oligotex (Qiagen). cDNA library constructed using Stratagene ZAP-cDNA synthesis kit. Oligo dt-primed, size fractionated ~1-6 kb, and directionally cloned at EcoRI and XhoI in Uni-ZAP XR. Following a single round of amplification pBlueScript SK phagemids were mass excised. A distribution channel for clones is being sought, but not currently available. Requests for clones cannot be honored."
 BASE COUNT 171 a 144 c 162 g 142 t
 ORIGIN
 Query Match 44.9%; Score 27.4; DB 12; Length 619;
 Best Local Similarity 59.8%; Pred. No. 4.9e+02;
 Matches 37; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 QY 6 GCACATCTTGGTTCCTCTGCGCCGCCCTCTCTCTACCGCATATCC 58
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 176 GCTCATCAAGGAGCTACCTGCTCTCTCTCTCTCTCTCTCTCTATATCC 124
 RESULT 6
 BE408262/c
 LOCUS BE408262 701 bp mRNA linear EST 21-JUL-2000
 DEFINITION 601302612F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637274 5', mRNA sequence.
 ACCESSION BE408262
 VERSION BE408262.1 GI:9344712
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 701)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: L10M336 row: g column: 03
 High quality sequence start: 7
 High quality sequence stop: 645.
 Location/Qualifiers
 1..701
 /organism="Homo sapiens"


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/db_xref="taxon:9606"
/clone="IMAGE:3637271"
/tissue_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/site="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT 170 a 185 c 215 g 131 t

Query Match 44.9%; Score 27.4; DB 10; Length 701;
Best Local Similarity 75.6%; Pred. No. 5e+02;
Matches 34; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TTCTCGACATCTTTGGTTCCTGCTGCCCGCCCTCTTCCTC 45
||||||| || ||| ||||||| ||||| ||| |||
Db 627 TTCTCGACCTCCATGGCTGCTGCTGCCAGAGCCCTGCTTGC 583

RESULT 7

LOCUS BG744371/c 706 bp mRNA linear EST 15-MAY-2001
DEFINITION 602723105F1 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:4849609 5', mRNA sequence.

ACCESSION BG744371

VERSION BG744371.1 GI:14055024

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 706)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLQM1689 row: i column: 02
High quality sequence stop: 704.
Location/Qualifiers
1. .706
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4849609"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 169 a 183 c 224 g 130 t

Query Match 44.9%; Score 27.4; DB 12; Length 706;
Best Local Similarity 75.6%; Pred. No. 5e+02;

Matches 34; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TTCTCGACATCTTTGGTTCCTGCTGCCCGCCCTCTTCCTC 45
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Db 612 TTCTCGACCTCCATGGCTGCTGCTGCCAGAGCCCTGCTTGC 568

RESULT 8

LOCUS BF488250/c 715 bp mRNA linear EST 23-APR-2001
DEFINITION AF23475.5prime AT Drosophila melanogaster adult testes pOTB7
Drosophila melanogaster cDNA clone AF23475 5 similar to CG4714;
Fnan004714 located on: 2R 49P15-50A1;; 04/09/2001, mRNA sequence.

ACCESSION BF488250

VERSION BF488250.2 GI:13753942

KEYWORDS EST.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 715)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, P., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celisner, S. and Rubin, G.M.
BDGP/HMM AT Drosophila EST Project
Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11571551.
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST_estefruitfly.berkeley.edu
hit genomic AS003819: arm:2R [8082036,8314191]
estimated-cyto:49F2-50A3; 04/09/2001
Plate: AT.234 row: G column: 3
High quality sequence stop: 674.
Location/Qualifiers
1. .715
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="AT23475"
/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
/sex="male"
/dev_stage="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DHS-alpha. Plates AT.121-AT.319: DHS-alpha tonA"
/note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; The mRNA for the testis library was made from testes and seminal vesicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into pOTB7. Plasmid cDNA library."

BASE COUNT 262 a 170 c 172 g 111 t

Query Match 44.9%; Score 27.4; DB 12; Length 715;
Best Local Similarity 69.8%; Pred. No. 5e+02;
Matches 37; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 6 GCACATCTTTGGTTCCTGCTGCCCGCCCTCTTCCTACCGCAATCC 58
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 623 GTCATCAAGGTGACTACCTGTTCTGCTCTTCTTCCTCATTCATTC 571

RESULT 9

LOCUS AI063338/c 754 bp mRNA linear EST 23-APR-2001
DEFINITION GH03085.5prime GH Drosophila melanogaster head pOT2 Drosophila

CDNA Library Prepared by: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Plate: DLM10409 ROW: 1 Column: 13
High quality sequence stop: 701.
Location/Qualifiers
1 913

Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.

RESULT 13	BC291149/c	BC291149	926 bp	mRNA	linear	EST 21-FEB-2001
LOCUS		602387180F1				
DEFINITION		Homo sapiens CDNA clone IMAGE:4516098 5', mRNA sequence.				

Stanford University
855 California Ave., Palo Alto, CA 94304, USA
Tel.: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952021 row: G column: 01

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 13, 2003, 02:39:09 ; Search time 4.64516 Seconds
(without alignments)
4027.262 Million cell updates/sec

Title: US-09-826-581-5_COPY_1007_1067

Perfect score: 61

Sequence: 1 ttctgcacatctttgttc.....cctctaccgcactccaag 61

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	42.6	387	4	US-08-148-708-7
2	26	42.6	909	4	US-08-148-708-9
3	26	42.6	1179	4	US-08-148-708-3
4	26	42.6	1378	1	US-08-759-848-2
5	26	42.6	1378	4	US-08-148-708-6
6	26	42.6	1378	5	PCT-US95-09383-2
7	24.8	40.7	1260	1	US-07-866-979-3
8	24.8	40.7	1260	3	US-08-466-906B-3
9	24.8	40.7	1260	3	US-08-706-281A-3
10	24.8	40.7	1260	4	US-09-201-746-3
11	24.8	40.7	1260	4	US-09-097-231-3
12	24.2	39.7	261	2	US-08-592-383-7
13	24.2	39.7	2561	4	US-09-347-878-25
14	24.2	39.7	2658	4	US-08-592-383-3
15	24.2	39.7	2928	2	US-08-095-728B-3
16	24.2	39.7	2928	5	PCT-US92-02320A-3
17	24.2	39.7	2940	2	US-08-592-383-1
18	24.2	39.7	2940	6	5171671-1
19	23.8	39.0	1929	4	US-09-040-229B-7
20	23.4	38.4	1101	1	US-08-759-848-7
21	23.4	38.4	1101	5	PCT-US95-09383-7
22	23.4	38.4	2051	4	US-09-399-913-52
23	23.4	38.4	3680	1	US-08-759-848-1
24	23.4	38.4	3680	5	PCT-US95-09383-1
25	23.4	38.4	4406	1	US-08-369-043-1
26	23	37.7	3258	2	US-08-729-955A-2
c 27	23	37.7	4403765	4	US-09-103-840A-2

c	28	23	37.7	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	29	22.8	37.4	3943	1	US-08-369-796-3	Sequence 3, Appli
	30	22.8	37.4	3943	2	US-08-852-091-3	Sequence 3, Appli
	31	22.8	37.4	3943	2	US-08-820-754-3	Sequence 3, Appli
	32	22.8	37.4	3943	3	US-08-956-652-3	Sequence 3, Appli
	33	22.8	37.4	3943	3	US-08-956-869-3	Sequence 3, Appli
	34	22.8	37.4	3943	3	US-08-948-547-3	Sequence 3, Appli
	35	22.8	37.4	3943	4	US-09-364-970-10	Sequence 10, Appli
	36	22.8	37.4	3943	4	US-08-956-653A-3	Sequence 3, Appli
	37	22.8	37.4	3943	5	PCT-US95-17025-3	Sequence 3, Appli
	38	22.8	37.4	4003	4	US-09-087-465-1	Sequence 1, Appli
c	39	22.8	37.4	35060	3	US-08-814-095-7	Sequence 7, Appli
	40	22.8	37.4	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	41	22.8	37.4	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	42	22.4	36.7	960	4	US-09-576-160B-10	Sequence 10, Appli
	43	22.4	36.7	1053	4	US-09-576-160B-11	Sequence 11, Appli
c	44	22.4	36.7	1161	4	US-09-199-637A-164	Sequence 164, App
c	45	22.4	36.7	4440	1	US-08-200-016-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-148-708-7
; Sequence 7, Application US/08148708
; Patent No. 6407207
; GENERAL INFORMATION:
; APPLICANT: Hess, John W
; Strader, Catherine D
; Borkowski, Joseph B
; Ransom, Richard W
; TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
; BK-2 Receptor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,708
; FILING DATE: 08-No. 6407207-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,709
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruso, Charles M
; REGISTRATION NUMBER: 30161
; REFERENCE/DOCKET NUMBER: 18713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4830
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-148-708-7

Query Match 42.6%; Score 26; DB 4; Length 387;
Best Local Similarity 65.5%; Pred. No. 3.7;

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Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 2 TCTGCACATCTTTGGTTCCTGCTGCGCGGCGCTCTCTCTACCGCACTATCCA 59
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Db 281 TCTGATGCTGCTGGCTTCTGCTGCCCTGAGTGTCAACCTTCTGCACGATGCA 338

RESULT 2
US-08-148-708-9
; Sequence 9, Application US/08148708
; Patent No. 6407207
; GENERAL INFORMATION:
; APPLICANT: Hess, John W
; Strader, Catherine D
; Borkowski, Joseph B
; Ransom, Richard W
; TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
; BK-2 Receptor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,708
; FILING DATE: 08-No. 6407207-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,709
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruso, Charles M
; REGISTRATION NUMBER: 30161
; REFERENCE/DOCKET NUMBER: 18713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4830
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 909 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-148-708-9

Query Match 42.6%; Score 26; DB 4; Length 909;
Best Local Similarity 65.5%; Pred. No. 4.2;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 2 TCTGCACATCTTTGGTTCCTGCTGCGCGGCGCTCTCTCTACCGCACTATCCA 59
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 352 TCTGATGCTGCTGGGCTTCTGCTGCCCTGAGTGTCAACCTTCTGCACGATGCA 409

RESULT 3
US-08-148-708-3
; Sequence 3, Application US/08148708
; Patent No. 6407207
; GENERAL INFORMATION:
; APPLICANT: Hess, John W
; Strader, Catherine D
; Borkowski, Joseph B
; Ransom, Richard W
```

```
; TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
; BK-2 Receptor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,708
; FILING DATE: 08-No. 6407207-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,709
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruso, Charles M
; REGISTRATION NUMBER: 30161
; REFERENCE/DOCKET NUMBER: 18713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4830
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1179 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-148-708-3

Query Match 42.6%; Score 26; DB 4; Length 1179;
Best Local Similarity 65.5%; Pred. No. 4.4;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 2 TCTGCACATCTTTGGTTCCTGCTGCGCGGCGCTCTCTCTACCGCACTATCCA 59
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Db 686 TCTGATGCTGCTGGGCTTCTGCTGCCCTGAGTGTCAACCTTCTGCACGATGCA 743

RESULT 4
US-08-759-848-2
; Sequence 2, Application US/08759848
; Patent No. 5750826
; GENERAL INFORMATION:
; APPLICANT: Borkowski, Joseph A.
; Strader, Catherine D.
; APPLICANT: Hess, John W.
; APPLICANT: Chen, Howard Y.
; APPLICANT: Trumbauer, Myrna E.
; TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
; NON-HUMAN ANIMALS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Wallen III
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,848
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/281,393
; FILING DATE: 27-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen III, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 19234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-759-848-2

Query Match          42.6%; Score 26; DB 1; Length 1378;
Best Local Similarity 65.5%; Pred. No. 4.5;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TCCTGCACATCTTTGCTCCCTGCTGCCGCGCCCTCTCTCTACCGCACTATCCA 59
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 821 TCCTGAATGCTGGGCTCTCTGCTGCCCTGAGTGATCATCATCCTTCTGCACGATGCA 878

RESULT 5
US-08-148-708-6
; Sequence 6, Application US/08148708
; Patent No. 6407207
; GENERAL INFORMATION:
; APPLICANT: Hess, John W
; Strader, Catherine D
; Borkowski, Joseph B
; Ransom, Richard W
; TITLE OF INVENTION: Cloned and Expressed Human Bradykinin
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P. O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,708
; FILING DATE: 08-NO. 6407207-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,709
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruso, Charles M
; REGISTRATION NUMBER: 30161
; REFERENCE/DOCKET NUMBER: 18713
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4830
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1378 base pairs
```

```
;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-148-708-6

Query Match          42.6%; Score 26; DB 4; Length 1378;
Best Local Similarity 65.5%; Pred. No. 4.5;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TCCTGCACATCTTTGCTCCCTGCTGCCGCGCCCTCTCTCTACCGCACTATCCA 59
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 821 TCCTGAATGCTGGGCTCTCTGCTGCCCTGAGTGATCATCATCCTTCTGCACGATGCA 878

RESULT 6
PCT-US95-09383-2
; Sequence 2, Application PC/YUS9509383
; GENERAL INFORMATION:
; APPLICANT: Borkowski, Joseph A.
; APPLICANT: Strader, Catherine D.
; APPLICANT: Hess, John W.
; APPLICANT: Chen, Howard Y.
; APPLICANT: Trumbauer, Myrna E.
; TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
; TITLE OF INVENTION: NON-HUMAN ANIMALS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Wallen III
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09383
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/281,393
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen III, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 19234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-09383-2

Query Match          42.6%; Score 26; DB 5; Length 1378;
Best Local Similarity 65.5%; Pred. No. 4.5;
Matches 38; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TCCTGCACATCTTTGCTCCCTGCTGCCGCGCCCTCTCTCTACCGCACTATCCA 59
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 821 TCCTGAATGCTGGGCTCTCTGCTGCCCTGAGTGATCATCATCCTTCTGCACGATGCA 878

RESULT 7
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```
US-07-866-979-3
; Sequence 3, Application US/07866979
; Patent No. 5532347
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Wilcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/866,979
; FILING DATE: 19920410
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532347nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..959
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 960..1260
; US-07-866-979-3

Query Match 40.7%; Score 24.8; DB 1; Length 1260;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CCTGCACATCTTGGTTCCTGCTGCCCGCCCTCTCTCTCTACCGCACT 54
Db 371 CGTGCATCTGTGGCTCCATGGTGCAGTCTCTCTCTGGGCATCAT 422

RESULT 8
US-08-466-906B-3
; Sequence 3, Application US/08466906B
; Patent No. 5849871
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,906B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5849871nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,154-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..959
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 960..1260
; US-08-466-906B-3

Query Match 40.7%; Score 24.8; DB 2; Length 1260;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CCTGCACATCTTGGTTCCTGCTGCCCGCCCTCTCTCTCTACCGCACT 54
Db 371 CGTGCATCTGTGGCTCCATGGTGCAGTCTCTCTCTGGGCATCAT 422

RESULT 9
US-08-706-281A-3
; Sequence 3, Application US/08706281A
; Patent No. 6100048
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Fan, Wei
; APPLICANT: Boston, Bruce A
; APPLICANT: Kesterton, Robert A
; APPLICANT: Lu, Dongsi
; APPLICANT: Chen, Wendiao
; TITLE OF INVENTION: Methods and Reagents for Discovering and
; TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagon:
; TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,906B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5849871nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,154-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..959
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 960..1260
; US-08-466-906B-3

Query Match 40.7%; Score 24.8; DB 2; Length 1260;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CCTGCACATCTTGGTTCCTGCTGCCCGCCCTCTCTCTCTACCGCACT 54
Db 371 CGTGCATCTGTGGCTCCATGGTGCAGTCTCTCTCTGGGCATCAT 422

RESULT 9
US-08-706-281A-3
; Sequence 3, Application US/08706281A
; Patent No. 6100048
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Fan, Wei
; APPLICANT: Boston, Bruce A
; APPLICANT: Kesterton, Robert A
; APPLICANT: Lu, Dongsi
; APPLICANT: Chen, Wendiao
; TITLE OF INVENTION: Methods and Reagents for Discovering and
; TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagon:
; TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,906B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5849871nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,154-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..959
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 960..1260
; US-08-466-906B-3

Query Match 40.7%; Score 24.8; DB 1; Length 1260;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CCTGCACATCTTGGTTCCTGCTGCCCGCCCTCTCTCTCTACCGCACT 54
Db 371 CGTGCATCTGTGGCTCCATGGTGCAGTCTCTCTCTGGGCATCAT 422

RESULT 8
US-08-466-906B-3
; Sequence 3, Application US/08466906B
; Patent No. 5849871
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
```


OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/706,281A
APPLICATION NUMBER: 04-SEP-1996
FILING DATE: 04-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100048nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..14
FEATURE:
NAME/KEY: CDS
LOCATION: 15..959
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 960..1260
US-08-706-281A-3
Query Match 40.7%; Score 24.8; DB 3; Length 1260;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 3 CTTGCACATCTTTGGTTCCTGCGCCGCGCCCTCTCTCTACCGCACT 54
DB 371 CGTGTCTATCTGTGGTCCATGTCAGTCTCTGCTTCTCTGGGCATCAT 422
RESULT 10
US-09-201-746-3
Sequence 3, Application US/09201746
Patent No. 6268221
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,746
FILING DATE: 01-DEC-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6268221nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154-J
TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..14
FEATURE:
NAME/KEY: CDS
LOCATION: 15..959
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 960..1260
US-09-201-746-3
Query Match 40.7%; Score 24.8; DB 4; Length 1260;
Best Local Similarity 67.3%; Pred. No. 11;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 3 CTTGCACATCTTTGGTTCCTGCGCCGCGCCCTCTCTCTACCGCACT 54
DB 371 CGTGTCTATCTGTGGTCCATGTCAGTCTCTGCTTCTCTGGGCATCAT 422
RESULT 11
US-09-097-231-3
Sequence 3, Application US/09097231
Patent No. 6278038
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
Chen, Wenbiao
Low, Malcolm J
TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,231
FILING DATE: 12-Jun-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6278038nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..14

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US-09-347-878-25/C
; Sequence 25, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25895-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 2561
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1131)..(2399)
; OTHER INFORMATION: Escherichia coli nucleic acid encoding
; OTHER INFORMATION: folsypolyglutamate synthetase-dihydrofolate
; OTHER INFORMATION: synthetase
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M32445/GenBank
; US-09-347-878-25

Query Match          39.7%; Score 24.2; DB 4; Length 2561;
Best Local Similarity 62.3%; Pred. No.19;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      1 TTCTGCACATCTTTGGTTTCCTGCTGCCCGCGCCCTCTTCTCTACCGCACTATCCAA 60
      || || || || || || || || || || || || || || || || || || || || || ||
Db      386 TTTCGGCTCAAGCTCGCTACCCAGCTCCACAAAGGCTTCTCTTCTTACACGGCTATGCAG 327
      || || || || || || || || || || || || || || || || || || || || || ||

QY      61 G 61
      |
Db      326 G 326

RESULT 14
US-08-592-383-3
; Sequence 3, Application US/08592383
; Patent No. 5830760
; GENERAL INFORMATION:
; APPLICANT: Tsai, S. and S.J. Collins
; TITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Rec
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows 5.01-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,383
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/099,242
; FILING DATE: July 28, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: EHC1-1-7190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-662-8100; 1-206-224-0709(direct)
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

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Result No.	Score	Query		Length	DB	ID	Description
		Match	8				
1	61	100.0	1647	10	US-09-826-581-5		Sequence 5, Appli
2	46.2	75.7	1722	10	US-09-826-581-3		Sequence 3, Appli
C 3	27.4	44.9	566	9	US-10-255-336-159		Sequence 159, App
4	26.6	43.6	2322	9	US-10-045-815-7		Sequence 7, Appli
5	26.6	43.6	2416	9	US-10-045-815-5		Sequence 5, Appli
6	26	42.6	1682	10	US-09-925-297-129		Sequence 129, App
C 7	25.8	42.3	12043	9	US-09-979-593-1		Sequence 1, Appli
8	25.8	42.3	12043	9	US-09-979-593-59		Sequence 59, Appli
C 9	25	41.0	635	9	US-09-764-891-2280		Sequence 2280, Ap
10	25	41.0	2285	9	US-09-764-891-6987		Sequence 6987, Ap
11	24.8	40.7	200	10	US-09-815-944-21		Sequence 21, Appli
12	24.8	40.7	1260	9	US-10-288-160-3		Sequence 3, Appli
13	24.8	40.7	1260	10	US-09-815-944-19		Sequence 19, Appli
C 14	24.8	40.7	99014	10	US-09-880-107-3428		Sequence 3428, App
C 15	24.4	40.0	733	12	US-10-044-090-92		Sequence 92, Appli
C 16	24.4	40.0	741	9	US-10-290-353-21		Sequence 21, Appli
C 17	24.4	40.0	741	10	US-09-790-264-21		Sequence 21, Appli
C 18	24.4	40.0	819	9	US-10-269-353-11		Sequence 11, Appli
C 19	24.4	40.0	819	10	US-09-790-264-11		Sequence 11, Appli

RESULT 2
US-09-826-581-3
; Sequence 3, Application US/09826581
; Patent No. US20020142310A1

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; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: JP 11/118806
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2322
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)...(1637)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2282
; OTHER INFORMATION: n = A,T,C or G
US-10-045-815-7

Query Match      43.6%; Score 26.6; DB 9; Length 2322;
Best Local Similarity 71.4%; Pred.No.2.3;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      3  CCTGCACATCTTGGTTCCTCTGCGCCGCCGCCCTCTCTCTCTACCGC 51
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Db      335  CCTGCGCTTCTCGGAGCGCTGCTGCGCGCTGCGCGCTACGCGC 383

RESULT 5
US-10-045-815-5
; Sequence 5, Application US/10045815
; Patent No. US20020160498A1
; GENERAL INFORMATION:
; APPLICANT: Wadhwa, Renu
; APPLICANT: Sugihara, Takashi
; APPLICANT: Ohide, Akiko
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: 06501-091001
; CURRENT APPLICATION NUMBER: US/10/045,815
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/JP00/02731
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: JP 11/118806
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)...(2252)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2376
; OTHER INFORMATION: n = A,T,C or G
US-10-045-815-5

Query Match      43.6%; Score 26.6; DB 9; Length 2416;
Best Local Similarity 71.4%; Pred.No.2.3;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      3  CCTGCACATCTTGGTTCCTCTGCGCCGCCGCCCTCTCTCTACCGC 51
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Db      335  CCTGCGCTTCTCGGAGCGCTGCTGCGCGCTGCGCGCTACGCGC 383

RESULT 6
US-09-925-297-129
; Sequence 129, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

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; APPLICANT: Phillips, Russell
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING MELANOCYTE
; TITLE OF INVENTION: STIMULATING HORMONE RECEPTOR GENE DISRUPTIONS
; FILE REFERENCE: R-654
; CURRENT APPLICATION NUMBER: US/09/815,944
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,236
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/215,214
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/218,075
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/219,167
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 200
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting vector
; US-09-815-944-21

Query Match 40.7%; Score 24.8; DB 10; Length 200;
Best Local Similarity 67.3%; Pred. No. 9.5;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0

QY 3 CCTGCGACATCTTGGTTCCTCGCTGCGCGCGCCCTCTCTCTACCGCACT 54
Db 82 CGTGCGCATCTGTGCTCCATGGTGTCCAGTCTGCTCTCTGCGGCATCAAT 133

RESULT 12
US-10-288-160-3
; Sequence 3, Application US/10288160
; Publication No. US20030105024A1
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; Fan, Wei
; Boston, Bruce A
; Kesterton, Robert A
; Lu, Dongsi
; Chen, Wenbiao
; TITLE OF INVENTION: Methods and Reagents for Discovering and
; Using Mammalian Melanocortin Receptor Agonists
; To Modulate Feeding Behavior in Animals
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/288,160
; FILING DATE: 05-NO. US20030105024A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,281
; FILING DATE: 04-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030105024A1nhan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001

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; TELEFAX: 312-913-0002
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1260 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA to mRNA
;   FEATURE:
;     NAME/KEY: 5'UTR
;     LOCATION: 1..14
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 15..959
;   FEATURE:
;     NAME/KEY: 3'UTR
;     LOCATION: 960..1260
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-288-160-3

Query Match      40.7%; Score 24.8; DB 9; Length 1260;
Best Local Similarity 67.3%; Pred. No. 9.7;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy      3 CCTGCACATCTTTGGTTCCCTGCTGCGCCGCCCTCTCTCTCTACCGCACT 54
Db      371 CGTGTCTATCTGTGGTCCATGGTGTCCAGTCTGTGTTCTCTGGGCATCAT 422

RESULT 13
US-09-815-944-19
; Sequence 19, Application US/09815944
; Patent No. US2002038467A1
; GENERAL INFORMATION:
;   APPLICANT: Allen, Keith D.
;   APPLICANT: Matthews, William
;   APPLICANT: Moore, Mark
;   APPLICANT: Phillips, Russell
;   TITLE OF INVENTION: TRANSGENIC MICE CONTAINING MELANOCYTE
;   FILE REFERENCE: R-654
;   CURRENT APPLICATION NUMBER: US/09/815,944
;   PRIOR FILING DATE: 2001-03-22
;   PRIOR APPLICATION NUMBER: US 60/191,236
;   PRIOR FILING DATE: 2000-03-22
;   PRIOR APPLICATION NUMBER: US 60/215,214
;   PRIOR FILING DATE: 2000-06-29
;   PRIOR APPLICATION NUMBER: US 60/218,075
;   PRIOR FILING DATE: 2000-07-12
;   PRIOR APPLICATION NUMBER: US 60/219,167
;   PRIOR FILING DATE: 2000-07-19
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 19
;   LENGTH: 1260
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   US-09-815-944-19

Query Match      40.7%; Score 24.8; DB 10; Length 1260;
Best Local Similarity 67.3%; Pred. No. 9.7;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy      3 CCTGCACATCTTTGGTTCCCTGCTGCGCCGCCCTCTCTCTACCGCACT 54
Db      371 CGTGTCTATCTGTGGTCCATGGTGTCCAGTCTGTGTTCTCTGGGCATCAT 422

RESULT 14
US-09-880-107-3428/c
; Sequence 3428, Application US/09880107
; Patent No. US20020142981A1
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; GENERAL INFORMATION:
;   APPLICANT: Horne, Darci T.
;   APPLICANT: Vockley, Joseph G.
;   APPLICANT: Scherf, Uwe
;   APPLICANT: Gene Logic, Inc.
;   TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;   FILE REFERENCE: 44921-5028-WO
;   CURRENT APPLICATION NUMBER: US/09/880,107
;   CURRENT FILING DATE: 2001-06-14
;   PRIOR APPLICATION NUMBER: US 60/211,379
;   PRIOR FILING DATE: 2000-06-14
;   PRIOR APPLICATION NUMBER: US 60/237,054
;   PRIOR FILING DATE: 2000-10-02
;   NUMBER OF SEQ ID NOS: 3950
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 3428
;   LENGTH: 99014
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 U78027
US-09-880-107-3428

Query Match      40.7%; Score 24.8; DB 10; Length 99014;
Best Local Similarity 67.3%; Pred. No. 10;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy      3 CCTGCACATCTTTGGTTCCCTGCTGCGCCGCCCTCTCTCTACCGCACT 54
Db      15006 CCTCGGCTCTTTGGTTCTCTGCTTCCCTTCCCTCCCTCGCGCTCTCTCCCT 14955

RESULT 15
US-10-044-090-92/c
; Sequence 92, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
;   APPLICANT: Olga Bandman
;   TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
;   FILE REFERENCE: PA-0028 US
;   CURRENT APPLICATION NUMBER: US/10/044,090
;   CURRENT FILING DATE: 2002-01-09
;   NUMBER OF SEQ ID NOS: 850
;   SOFTWARE: PERL Program
;   SEQ ID NO 92
;   LENGTH: 733
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020137081A1 416842.32
;   NAME/KEY: unsure
;   LOCATION: 665, 690, 698
;   OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-92

Query Match      40.0%; Score 24.4; DB 12; Length 733;
Best Local Similarity 63.8%; Pred. No. 13;
Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy      2 TCCTGCACATCTTTGGTTCCCTGCTGCGCCGCCCTCTCTCTACCGCACTCCA 59
Db      192 TCCAGCAGGTCCACCCCTGGAGCTGCAGCCTCTGCACTTCTTCCCTTCATTGCATGTGCA 135

Search completed: June 13, 2003, 09:00:42
Job time : 20.2903 secs
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